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(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

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This application claims priority to USSN 60/323,469, filed Setember 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the charactaristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis and treatment of cancer patients.

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Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

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Compostions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. 20 (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 25 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, 30 ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

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al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library 5 Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and 10 Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznek (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) 15 Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et 20 al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell 25 Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) <u>Textbook of Medical Oncology</u> Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenisis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

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The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

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A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

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The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negativescoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) <u>Proc. Natl. Acad. Sci. USA</u> 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

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The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain somebasic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules

Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

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"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) <u>Tetrahedron</u> 49:1925-1963 and references therein; Letsinger (1970) <u>J. Org. Chem.</u> 35:3800-3803; Sprinzl, et al. (1977) <u>Eur. J. Biochem.</u> 81:579-589; Letsinger, et al. (1986) <u>Nucl. Acids Res.</u> 14:3487-499; Sawai, et al. (1984) <u>Chem. Lett.</u> 805, Letsinger, et al. (1988) <u>J. Am. Chem. Soc.</u> 110:4470-4471; and Pauwels, et al. (1986) <u>Chemica Scripta</u> 26:141-149), phosphorothioate (Mag, et al. (1991) <u>Nucleic Acids Res.</u> 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) <u>J. Am.</u>

Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; 5 Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) 10 Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in 15 Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp. 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I, electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

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As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

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Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

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The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

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Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Maliganant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

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In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

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The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multidimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guuide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the

Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

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The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning:

Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

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Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

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An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

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As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and 15 the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

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Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) <u>PCR Protocols</u>, A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

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In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

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In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

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In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of nonbacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (grampositive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

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In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anticancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

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Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

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In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Substantial changes in function or immunological identity are sometimes made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threone is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include dearnidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

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Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) <u>CRC Crit. Rev. Biochem.</u>

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57 and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u> 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

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Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxylterminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

Antibodies to cancer proteins

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In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 15 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) <u>J. Mol. Biol.</u> 227:381-388; Marks, et al. (1991) <u>J. Mol. Biol.</u> 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) <u>Monoclonal Antibodies and Cancer Therapy</u> Liss; and Boerner, et al. (1991) <u>J. Immunol.</u> 147:86-95).

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Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

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In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChipTM expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferred.

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Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology:

Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

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Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

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In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. 10 (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, 15 Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum 20 (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

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The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins. describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

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In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

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Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

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Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

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Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

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In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss; Freshney (2000) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) <u>Nature Genet.</u> 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al.(1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

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Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal. counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; Freshney (1985) <u>Anticancer Res.</u> 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

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A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is reimplanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263-272; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) <u>Adv. in Pharmacology</u> 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990)

Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.
5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993)

Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human

Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386.

Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

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Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacologial Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294,; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in 5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. 15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de 20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, 30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

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biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gum") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

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For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are availablel for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

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Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A-68, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

od vessels/anglogenesis: hemangiomas, lymphangiomas, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atheroscierosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumora, lymphomas, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented vibonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macutar degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (teatold), birth control, uterine throtic 5

bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinom bone marrow. Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the pertoheral nervous system

10 brain: glioblastoma, oligodendroglioma, anablastic astrocytoma, meningioma, medulablastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma

breast ductal carcinoma in situ, lobular carcinoma in situ

cervic cancer of the cervic, vagina, or vulva color/rectum: precancerous coloractal disease (e.g., neoptastic polyps (adenomas), familial adenomatous polyposis, utcerative colitis), colon cencer, e.g., epithelial tumor (e.g., adenocarcinoma, auctinous adenocarcinoma, signel-ring cell adenocarcinoma, sugamous cell carcinoma, adenocarcinoma, undifferentiated carcinoma, unclassified carcinoma), cartinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leimyo sarcoma, others), inflammatory bowel disease (e.g., utcerative colitis, Crohris disease (granuformatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, nuclnous adenocarcinoma, melanoma) 15

phagus: premailignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, tung, or cervix), gastrodigestive carcinomas (e.g., cancers of the stomach, colon, or rectum) 20

(e.g., cancers of the stomach, coton, or rectum)
fibrosis: timp fibrosis (diopathic potentionary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific Idiopathic pneumonitis), chronic obstructive pulmonary disease
(e.g., emphysema, chronic bronchitis), asthran, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scieroderma, wound heating
head and nack: tumors of the nasad cavity, paranesal sinuses, nasopharyror, oral cavity, oral pharyror, lip, laryror, hypopharyror, salivary glands, paragangtiomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, activomophobe renal carcinoma, hypemenhiroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal
carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma
leukocytes; caute lymphotiastic leukemia/lymphoma, malignant transformation of immature, precursor 8 (pre-B) or precursor 1 (pre-T) lymphocytes, or lymphoblasts, arthritis,
Inflammation, wound heating 25

inflammation, wound healing

liver: hepatilis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the grafibladder or bile duct

granisation of the duct
lung: lung cancer, small cell lung carcinoma (eat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinold,
granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, intersitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary
disease (e.g., emphysema, chronic bronchitis), ashma, bronchiectasis, esophageal cancer
ovary: ovarian carcinoma (e.g., epithelial (serous tumors, muchous tumors, endometricid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryomal
carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosal stromal cell tumors)), falloptan tube carcinoma, peritoneal carcinoma, 30

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pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma pancreatoblastoma, duct-ectatic mucin-hypersecreting turnor, mucinous cyst adenoma, pantillary cystic neoptasm, serous cyst adenoma, diabetes melitis, chronic pancreatitis prostate: epithelial neoptasms (e.g., adenocarcinoma, small cell turnors, transitional cell carcinoma, carcinoma in stu, and basel cell carcinoma), carcinosarcoma, non-epithelial neoptasms (e.g., mesenchymal and lymphoma), germ cell turnors, prostatic intreprihelial neoptasia (PIN), hormone independent prostate cancer, benign prostate hyperplasta, 40

skin/metanoma: metanoma, tentigo (common benign localized hyperplasia of metanocytes), nevocellular nevi (congenital or acquired neoplasm of metanocytes), actinic keratosis (overgrowth of outer layers of skin), based cell carcinoma, Merical cell carcinoma, benign fibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histocytes within the dermis), dermal vascular tumors, seborrheic kerstoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasta and hyperplasta and hyperplasta of skin), and squamous cell carcinomas of the skin, lung, carrix, esophagus, uterus, head, neck, or bladder

stomach: adenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoid, laiomyosarcoma, gastrifis (chronic atrophic, H. pylori associated), hyperplastic polyps, tipoma, leiomyoma, esophageal adenocarcinomas

testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Seriol cell turnors, and Granulosa cell turnors), germ cell and gonada stromal elements (e.g., gonadoblastomas), adnaval and paratesticular turnors (e.g., mesotheliomas, soft tissue sercomas, and adnaval of the rate testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)

uterus: epithelial lumors (e.g., endometriold, papillary endometriold, papillary serous, clear cell, mudinous), mescarchymal tumors (e.g., endometriol stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed mullerian tumors, adenosarcoma)

55 Tables 28-66C list accession numbers for Pkeys lacking UnigenetD's for Tables 2A-66C, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 2C-66C list genomic positioning for Pikeys tacking Unigene ID's and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 60

TABLE 2A: ABOUT 1031 GENES UP-REGULATED IN ACUTE LYMPHOCYTIC LEUKEMIA (ALL)

Table 2A BOUT NOT GENES UF-REGULATED IN ACUTE LYMPHOLYTIC LEUREMA (ALL)

Table 2A lists about 1031 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult tissues. These were selected from 35403 probesets on the

AffymetrixEos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult tissues was greater than or equal to 1.7. The "average" leukemia level was set to the 85° percentile amongst various non-meilignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5° percentile value amongst various non-mailignant tissues was subtracted from both the numerator and the denominators before the office and exhibited. 65 the denominator before the ratio was evaluated.

Unique Eos probeset Identifier number Exemplar Accession number, Genbank accession number Pkev:

Unigene number Unigene gene title UnigeneiD:

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Unigene Title:

Ratio of leukernla to normal body tissue

75	Pkey	ExAcc	UniGeneID	UniGene Tille	Ri
75	100458	874019	Hs.247979	pre-8 lymphocyte gene 1	46.8
	113089	T40707	Hs.270862	ESTs	20.4
	106956	R06428	Hs.226351	ESTs	15.8
	101447	M21305		gb:Human alpha satellite and satellite 3	13.8
00	113009	T23699	Hs.7246	ESTs	12.5
80	126947	Z40778	Hs.191837	ESTs	11.4
	100893	BE245294	Hs.180789	S164 protein	1 1.1
	101050	AU077324	Hs.1832	neuropepilde Y	11.0
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein	10.7

	404004	4 4 504 604	11-0000		
	101304 105667	AA001021 AA767528	Hs.6685 Hs.22030	thyroid hormone receptor interactor 8	10.4
	112727	T91029	Hs.15069	paired box gene 5 (B-cell lineage specif ESTs	9.1 9.0
_	109788	T79971	Hs.12432	Homo sepiens clone 24407 mRNA sequence	8.7
5	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.8
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20553 fis, clone KA	7.7
	109384 112602	AA219172	Hs.86849	ESTS	7.6
	125278	AW004045 Al218439	Hs.203365 Hs.129998	ESTs enhancer of polycomb 1	6.6
10	112167	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	6.5 6.4
	116355	AA789133	Hs.88650	ESTs	5.8
	123440	AJ733692	Hs.112488	ESTs	5.5
	100918	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	5.4
15	101879 109260	AA176374 AW978515	Hs.243886 Hs.131915	nuclear autoantigenic sperm protein (his	5.4
	129213	Al146494	Hs.109525	KIAA0863 protein ESTs, Weakly similar to IRX2_HUMAN IRQQU	5.4
	120809	AA346495	10.100020	gb:E8T52657 Fetal heart II Homo saptens	5.4 5.4
	105498	H68279	Hs.24937	transformer-2 alpha (htra-2 alpha)	5.1
20	114840	AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	5.0
20	103304	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	4.9
	113983 115844	W87415 Al373062	Hs.55298 Hs.332938	HLA-B associated transcript-1	4.8
	120712	AF193339	Hs.102506	hypothetical protein MGC5370 eukaryotic translation initiation factor	4.8 4.8
~ ~	107794	AA019255		gb:ze56e10.s1 Soares retina N2b4HR Homo	4.7
25	135101	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	4.6
	129898	A1672731	Hs.13258	ESTs	4.6
	113494 115004	T91451 AA329340	Hs.86538	ESTs	4.6
	113074	AK001335	Hs.4867 Hs.31137	mannosyl (alpha-1,3-)-glycoprotein beta- protein tyrosine phosphatase, receptor t	4.5
30	112326	R55822	Hs.4268	ESTs	4.5 4.4
	105169	BE245294	Hs.180789	S164 protein	4.4
	117048	H89732	Hs.230113	EST	4.3
	123133	AA487264	Hs.154974	Homo saplens mRNA; cDNA DKFZp667N064 (fr	4.3
35	111394 106112	AA412227 AL117518	Hs.16131 Hs.3686	hypothetical protein FLJ12876 KIAA0978 protein	4.3
	114414	AW152166	Hs.182113	EST8	4.2 4.2
	125219	Al804331	Hs.99423	ATP-dependent RNA helicase	4.2
	114995	AA769266	Hs.193657	ESTs	4.2
40	123338	AA504249	Hs.187585	ESTs	4.1
40	126666 112908	AA648886 BE281000	Hs.151999	ESTS	4.1
	116640	X89984	Hs.3530 Hs.211563	TLS-associated serine-arginine protein 2 B-cell CLL/lymphoma 7A	4.1
	109292	AW975746	Hs.188662	KIAA1702 protein	4.0 4.0
45	131724	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.0
45	119772	AJ250839	Hs.58241	gene for serine/threonine protein kinase	4.0
	134453 123562	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	4.0
	103226	AA177088 X75042	Hs.190065 Hs.44313	ESTs v-rei avian reticuloendotheliosis virsi	4.0
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	3.9 3.9
50	119873	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.9
	115553	AJ275986	Hs.71414	transcription factor (SMIF gene)	3.9
	131844 123360	AJ419294	Hs.324342	ESTs	3.8
	111180	AA532718 AI798851	Hs.178604 Hs.283108	ESTs hemoglobin, gamma G	3.8
55	129426	AF077953	Hs.111323	Protein Inhibitor of activated STAT X	3.8 3.8
	105434	AA252111	Hs.15200	ESTs	3.8
	119073	BE245360	Hs.279477	ESTs	3.8
	127003 118325	AW816515		ATPase, Class V, type 100	3.7
60	115998	T51138 AA448488	Hs.90489 Hs.336829	ESTs ribosomal protein L44	3.7
• •	119830	AW054922		Homo saplens cDNA FLJ12366 fis, clone MA	3.7 3.7
	104584	AA704538	Hs.193777	ESTs	3.6
	105212	AA205334	Hs.324278	Homo sapiens mRNA; cDNA DKFZp566M063 (f	3.6
65	109223 112605	AW000714		ESTs	3.6
05	105733	R79374 AA767669	Hs.29852 Hs.10242	ESTs ESTs	3.5
	120562		Hs.302267	hypothetical protein FLJ10330	3.5 3.5
	112268		Hs.22003	solute carrier family 6 (neurotransmitte	3.5 3.5
70	127834			EST	3.5
70	115147		Hs.38399	hypothetical protein MGC2454	3.5
	115185 113921		Hs.105461	hypothetical protein FLJ20357	3.5
	115835		Hs.28355 Hs.41371	hypothetical protein FLJ22402 ESTs	3.5 3.5
-	123503			ESTs, Wealdy similar to 178885 serine/th	3.5 3.5
75	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.4
	128743		Hs.2730	heterogeneous nuclear ribonucleoprotein	3.4
	117031		No 10core	gb:yw21a02.s1 Morton Fetal Cochlea Homo	3.4
	123149 102581		Hs.105676 Hs.77256	ESTs enhancer of zeste (Drosophila) homolog 2	3.4
80	103158			hematopoietically expressed homeobox	3.4 3.4
	107599	AW664072	Hs.60136	ESTs	3.4 3.4
	125556		Hs.334808	KIAA1238 protein	3.4
	103331	AJ825463	Hs.147996	protein kinase, X-linked	3.4

	114387	AICCC4 44	//		
	119040	AI655141 R02394	Hs.107720 Hs.269436	ESTs, Weakly similar to A\$4295 Interfer ESTs, Moderately similar to PC4259 fem	3.4
	100305		Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.4 3.4
5	129818 133445	771092 AC005262	Hs.172572	nypothetical protein FLJ20093	3.4
-	132111	AW500857	Hs.73797 Hs.40137	guantne nucleotide binding protein (G pr anaphase-promoting complex 1; melotic ch	3.3
	105292	AF128542	Hs.166846	polymerase (DNA directed), epsilon	3.3 3.3
	118397 118922	BE139479 AW206193	Hs.161492 Hs.91065	ESTs	3.3
10	132344	AW977189	Hs.45719	hypothetical protein DKFZp761B2423 KIAA0823 protein	3.2
	129889	AA810932	Hs.131899	ESTs, Wealdy strallar to T00370 hypotheti	3.2 3.2
	123670 116291	Al189844 AW410377	Hs.112708 Hs.41502	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
1.5	105289	AB020638	Hs.103000	hypothetical protein FLJ21276 KIAA0831 protein	3.2
15	105583 104796	AA278907	Hs.3530	TLS-associated serine-arothine protein	3.2 3.2
	111657	BE620712 R07364	Hs.33026 Hs.268667	hypothetical protein PP2447	3.2
	134174	AF283770	Hs.79630	ESTs, Weakly similar to ALU1_HUMAN ALU CD79A antigen (immunoglobulin-associated	3.2 3.2
20	126077 133733	M78772 AK000476	Hs.210836	ES18	3.2 3.1
	124847	W07701	Hs.75798 Hs.304177	hypothetical protein Homo sapiens clone FLB8503 PRO2266 mRNA	3.1
	127879	AA768098	Hs.189079	ESTs	3.1 3.1
	113108 110343	AW516695 AW138703	Hs.8438	ESTs	3.1
25	102935	BE561850	Hs.17268 Hs.80506	ESTs small nuclear ribonucleoprotein polypept	3.1
	111676	AB040882	Hs.109778	KIAA1449 protein	3.1 3.1
	127311 108830	AA492582 AA131743	Hs.322404 Hs.193352	hypothetical protein MGC4175 ESTs	3.1
20	111330	BE247767	Hs.18166	KIAA0870 protein	3.1
30	104246 126668	AF016032	Hs.201377	lysosomal apyrase-like 1	3.1 3.1
	124724	AA011616 H20816	Hs.269877 Hs.112423	ESTS Home serious mental conta over-seguance	3.1
	114794	AI751157	Hs.101395	Homo saplens mRNA; cDNA DKFZp586i1420 (f hypothetical protein MGC11352	3.1 3.1
35	134599 130314	X99226 NM 014674	Hs.284153 Hs.154332	Fanconi anemia, complementation group A	3.0
	100265	D38521	Hs.112396	KIAA0212 gene product KIAA0077 protein	3.0
	115005	A1760825	Hs.111339	ESTs	3.0 3.0
	123433 127798	AW450922 AA737068	Hs.112478 Hs.294078	ESTs EST-	3.0
40	117403	H84455	Hs.40639	ESTs ESTs	3.0
	107111 105698	A1298448	Hs.22670	chromodomain helicase DNA binding protei	3.0 3.0
	108358	AW957300 MB1933	Hs.294142 Hs.1634	ESTs, Weakly similar to C55663 oligodend cell division cycle 25A	3.0
45	132066	A1929392	Hs.181195	OnaJ (Hsp40) homolog, subfamily B, membe	3.0 2.9
43	130303 104596	BE245294 AF067804	Hs.180789	S164 protein	2.9
	112197	NM_003655	Hs.15423 Hs.5637	hypothetical protein HOCMC04P ESTs	2.9
	132809 100877	AF036144	Hs.5734	meningioma expressed antigen 5 (hyaluron	2.9 2.9
50	108147	X80821 Al972094	Hs.27973 Hs.286221	KIAAU8/4 protein	2.9
	133674	AW851121	Hs.75497	Homo sepiens cDNA FLJ13741 fis, clone PL Homo sepiens cDNA: FLJ22139 fis, clone H	29 29
	129001 131920	AA443323 BE002320	Hs.107812	BPOZ protein	2.9
	134709	NM_006290	Hs.287864 Hs.211600	Homo sapiens cDNA FLJ14030 fis, clone HE tumor necrosis factor, alpha-induced pro	2.9
55	113577	Al300699	Hs.278937	PRO0470 protein	2.8 2.8
	115839 129969	BE300266 N57818	Hs.28935	transducin-like enhancer of split 1, hom	2.8
	128659	AW630087	Hs.103315	gb:yv59d07.s1 Soares fetal liver spleen trinucleotide repeat containing 1	2.8
60	105011 129294	BE091926 AF172940	Hs.15244	mitotic spindle colled-coil related prot	2.8 2.8
	104518	H20816	Hs.184542 Hs.112423	CGI-127 protein	2.8
	107796	AA058848	Hs.60797	Homo sapiens mRNA; cDNA DKFZp5861420 (f ESTs	2.7 2.7
	106331 127692	AB037742 Al021912	Hs.24336 Hs.187983	KIAA1321 protein	2.7
65	131916	AA02597B	Hs.34569	ESTS ESTS .	27
	124971 129428	T23800	Hs.151001	hypothetical protein FLJ14728	2.7 2.7
	118348	AA256906 AW408588	Hs.111364 Hs.91052	ESTs, Wealdy similar to ubiquitous TPR m	27
70	113219	T59257	Hs.269528	ESTs, Moderately similar to ALU5_HUMAN A ESTs, Moderately similar to ALU8_HUMAN A	27
70	131720 109593	Z68128 AW196801	Hs.3109	Rho GTPase activating protein 4	2.7 2.7
	135359	AF043722	Hs.6685 Hs.99491	thyroid hormone receptor interactor 8 RAS guanyt releasing protein 2 (calcium	2.7
	131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.7 2.7
75	117457 121073	N29682 H48199	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALLI	2.7
	125069	H81306	Hs.112184 Hs.194485	DKFZP586J0619 protein ESTs	2.7
	116456	Al381911	Hs.334859	KIAA1814 protein	27 27
00	124271 112369	AW293223 AW966243	Hs.8928 Hs.4243	hypothetical protein FLJ20291	27
80	115866	AW082829	Hs.52081	hypothetical protein FLJ12650 KIAA0867 protein	27
	132543 124494	BE568452 N54831	Hs.5101	protein regulator of cytokinesis 1	2.7 2.7
	104799	AA029703	Hs.271381	ESTs, Weakly similar to 138022 hypothet gb:ze95h08.s1 Soares_fetal_heart_NbHH1gW	2.7
				9	27

	120510	AI796395	Un 111377	ESTs	•
	129781		Hs.111377 Hs.124707	ESTs	2.6 2.6
	122698	AA456112	Hs.99410	ESTs	2.6 2.6
_	106995	AB023139	Hs.37892	KIAA0922 protein	26
5	105502	BE464016	Hs.238958	ESTs	2.6
	128671 107059	A1885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	26
	126502	BE614410 T10077	Hs.23044 Hs.13453	RAD51 (S. cerevisiae) homolog (E coli Re hypothetical protein FLJ14753	2.6 2.6
	129703	BE388665	Hs.179999	Homo saplans, clone IMAGE:3457003, mRNA	26
10	111219	N68836	Hs.19247	ESTs, Moderately similar to ALUC_HUMAN	26
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	26
	125626 111189	A1038854	Hs.180789	S164 protein	2.6
	113146	N67603 BE151985	Hs.272130 Hs.5722	ESTs, Weatdy similar to S65824 reverse hypothetical protein FLJ23316	26
15	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	2.6 2.6
	102263	U29171	Hs.75852	casein kinase 1, della	26
	118835	AA535246	Hs.50852	ESTs	2.6
	103141	X66113	Hs.75584	polymyositis/scleroderma autoantigen 2 (2.6
20	109598 127262	R40515 AA828125	Hs.21248	ESTs	26
20	129620	D79338	Hs.239720	gb:od71a09.s1 NCL_CGAP_Ov2 Homo saptens CCR4-NOT transcription complex, subunit	26 26
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	26
	123255	AA830335	Hs.105273	ESTs	2.6
25	133160	N54968	Hs.66309	hypothetical protein MGC11061	26
25	109638 119896	AW977747 AA731836	Hs.119120 Hs.137319	E3 ubiquitin ligase SMURF1	2.6
	134770	M89957	Hs.89575	ESTs CD798 antigen (immunoglobulin-essociated	26 26
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	2.6
20	129563	AF119664	Hs.27299	transcriptional regulator protein	2.6
30	111719	AI655806	Hs.179262	ESTs .	2.6
	103982 125032	AA218558	Hs.7905	sorting nextn 9	2.6
	131428	T74884 AL122045	Hs.26703	gb:yc58d02.s1 Stratagene liver (937224) CCR4-NOT transcription complex, subunit	2.5
	131938	AF176085	Hs.34956	neural polypyrimidine tract binding prot	2.5 2.5
35	102450	U48251	Hs.75871	protein kinase C binding protein 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	126339 118967	AA152106	Hs.4859	cyclin L ania-6a	2.5
	123110	A1668670 AA486256	Hs.216756 Hs.193510	ESTs EST	2.5 · 2.5
40	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.5
	113247	T63856	Hs.193430	ESTs, Wealdy similar to 2109260A B cett	2.5
	122024	AA431296	Hs.139433	ESTs	2.5
	106657 126127	AW854339 N95428	Hs.33476	hypothetical protein FLJ11937	2.5
45	111836	R58394	Hs.25119	gb:zb80d09.s1 Soares_senescent_fibroblas ESTs, Weakly similar to YEX0_YEAST HYPOT	2.5 2.5
	121470	AA558958	Hs.324751	ESTs	2.5
	120132	W57554	Hs.125019	ESTs ·	2.5
	107731	AA016086	Hs.272106	ESTs, Weakly strnilar to 138022 hypotheti	2.5
50	118122 106589	Al186671 AK000933	Hs.48008	ESTS	2.5
	129948		Hs.28661 Hs.263988	Homo saplens cDNA FLJ10071 fis, clone HE ESTs	2.5 2.5
	115652		Hs.38178	hypothetical protein FLJ23468	2.5
	103076	NM_001034		ribonucleolide reductase M2 polypeptide	2.5
55	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.5
55	100512 105393	D13317 AF167570	Hs.78915 Hs.256583	GA-binding protein transcription factor,	2.5
	100571	L14581	Hs.78546	interleukin enhancer binding factor 3, 9 ATPase, Ca++ transporting, plasma membra	2.5 2.5
	106890		Hs.88500	mitogen-activated protein kinase 8 inte	2.5
60	104276		Hs.284288	hqp0256 protein	2.5
60	113283 118078		Hs.12947	EST	2.5
	120796		Hs.47790 Hs.96820	EST ESTs	2.5
	106265		Hs.236463	Homo sapiens mRNA; cDNA DKFZp586i0521 (f	2.5 2.5
15	102507		Hs.193044	potassium inwardly-rectifying channel, a	2.5
65	106508		Hs.30348	ESTs	2.5
	104568 103698		Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.5
	113947		Hs.6685	thyroid hormone receptor interactor 8 gbzh53d03.s1 Soares_fetat_liver_spieen_	2.5 2.5
	132112		Hs.40154	jumonji (mouse) homolog	2.5 2.5
70	129052	BE275031	Hs.158210	hypothetical protein MGC2555	24
	117265		Hs.43005	RAB9-like protein	24
	107834		Hs.40838	ESTs	24
_	113119 133726		Hs.252716	gbryb18b11.s1 Strategene fetal spieen (9 oxysterol-binding protein-related protei	2.4
75	120548		Hs.187634	ESTs	24 24
	121545	AA412442	Hs.98132	ESTs	24
	131136		Hs.23413	KIAA1273 protein	2.4
	126589 115475			Homo saplens cytomegalovirus partial fus	. 24
80	103760		Hs.40193 Hs.183842	hypothelical protein KIAA 1259 ubiquitin B	2.4
	127889	Al147408	Hs.144941	ESTs .	2.4 2.4
	124457	AK000680	Hs.266175	phosphoprotain associated with GEMs	2.4
	113721	AF143885	Hs.18190	EST	2.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.4
		AA608705	Hs.187772	ESTs	2.4
	123592 113474	AA805331 R50752	Hs.112837 Hs.23856	ESTs hypothetical protein MGC5297	24 24
5		F13687	Hs.227976	EST	24
	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	24
	131686 127841	NM_012296		GRB2-associated binding protein 2 ESTs	2.4
	102737	AW136558 R51790	Hs.125246 Hs.239483	Human clone 23933 mRNA sequence	2.4 2.4
10	129673	D38552	Hs.1191	KIAA0073 protein	24
	133095	BE046490	Hs.180677	zinc finger protein 162	2.4
	124540 113609	N63232 T93263	Hs.16875	gb:yz39a12.s1 Morton Fetal Cochlea Homo ESTs, Weakly similar to S23650 retrovir	2.4 2.4
	128826	Z40313	Hs.106330	Homo sapisns clone IMAGE:23371, mRNA seq	2.4
15	129059	AW069534	Hs.279583	CGI-81 protein	2.4
	134092 132317	AA218558 BE262438	Hs.7905	sorting nextin 9	2.4
	135278	AA399542	Hs.44592 Hs.229671	beta-1,4 mannosyltransferase EST, Moderately similar to PEPTIDYL-PROL	2.4 2.4
00	128468	T23625	Hs.150580	putative translation initiation factor	24
20	127407	AW089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	24
	132342 113518	AW162758 AW367788	Hs.45232 Hs.323954	ESTs, Weakly similar to ALUS_HUMAN ALU S postmetotic segregation increased 2-lik	2.4 2.4
	100330	AW410976		minichromosome maintenance deficient (S.	24
25	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	24
25	123910	AA621262	Hs.179923	ESTs, Wealdy similar to S65657 alpha-1C-	2.4
	101651 100114	AL037111 X02308	Hs.75641 Hs.82962	galactose-1-phosphate uridylyltransferas thymidylate synthetase	24 24
	125038	AA812234	Hs.270134	hypothetical protein FLJ20280	2.4
30	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.4
30	123258 132380	AA490929 AW373665	Hs.105274 Hs.46853	ESTs, Weakly similar to RMS1_HUMAN REGUL ESTs	2.4
	114046	BE018658	Hs.141003	Homo saplens cDNA: FLJ21691 fis, clone C	2.4 2.3
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.3
35	134839	D63479	Hs.115907	diacylglycerol kinase, delta (130kD)	2.3
33	105734 101086	Al952797 AA382524	Hs.10888 Hs.250959	hypothetical protein FLJ21709 histatin 1	2.3 2.3
	118349	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	101194	L20971	Hs.188	phosphodiesterase 48, cAMP-specific (dun	2.3
40	130588 101875	AL030996 BE241753	Hs.16411	hypothetical protein LOC57187	2.3
70	118751	N74210	Hs.74592 Hs.50454	special AT-rich sequence binding protein ESTs	2.3 2.3
	125174	W51835	Hs.231082	EST	23
	105966	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	2.3
45	104624 131263	AA353125 AU077002	Hs.184721 Hs.24950	ESTs regulator of G-protein signalling 5	2.3 2.3
	105014	AA121123	Hs.269267	ESTs, Wealthy similar to AF161361 1 HSPC	23
	123423	AA598484		gb:ae38/04.s1 Gessler Wilms tumor Homo s	23
	128531 108876	H03721	Hs.2953	ribosomal protein \$15a	23
50	130215	AI733860 BE301883	Hs.191453 Hs.152707	ESTs glioblastoma amplified sequence	2.3 2.3
	132232	Al522273	Hs.42640	ËSTs	2.3
	132664	Al740461	Hs.54542	ESTs	2.3
	105991 100253	AA215701 D38024	Hs.186541 Hs.157425	ESTs, Wealdy similar to 138022 hypotheti double homeobox, 2	2.3 2.3
55	105574	AA045281	Hs.268175	phosphoprotein associated with GEMs	2.3
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.3
	134964 132786	AI803516 BE083422	Hs.272891 Hs.56851	hippocalcin-like protein 4	2.3
	104952	AW076098		hypothetical protein MGC2668 desmoplaldn (DPI, DPII)	2.3 2.3
60	119127	AA708035	Hs.12248	ESTs	23
	104857	A1920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.3
	107592 113378	AA694264 T80738	Hs.60049 Hs.14757	ESTs ESTs	23 23
65	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	23
65	106898	AA490069	Hs.306676	Homo sepiens cDNA FLJ14302 fis, clone PL	2.3
	130734 125728	AW137091 AW954565		KIAA1052 protein B-cell CLL/lymphoma 118 (zinc finger pro	2.3 2.3
	113697	197183	Hs.17992	Homo sepiens mRNA; cDNA DKFZp434J1726 (f	2.3
70	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.3
70	134267 105777	A1174596 R42755	Hs.196209 Hs.23096	RAE1 (RNA export 1, S.pombe) homotog	23
	115308			ESTs ESTs	23 23
	133363	AI866286	Hs.71962	ESTs, Wealdy similar to B36298 proline-r	2.3
75	129535			chimerin (chimaerin) 1	2.3
, ,	121520 123808			ESTs gb:ae58g11.s1 Stratagene lung carcinoma	2.3 2.3
	105700	AW580830		hypothetical protein FLB6421	23
	120820	AA347417	Hs.96869	EST	2.3
80	128721 107711			phosphoprotein associated with GEMs ESTs	23
	102564		Hs.220687 Hs.79067	MAD (mothers against decapentaplegic, Dr	23 23
	131868	AW408298	Hs.33532	zino finger protein 151 (pHZ-67)	23
	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.3
				· 88	

	118865	AA736405	Hs.54530	ESTs	2.3
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.3
	133772	BE379867	Hs.76038	isopentenyl-diphosphate della isomerase	2.3
5	111795	A1435437	Hs.24567	ESTs, Wealthy similar to KBF3_HUMAN NUCL	23
5	103437	AV655598	Hs.184211	peptidase (mitochondrial processing) bet	23
	123060 125466	AA482027 R08234	Hs.142569	ESTs, Weakly similar to 138022 hypotheti	2.3
	100892	BE245294	Hs.180461 Hs.180789	ESTs C164 contrib	2.3
	121613	AA416879	Hs.193195	S164 protein ESTs, Wealdy similar to 2109260A B cett	2.3
10	133665	AL036883	Hs.75450	delta steep inducing peptide, immunoreac	2.3
	129248	W04606	Hs.171637	hypothetical protein MGC2528	2.2
	126153	H85692	Hs.40730	ESTs	2.2 2.2
	125590	R23858	Hs.143375	Homo sapians, clone IMAGE:3840937, mRNA	2.2
	104960	AA558877	Hs.8928	hypothetical protein FLJ20291	2.2
15	113941	AA531016	Hs.22399	hypothetical protein FLJ14824	2.2
	112540	R69751		gb:yl40a10.s1 Soares placenta Nb2HP Homo	22
	105322	TB7179	Hs.16346	ESTs, Wealdy similar to S57447 HP8RII-7	2.2
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.2
20	134733	N87353	Hs.89421	CBF1 Interacting corepressor	2.2
20	114620	AA842974		gb:nr60h01.s1 NCI_CGAP_Lym3 Homo saplens	2.2
	123451	Al793211	Hs.165372	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	130850	AB040922	Hs.20237	OKFZP566C134 protein	2.2
	105561	AA262881	Hs.323835	ESTs, Weakly similar to alternatively s	2.2
25	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	2.2
23	130362	BE513050	Hs.279681	heterogeneous nuclear ribonucleoprotein	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	124250	AA350256	Hs.323875	EST, Wealdy similar to 2109260A B cell	2.2
	131392 128845	AA235153	Hs.26320	TRABID protein	2.2
30	130453	AW503976 U80735	Hs.10649	basement membrane-induced gena	2.2
-	126973	W46653	Hs.173854 Hs.251928	PAX transcription activation domain inte	2.2
	103156	BE259039	Hs.129953	nuclear pore complex interacting protein	2.2
	103163	AU077018	Hs.3235	Ewing sarcoma breakpoint region 1 keratin 4	2.2
	109252	BE440157	Hs.85944	ESTs	2.2 2.2
35	131163	AA099524	Hs.23754	ESTS	. 2.2
	115292	AA279956	Hs.88872	ESTs	2.2
	122591	AJ188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.2
	124977	F04819	Hs.190452	KIAA0365 gene product	2.2
40	103319	XB3492	Hs.82359	tumor necrosis factor receptor superfami	22
40	100370	D79989	Hs.184884	KIAA0167 gene product	2.2
	128992	H04150	Hs.107708	ESTs	22
	129928	AJ338993	Hs.134535	ESTs	2.2
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
45	133910	AW835281	Hs.77500	ublquitin specific protease 4 (proto-onc	2.2
45	106288	AB037742	Hs.24336	KIAA1321 protein	22
	134125	NM_014781		KIAA0203 gene product	2.2
	101379	X02994	Hs.1217	adenosine deaminase	2.2
	112276 106251	R53442	Hs.26038	ESTs, Wealdy similar to 138022 hypothet	2.2
50	125394	R12607 BE178502	Hs.35101 Hs.173772	profine-rich Gla (G-carboxyglutamic acid	2.2
	103392	X94563	16.173/12	ESTs, Weakly similar to 178885 serine/th	2.2
	112853	T02843		gb:H.saplens dbi/acbp gene exon 1 & 2. gb:F811H5 Fetal brain, Stratagene Homo s	2.2
	133195	Al434760	Hs.279949	KIAA1007 protein	2.2
	135050	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.2 2.2
55	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.2
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.2
	105225	AA211777		gb:zn57d02.s1 Stratagene muscla 937209 H	2.2
	131320	AA505691	Hs.145696	splicing factor (CC1.3)	22
60	114419	AI248013	Hs.106532	ESTs, Weakly similar to 138588 reverse t	2.2
oo	103634	BE541733	Hs.180877	H3 histone, family 3B (H3.3B)	2.2
	134624	AF035119	Hs.8700	deleted in liver cancer 1	2.2
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.2
	115556 111898	AL031778 R38944	Hs.797	nuclear transcription factor Y, alpha	2.2
65	100415	D86970	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.2
00	103898	AA248884	Hs.75822	TGFB1-induced anti-apoptotic factor 1	2.2
	129501	AI631811	Hs.180403	gb:k3517.seq.F Human fetal heart, Lambda STRIN protein	2.2 2.2
	127251	AA936428	Hs.128638	ESTs	2.2
	100613	X52078	Hs.101047	transcription factor 3 (E2A immunoplobut	2.2
70	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2 2.2
	128897	AW979134	Hs.10700	hypothetical protein	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.2
76	125585	AW298113	Hs.92909	SON DNA binding protein	22
75	129584	AV656017	Hs.184325	CGI-76 protein	2.2
	114461	AA531187	Hs.126705	ESTs	22
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.2
	109339	AA314554	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	2.2
80	129179	AW969025	Hs.109154	ESTs	2.2
50	106711	BE390125	Hs.143187	hypothetical protein	22
	106424		Hs.37902	ESTs	2.2
	123949 127256		Hs.208957	EST	2.2
	-41230	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.2

	404060	A.C472007			
	104868 132984	AF173867	Hs.28906	glucocorticoid modulatory element bindin	2.2
	126383	BE539199 AB032977	Hs.62112 Hs.6298	zinc finger protein 207	2.2
	130557	H51825	Hs.268911	KIAA1151 protein	2.2
5	119232	AI855226	Hs.117659	ESTs, Weakly similar to S65824 reverse ESTs, Weakly similar to T46481 hypotheti	2.2
•	105715	BE621800	Hs.29444	putative small membrane protein NIO87	2.2
	124691	R05835	Hs.110153	ESTs	2.2 2.2
	113849	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	22
10	117040	AW970600	Hs.303261	ESTs	2.2
10	128767	M85169	Hs_1050	pleckstrin homology, Sec7 and colled/col	2.2
	120602	AA808018	Hs.109302	ESTs	2.2
	107182	Al311782	Hs.20013	GCIP-Interacting protein p29	2.2
	107357	U63973	Hs.103501	modopsin kinase	2.2
15	125499 126872	H10543		gb:ym04c08.r1 Soares infant brain 1NIB H	2.1
13	113233	AW450979 T61955	Hs.279867	gb:UI-H-BI3-gla-g-12-0-UI.s1 NCL_CGAP_Su	2.1
	128367	AWB11791	Hs.150742	CGI-59 protein ESTs	2.1
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	21
	114021	AW235215	Hs.16145	ESTs	2.1
20	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.1 2.1
	134966	AW402389	Hs.920	modulator recognition factor I	21
	129765	M86933	Hs.1238	amelogentn (Y chromosome)	21
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	21
25	109639	AA082650	Hs.6217	Homo saplens cDNA FLJ12521 fis, ctone NT	2.1
25	129794	AF161399	Hs.23259	hypothetical protein FLi 13433	21
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
	110256	H63947	Hs.237955	RAB7, member RAS encogene family	2.1
	128817 120906	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.1
30	134354	NM_000734 M90391	Hs.82127	CD3Z antigen, zeta polypeptide (TIT3 com	2.1
-	106048	AW883367	Hs.301732	Interleukin 16 (lymphocyte chemoattracta hypothetical protein MGC5306	2.1
	128352	AW137413	Hs.169942	ESTs	21
	115348	AA281562	Hs.292100	ESTs	21 21
~ -	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	2.1
35	107121	AB015427	Hs.250493	zinc finger protein 219	2.1
	118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HE	21
	135051	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	2.1
40	126661	AA009835	Hs.269521	ESTs .	2.1
- 0	129270 125568	AA357185	Hs.109918	ras homolog gene family, member H	2.1
	132867	AW615398 AF226667	Hs.105613	ESTs CTD combace II	21
	124656	AW297702	Hs.58553 Hs.102915	CTP synthese II	21
	128954	AA346839	Hs.209100	ESTs DKFZP434C171 protein	2.1
45	132985	AL045579	Hs.62113	KIAA0717 protein	2.1 2.1
	119247	BE269047	Hs.65234	hypothetical protein FLJ20596	2.1
	106686	N66397	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	21
	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	2.1
50	112170	BE246743	Hs.288529	hypothetical protein FLJ22635	21
50	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.1
	117357	N24829	11 450000	gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.1
	101613	M24283	Hs.168383	Intercellular adhesion molecule 1 (CD54)	2.1
	127644 101183	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	21
55	100420	AA442324 D86983	Hs.795 Hs.118893	H2A histone family, member O Melanoma associated gene	2.1
	129879	AK001696	Hs.13109	Ran binding protein 11	21
	122311		Hs.131915	KIAA0863 protein	2.1
	130566	R85474	Hs.16073	ESTs	21 21
C 0	113517	AI874223	Hs.293560	ESTs	2.1
60	115810	AA426026	Hs.187615	ESTs	2.1
	108743	AI580150	Hs.71074	ESTs .	21
	129255	Al961727	Hs.109804	H1 histone family, member X	2.1
	120766 126893	AA764879	Hs.12570	tubulin-specific chaperone d	2.1
65	115254	AJ252060	Hs.26320	TRABID protein	2.1
00	105865	AA279024 BE279383	Hs.269316 Hs.26557	ESTs, Weakly similar to S65657 alpha-1C	2.1
	120999	AI972375	Hs.29826	plakophilin 3 hypothetical brain protein my038	21
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	2.1
	117997	N52090	Hs.47420	EST	2.1
70	104333	D82418	Hs.29626	hypothetical brain protein my038	2.1 2.1
	134315	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	21
	135332	AW3938B3	Hs.98968	hypothetical protein FLJ23058	21
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic laukernia	2.1
75	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
13	112563	AW961220	Hs.29282	milogen-activated protein kinase kinase	2.1
	121782	AW452957	Hs.334698	Homo saptens, clone MGC:15203, mRNA, com	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC15040	21
	133912	H42679 AF086215	Hs.77522	major histocompatibility complex, class	2.1
80	134076 116665	F04405		gb:Homo sapiens full length insert cDNA	2.1
-5	133562	M60721	Hs.74870	gb:HSC2SB082 normalized infant brain cDN	2.1
	129092	D56365	Hs.63525	H2.0 (Drosophila)-like homeo box 1 poly(rC)-binding protein 2	2.1
	106869	AW975362	Hs.292679	ESTs	2.1 2.1
	•				4.1
				00	

	130820		Hs.288798	hypothetical protein FLJ21012	21
	126277 106392	AB037847 BE350058	Hs.15441 Hs.36787	Crm (Cramped Drosophila)-like chromodomain helicase DNA binding protel	2.1 2.1
-	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	21
5	120734 113070	AA299948 AB032977	Hs.6298	gb:EST12544 Uterus turnor I Horno sapiens	2.1
	116031	AA452239	Hs.103329	KIAA1151 protein KIAA0970 protein	2.1 2.1
	123869	AA620924	Hs.112923	EST	2.1
10	108145 109061	AA424791 AA160898	Hs.5734	meningioma expressed antigen 5 (hyzłuron	21
10	126348	T16243	Hs.6473	gb:zo79c07.s1 Stratagene pancreas (93720 Homo sapiens cDNA FLJ13992 fis, clone Y7	21 21
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	123132 117452	AI061582	Hs.324179	Homo saplens cDNA FLJ12371 fls, clone MA	21
15	128538	N34687 R44214	Hs.44054 Hs.101189	ninein (GSK3B interacting protein) ESTs	2.1 2.1
	111945	R40683	Hs.124944	ESTs	2.1
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	21
	124362 129198	ALD46406 N57532	Hs.103483 Hs.109315	KIAA1798 protein KIAA1415 protein	21 21
20	122059	AA431737	Hs.98749	EST, Moderately similar to T42871 hypoth	21
	115843	AA404276	Hs.123253	hypothetical protein FLJ22009	2.0
	112558 115355	AK001621 AA262292	Hs.15921 Hs.88445	hypothetical protein FLJ10759 ESTs	2.0 2.0
26	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	20
25	125360 104926	AW898892	Hs.189741	EST8	20
	119468	BE298808 Al911535	Hs.33363 Hs.6657	DKFZP434N093 protein hypothetical protein bK1048E9.5	2.0 2.0
	132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxillary fac	20
30	100237 105335	D30715	Hs.305333	Human PAP (pancreatitis-associated prot	2.0
30	105333	AW291165 AA357001	Hs.25447 Hs.34045	ESTs hypothetical protein FLJ20764	2.0 2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	20
	115084 128408	BE383668	Hs.42484	hypothetical protein FLJ 10618	2.0
35	132311	Al183407 Al765559	Hs.143704 Hs.20072	EST myosin regulatory light chain interactin	2.0 2.0
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	116379 105474	AA448588 AL134843	Hs.71252	hypothetical protein DKFZp761C169	20
	108922	AA115268	Hs.219614 Hs.269263	f-box and leucine-rich repeat protein 11 ESTs	2.0 2.0
40	123720	AA609734	Hs.112755	EST	2.0
	128902 113226	AA036637 Al821008	Hs.107052 Hs.10697	ESTs ECT-	2.0
	106798	8E252749	Hs.20558	ESTs hypothelical protein FLJ20345	20 20
A E	106665	BE090009	Hs.323164	hypothetical protein MGC2217	2.0
45	105952 127248	Al767152 AA364195	Hs.181400	ESTs, Wealdy similar to 178885 serine/th	20
	112972	AI684745	Hs.165983	gb:ES175015 Pineal gland II Homo saplens hypothetical C2H2 zinc finger protein FL	2.0 2.0
	128148		Hs.126637	ESTs	2.0
50	118176 126457	AA311152 AA007489	Hs.288708 Hs.50382	hypothetical protein FLJ21562	2.0
50	112610		Hs.23643	ESTs serine/threonine prolein kinase MASK	2.0 2.0
	109249		Hs.268189	hypothetical protein FLJ20436	2.0
	121292 128606		Hs.102402	gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_ Mad4 homolog	2.0 2.0
55	127705		113.102402	gb:AJ003322 Selected chromosome 21 cDNA	2.0
	134674		Hs.87726	KIAA0154 protein; ADP-ribosylation facto	2.0
	107529 116411		Hs.296585 Hs.321618	nucleolar protein (KKE/D repeat) hypothetical protein FLJ12525	2.0 2.0
	111576	T88827	Hs.15489	ESTs	2.0
60	127002		Hs.24979	hypothetical protein DKFZp761P1010	2.0
	112662 126250		Hs.268814 Hs.321247	ESTs Homo saplens mRNA; cDNA DKFZp586A181 (fr	2.0 2.0
	101045	J05614		gb:Human proliferating cell nuclear anti	2.0
65	117188		Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
05	122110 119849		Hs.301240 Hs.58440	melanocortin 1 receptor (alpha melanocyt ESTs	20 20
	124395	N29963	Hs.272095	ESTs, Weakly similar to 138022 hypotheti	2.0
	131600		7 Hs.29331	camitine palmitoyltransferase I, muscle	2.0
70	112774 109751		Hs.35455 Hs.6679	ESTs hHDC for homotog of Drosophila headcase	20 20
	102377	7 U40343	Hs.29656	cyclin-dependent kinase inhibitor 2D (p1	20
	115197		Hs.6749	ESTs	2.0
	102808 128869		Hs.179606 Hs.80618	nuclear RNA halicase, DECD variant of DE hypothetical protein	2.0 2.0
75	111229	AW389845		ESTs	20
	129330		Hs.92260	high-mobility group protein 2-like 1	2.0
	105448 127391			BTB and CNC homology 1, basic leucine zi hypothetical protein MGC2722	2.0 2.0
00	102337	7 Al814663	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	2.0
80	121897		Hs.229162 Hs.61358	EST, Weakly similar to ZN91_HUMAN ZINC	2.0
	10790: 12934		Hs.11050	ESTs F-box only protein 9	2.0 2.0
	10109			chemokine (C-X-C matif), receptor 4 (fus	2.0
				. 91	
				>1	
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	124864	AW970168	Hs.185706	ESTs	2.0
	118485 116715	AA508515	Hs.291049	ESTs	2.0
	130743	AL117440 AL049266	Hs.170263 Hs.18724	tumor protein p53-binding protein, 1	2.0
5	118877	AW971146	Hs.293187	Homo saplens mRNA; cDNA DKFZp564F093 (fr ESTs	2.0 2.0
	100020				20
	123252	AW968776	Hs.287586	Homo sapiens cDNA FLJ13648 ffs, clone PL	2.0
	134977	AL044963	Hs.308121	leukocyte receptor cluster (LRC) encoded	2.0
10	115334 111790	AA702972	Hs.65300	ESTS	2.0
10	129101	AW769683 NM_013403	Hs.6734	ESTs, Wealdy similar to \$26650 DNA-bindi zinedin	2.0
	132676	N92589	Hs.261038	ESTs, Wealtly similar to 138022 hypothet	2.0 2.0
	111018	Al287912	Hs.3628	mitogen-activated protein kinase kinase	2.0
1.0	105933	AF078544	Hs.194686	solute carrier family 25 (mitochondrial	2.0
15	110679	AA004798	Hs.108311	ESTs, Wealdy similar to TD0351 hypotheti	2.0
	120861	AA350394	Hs.96952	ESTs .	2.0
	132430 115026	AW973652 AA251972	Hs.283105	ESTs .	2.0
	128660	AA011597	Hs.188718 Hs.177398	ESTs ESTs	2.0
20	134554	AI184316	Hs.85273	retinoblastoma-binding protein 6	20 20
	109592	Al198059	Hs.26370	ESTs .	20
	123636	AA609263		gb:af13c08.s1 Soares_testis_NHT Homo sap	2.0
	132610	AA160511	Hs.5326	amino acid system N transporter 2; porcu	2.0
25	122652 120467	AA454641	U. 107000	gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sepi	2.0
2,5	126048	AW292582 AA804957	Hs.187628 Hs.119840	ESTs ESTs	2.0
	128179	AW293689	Hs.127116	ESTS	20 20
	123349	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona	20
20	10620B	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
30	125832	AA628600	Hs.117587	ESTs	2.0
	133317 132886	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	2.0
	127447	AW978168 AA386192	Hs.5912 Hs.193482	F-box only protein 7	2.0
	133149	AA370045	Hs.6607	Homo sapiens cDNA FLJ11903 fis, clone HE AXIN1 up-regulated	2.0 2.0
35	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	20
	106487	A1697340	Hs.135265	Homo saplens clone FLB8436 PRO2277 mRNA,	2.0
	126770	Al292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.0
	120592	AA830664	Hs.143974	ESTs	2.0
40	100944 101887	L07518 AW987413	Hs.159593 Hs.83958	mucin 6, gastric	2.0
-10	125324	R07785	115.03330	transducin-like enhancer of split 4, hom gb:yf15c06.r1 Soares fetal liver spleen	2.0
	133906	BE386038	Hs.77492	haterogeneous nuclear ribonucleoprotein	2.0 2.0
	113408		Hs.115945	mannosidase, beta A, lysosomal	20
15	115613	AW136951	Hs.173946	hypothetical protein FLJ 10486	2.0
45	107468	AA740979	Hs.91389	ESTs	2.0
	100554 120476	M95923	U- 10/20E	gb:Human 12-lipoxygenase mRNA, partial c	2.0
	117160	AA322302	Hs.104305 Hs.183302	death effector filament-forming Ced-4-II PCTAIRE protein kinase 2	2.0
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tu	2.0 2.0
50	125536	F08266	Hs.77948	ESTs, Wealdy similar to ALU1_HUMAN ALU S	20
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	2.0
	133207	AI561173	Hs.67688	ESTs	2.0
	122053 121080	AI637498 AA617830	Hs.98745 Hs.28310	ESTs	2.0
55	113316	T70318	Hs.268581	ESTs ESTs	20 20
-	113137	AW952129	Hs.293225	ESTs, Weakly similar to FLDED-1 [H.sapie	1.9
	100416	AW505086	Hs.196914	minor histocompatibility antigen HA-1	1.9
	133975	C18358	Hs.295944	tissue factor pathway inhibitor 2	1.9
60	103872		Hs.21756	translation factor sui1 homotog	1.9
00	132439 126082	AK001942 H81188	Hs.4863	hypothetical protein DKFZp566A1524	1.9
	124877	R01073	Hs.269571	ESTs gb:ye84c03.s1 Soares fetal liver spleen	1.9
	123385		Hs.17767	KIAA1554 protein	1.9 1.9
~~	103138			gb:H.seplens SOD-2 gene for manganese su	1.9
65	104867	AA278898	Hs.225979	hypothetical protein similar to small G	1.9
	128668		Hs.103422	Homo sapiens cDNA FLJ14630 fis, clone NT	1.9
	125826 113701		Hs.7594	solute carrier family 2 (facilitated glu	1.9
	134447	T97301 M58603	Hs.18026 Hs.83428	EST8	1.9
70	128895			nuclear factor of kappa light polypeptid ESTs	1.9
	112719		Hs.19301	Homo saplens, Similar to Nedd-4-like ubi	1.9 1.9
	102552			tumor protein p53-binding protein, 2	1.9
	131186		Hs.246112	KIAA0788 protein	1.9
75	133347		Hs.71475	acid cluster protein 33	1.9
15	133388			heterogeneous nuclear ribonucleoprotein	1.9
	112266 100336		Hs.25934 Hs.8127	ESTs, Wealdy similar to HSHU11 histone H	1.9
	113479		Hs.10739	KIAA0144 gene product ESTs	1.9
00	135231		Hs.74280	hypothetical protein FLJ22237	1.9 1.9
80	123783	AA610112		gb:a/19g05.s1 Soares_total_fetus_Nb2HF8_	1.9
	113016		7 Hs.127649	KIAA0414 protein	1.9
	132761		Hs.323502	nuclear RNA export factor 1	1.9
	128536	AW955085	Hs.101150	Homo seplens, clone IMAGE:4054156, mRNA,	1.9

	126663	AW518478	Hs.181297	ESTs	1.9
	103973 106742	AA305729	Hs.18272	amino acid transporter system A1	1.9
	129793	AW591428 AW207000	Hs.27556 Hs.126857	hypothetical protein FLJ22405	1.9
5	105888	AW970872	Hs.9247	Homo seplens cDNA FLJ12935 fis, clone NT protein kinase, AMP-activated, alpha 1 c	1.9 1.9
	101892	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	1.9
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.9
	126751	AI378328	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.9
10	129111 128750	AL080155 T80270	Hs.226372 Hs.104788	DKFZP434J154 protein	1.9
	133531	BE276738	Hs.74578	hypothetical protein LOC55565 DEAD/H (Asp-Glu-Ata-Asp/His) box polypep	1.9 1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	100157	D14661	Hs.119	Wilms' tumour 1-associating protein	1.9
15	125845	AK001440	Hs.131840	hypothetical protein FLJ10578	1.9
13	134682 106565	AW882645 NM_014892	Hs.88044	sprouty (Orosophila) homolog 1 (antagoni	1.9
	106706	AB037810	Hs.18760	KIAA1116 protein KIAA1389 protein	1.9 1.9
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	1.9
20	116470	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	1.9
20	123264	AJ681270	Hs.99824	BCE-1 protein	1.9
	126096 104995	F08208 AK001690	Hs.283844 Hs.16390	similar to rat tricarboxylate carrier-li	1.9
	133424	AA350994	Hs.20281	hypothetical protein FLJ10035 KIAA1700	1.9 1.9
05	132450	AA100012	Hs.48827	hypothetical protein FLJ12085	1.9
25	131803	U73737	Hs.284289	vitiligo-associated protein VIT-1	1.9
	116548 113815	D20433 AA386192	Un 403400	gb:HUMGS01407 Human promyelocyle Homo sa	1.9
	100245	AL039248	Hs.193482 Hs.3094	Homo saplens cDNA FLJ11903 fis, clone HE KIAA0063 gene product	1.9
	113877	Z70200	Hs.246112	KIAA0788 protein	1.9 1.9
30	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
	134937	AI251449	Hs.171939	ESTs .	1.9
	134506 126469	AW247364	Hs.84285	ubiquifin-conjugating enzyme E2i (homolo	1.9
	115261	BE384361 AA938293	Hs.182885 Hs.60088	ESTs, Weakly similar to JC5024 UDP-galac hypothetical protein MGC11314	1.9
35	125198	W69474	Hs.323140	ESTs	1.9 1.9
	115317	AA303799	Hs.300141	ribosomal protein L39	1.9
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	1.9
	117329 116353	AA524065 AB032968	Hs.93670	Homo septens cDNA: FLJ22664 fls, clone H	1.9
40	114459	AW445217	Hs.131728 Hs.103362	KIAA1140 protein ESTs	1.9
	133903	X63692	Hs.77482	DNA (cytosine-5-)-methyltransferase 1	1.9 1.9
	116083	AA455706	Hs.44581	heat shock protein hsp70-related protein	1.9
	130037	AJ498631	Hs.111334	ferrilin, light polypeptide	1.9
45	102273 120452	BE391815 AL022328	Hs.75981 Hs.104335	ubiquitin specific protesse 14 (tRNA-gua	1.9
	116432	BE271922	Hs.71243	hypothetical protein IMAGE3510317 ESTs, Weakly similar to zinc finger prot	1.9 1.9
	115916	AI052731	Hs.91910	ESTs	1.9
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	1.9
50	129602 105693	AI282193	Hs.198298	v-src avlan sarcoma (Schmidt-Ruppin A-2)	1.9
50	102316	BE250951 U34301	Hs.181368	U5 snRNP-specific protein (220 kD), orth gb:Human nonmuscle myosin heavy chain II	1.9
	131422	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.9 1.9
	128434	Al190914	Hs.143880	ESTs	1.9
55	117086	AA581602	Hs.41840	ESTs	1.9
"	102006 121335	AL048967 AA404418	Hs.172207	non-POU-domain-containing, octamer-bindi	1.9
	105905	AA401533	Hs.19440	gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_ ESTs	1.9 1.9
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	1.9
60	109875	H03260	Hs.30385	ESTs	1.9
00	109152 126203	AW380723 AK001035	Hs.73451	ESTs, Weakly similar to S55024 nebulin.	1.9
	122530	AW959741	Hs.130881 · Hs.40368	B-cell CLL/lymphoma 11A (zinc finger pro adaptor-related protein complex 1, sigma	1.9
	124508	BE273688	Hs.182447	heterogeneous nuctear ribonucleoprotein	1.9 1.9
65	130525	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.9
65	127226	AL036559	Hs.3463	ribosomal protein S23	1.9
	106465 106970	AA521368	Hs.225951 Hs.24252	topoisomerase-related function protein 4 ESTs	1.9
	134275	AJ878910	Hs.3688	cisplatin resistance-associated overexpr	1.9
70	126825	AA100230		gb:zi81c01.s1 Stratagane colon (937204)	1.9 1.9
70	132443	AW246148	Hs.268371	hypothetical protein FLJ20274	1.8
	104631 111468	AA002064	Hs.18920	ESTs	1.8
	114317	H62647 AA524839	Hs.205481 Hs.469	ESTs succinate dehydrogenase complex, subunit	1.8
	126158	N55989	Hs.16390	hypothetical protein FLJ10035	1.8 1.8
75	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.8
	119229	T03229		gb:FBSC2 Fetal brain, Stratagene Homo sa	1.8
	105930 127245	AF016371 AA323958	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.8
	100967	8E011845	Hs.251064	gb:EST26810 Cerebellum II Homo sapiens c high-mobility group (nonhistone chromoso	1.8
80	105149	BE089288	Hs.8958	Homo septens cDNA FLJ 12024 fis, clone HE	1.8 1.8
	104542	R29657		gb:F1-11790 22 week old human fetal live	1.8
	124236	AF086006 AA284993		gb:Homo sapiens full length insert cDNA	1.8
	127155	**********		gb:zt23e10.r1 Soares ovary tumor NbHOT H	1.8

	400004	4 1075000			
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.8
	107021	AK001342	Hs.14570	hypothetical protein FLJ22530	1.8
	110023	AW294701	Hs.31040	ESTs	1.8
_	114899	AK000342	Hs.77646	Homo sapiens mRNA; cONA DKFZp761M0223 (f	1.8
5	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	1.8
	110384	H45282	Hs.268798	ESTs	1.8
	132693	BE244200	Hs.55075	KIAA0410 gene product	1.8
	127684	AA568631	Hs.32556	KIAA0379 protein	1.8
10	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
10	104249	AF004231	Hs.22405	teukocyte immunoglobulin-like receptor,	1.8
	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.8
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	1.8
	100417	NM_014003		pre-mRNA splicing factor similar to S. c	1.8
	120532	AA262354	Hs.186648	ESTs, Weakly similar to I38022 hypothefi	1.8
15	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	100739	M59287	Hs.2083	CDC-like kinase 1	
	110636	H72868	Hs.19110	ESTs	1.8 1.8
	132957	BE244044	Hs.61469	hypothetical protein	
	115467	Al366784	Hs.48820	TATA box binding protein (TBP)-essociate	1.8
20	132161	W31634	Hs.180799	hypothetical protein FLJ22561	1.8
	129510	AW968504	Hs.123073	CDC2-related protein kinase 7	1.8
	126805	F32658	Hs.101359	chromosome 6 open reading frame 32	1.8
	129295	U63127	Hs.110121	SEC7 homolog	1.8
0.5	127823	AW972893	Hs.78859	transcription elongation factor A (Sii),	1.8
25	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	1.8
	111959	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	1.8
	109303	AA199857	Hs.269291	ESTs	1.8
	112501	AA972447	Hs.288833	Homo septens mRNA; cONA DKFZp434K087 (tr	1.8
20	127303	AA366951		gb:EST77963 Pancreas lumor III Homo sapi	1.8
30	115982	W92113		gbtzh48e01.r1 Soares_fetal_liver_spleen_	1.8 1.8
	123331	AA497013		gb:ae32g02.s1 Gessler Wilms turnor Homo s	
	111598	R11505	Hs.268912	ESTs	1.8 1.8
	121643	AA640987	Hs.193767	ESTa	1.8
25	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.8
35	118761	AW799109	Hs.226755	ESTs	1.8
	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.8
	118103	AA401733	Hs.184134	ESTs	1.8
	134595	NM_002401	Hs.29282	mitogen-activated protein kinase kinase	1.8
40	134212	AA654353	Hs.17719	EBP50-PDZ Interactor of 64 kD	1.8
40	128033	AI248705	Hs.149321	ESTs	1.8
	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.8
	111122	N63753	Hs.16492	DKFZP564G2022 protein	1.8
	114798	AA159181	Hs.54900	serologically defined colon cancer antig	1.8
15	106349	AW954310	Hs.127270	KIAA1545 protein	1.8
45	135358	BE622827	Hs.99488	hypothetical protein FLJ13044	1.8
	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kinase 1	1.8
	116654	Z26324	Hs.79204	ESTs, Wealdy similar to I38022 hypotheti	1.8
	124554	N65961		gb:za27d03.s1 Soares felal liver spleen	1.8
50	120259	AW014786	Hs.192742	hypothetical protein FLJ12785	1.8
50	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.8
	125261	W90351	Hs.110134	ESTs, Highly similar to CREB-binding pro	1.8
	135026	N92165	Hs.93231	ESTs	1.8
	129951	AL110282	Hs.268024	Homo saplens, clone IMAGE:3873720, mRNA	1.8
55	125768	AI557486	Hs.119122	ribosomai protein L13a	1.8
55	114122	R46128	Hs.12751	ESTs	1.8
	133047	AA310600	Hs.63657	peplide:N-glycanase similar to yeast PNG	1.8
	133589	L37368	Hs.75104	RNA-binding protein S1, serine-rich doma	1.8
	130872 133498	U81084	Hs.226307	phorbolin (similar to apolipoprotein 8 m	1.8
60		DE299587	Hs.85301	calcium binding protein P22	1.8
~	131144 104261	AA305255	Hs.23528	HSPC038 protein	1.8
		AW248364	Hs.5409	RNA polymerase I subunit	1.8
	115507	AI083568	Hs.50601	hypothetical protein MGC10986	1.8
	109073 115363	T05003	Hs.10056	hypothetical protein FLJ14621	1.8
65	112657	AA214618	Hs.152759	activator of S phase kinase	1.8
05	102960	AW844878	Hs.19769	hypothetical protein MGC4174	1.8
	125549	Al904738 R20215	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.8
	133797	AL133921	U. 70070	gb:yg18b09.r1 Soares intent brein 1NIB H	1.8
	125048	AW440068	Hs.76272	retinoblastoma-binding protein 2	1.8
70	103403		Hs.59425	hypothetical protein FLJ23323	1.8
	123546	X95406	U- 442007	gb:H.sapiens cyclin E gens.	1.8
	124694	AA608817	Hs.112597	EST	1.8
	102406	R06108		gb:ye94h05.s1 Soares fetal liver spleen	1.8
	130695	U43177 T97205	Hs.17998	(NONE)	1.8
75	123951	AB012922		ESTs, Wealdy similar to 2109260A B cell	1.8
	118533	N71861	Hs.173043	metastasis-associated 1-like 1	1.8
	123197	AA489250	Hs.49413	ESTs	1.8
	125658	AW516428	Un 70007	gbras57h12s1 NCI_CGAP_GC81 Homo saplens	1.8
	100154	H80720	Hs.78687 Hs.81892	neutral sphingomyelinase (N-SMase) activ	1.8
80	106876	N52821	Hs.269412	KIAAD101 gene product	1.8
	128339	AL121087	Hs.296406	ESTs, Moderately similar to ALU7_HUMAN A	1.8
	105939	AL137728	Hs.12258	KIAA0685 gene product	1.8
	102495	NM_006762	Hs 79356	Homo saplens mRNA; cDNA DKFZp43480920 (/	1.8
				Lysosomal-associated multispanning membr	1.8
				0.4	

	100221	Dagge		abilition - But a company	
	101741	D28383 NM_003199	W- 226108		1.8
	101701	NM_002438	Hs.1861		1.8
_	107119	Al375499	Hs.27379		1.8 1.8
5	134362	U47742	Hs.82210		1.8
	127964	F06298		gb:HSC13F081 normalized Infant brain cDN	1.8
	101437	M20681	Hs.7594		1.8
	106204 112716	AA188734 AW590680	Hs.21479		1.8
10	109779	AB029396	Hs.110802 Hs.3353		1.8
	111369	AA535740	Hs.170263		1.8 1.8
	135204	AF087515	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	1.8
	105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	1.8
15	110997	AW882823	Hs.168052	KIAAD421 protein	1.8
13	111620 115618	R14853	Hs.307478		1.8
	115904	H11695 Al167560	Hs.322901 Hs.61297	disrupter of silencing 10 ESTs	1.8
	107510	BE613332	Hs.132055	ESTs, Wealty similar to GNMSLL retroviru	1.8
••	116435	AA186761	Hs.334812		1.8 1.8
20	112399	R60920	Hs.296770		1.8
	127426	AA854756	Hs.124076	ESTs .	1.8
	125175 132972	W52355	Hs.303030	EST	1.8
	125982	AA034365 R98091	Hs.288924	Homo saplens cDNA FLJ11392 fls, clone HE	1.8
25	115620	AA399997	Hs.211610	gb:yr30e11.r1 Soares fetal liver spleen CUG triplet repeat, RNA-binding protein	1.8
	128115	AJ435590	Hs.130168	ESTs	1.8 1.8
	106880	A1493206	Hs.32425	ESTs	1.7
	101199	L22075	Hs.1666	guanine nucleotide binding protein (G pr	1.7
30	104159	BE386983	Hs.283685	hypothetical protein FLJ20396	1.7
50	101368 103648	M13058	Hs.73952	proline-rich protein Haeill subfamily 2	1.7
	130717	AW248439 AA334274	Hs.2340 Hs.18368	junction plakoglobin OKFZP56480769 protein	1.7
	124981	N25485	Hs.330310	maternal G10 transcript	1.7
~ ~	124770	AA984414	Hs.120429	ESTs	1.7 1.7
35	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	1.7
	101636	BE392781	Hs.89474	ADP-ribosylation factor 6	1.7
	123553	A1494291	Hs.111977	ESTs	1.7
	127172 130621	AA292208	Hs.251278	KIAA1201 protein	1.7
40	116925	AW513087 H73110	Hs.16803 Hs.260603	LUC7 (S. cerevisiae)-like ESTs, Moderately similar to A47582 B-ce	1.7
	108845	AW382901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.7 1.7
	128092	AA904817	Hs.166229	ESTs	1.7
	128193	AJ224442	Hs.155020	putative methyltransferase	1.7
45	113965	Al268666	Hs.19631	ESTs, Wealdy similar to I38022 hypotheti	1.7
43	106620	D52562	Hs.296317	KIAA1789 protein	1,7
	102926 114964	W28363 BE085271	Hs.239752	nuclear receptor subfamily 2, group F, m	1.7
	101800	NM_006433	Hs.8834 Hs.105806	ring finger protein 3	1.7
	130094	NM_001471		granulysin gamma-aminobutyric acid (GABA) B recepto	1.7
50	120112	AA180240	Hs.6083	Homo saplens cDNA: FLJ21028 fis, ctone C	1.7 1.7
	109978	H09356	Hs.22528	ESTs	1.7
	121252	AA393907	Hs.97179	ESTs	1.7
	127768 125445	AW085002	Hs.156187	ESTs	1.7
55	100052	Al452722	Hs.7709	WW domain binding protein 1	1.7
	119863	AA081218	Hs.58608	Homo sapiens cDNA FL114206 fis, clone NT	1.7
	134333	AW888411	Hs.81915	teukemia-associated phosphoprotein p18 (1.7 1.7
	123541	AW976511	Ha.112592	ESTs	1.7
60	134191	W28632	Hs.7979	KIAAD736 gene product	1,7
UU	103305 112411	X82279	N- 094546	gb:H.saptens Fas, Apo-1 gene (promoter a	1.7
	100598	R43090 AL121734	Hs.271510 Hs.146409	ESTs, Moderately similar to ALU1_HUMAN A	1.7
	113610	T93279	118.140409	cell division cycle 42 (GTP-binding prot gb:ye25f01.e1 Stratagene lung (937210) H	1.7
	105593	AA279341	Hs.174151	aldehyde oxidase 1	1,7 1.7
65	125317	Z99348	Hs.112461	ESTs, Weakly similar to 138022 hypotheti	1.7
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.7
	105105	R81532	Hs.87016	hypothetical protein FLJ22938	1.7
	132791 116996	AB029551	Hs.7910	RING1 and YY1 binding protein	1.7
70	133335	H83935 BE251012	Hs.40535 Hs.263812	ESTs	1.7
. •	120959	BE247692	Hs.102469	nuclear distribution gene C (A.nidulans) putative nuclear protein	1.7
	105621	AL040058	Hs.6375	uncharacterized hypothalamus protein HTO	1.7 1.7
	106181	AI803651	Hs.191608	ESTs	1.7
75	125661	AA491830	Hs.25689	ESTs	1.7
13	127585	AA604144	Hs.190632	ESTs .	1.7
	112035		Hs.300759	ribosomal protein L38	1.7
	102870 108039	M64437 AA280319	Hs.234799 Hs.288840	breakpoint cluster region PRO1575 protein	1.7
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.7
80	114740	N70103		gb:za53e10.s1 Soares fetal liver spicen	1.7 1.7
	120304	AA192469	Hs.271838	ESTs	1.7
	103433	X38001	Hs.78948	Rab geranylgeranyltransferase, beta subu	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
				0.6	

	105269	AF174499	Hs.6764	histone deacetytase 6	1.7
	125431 133579	AW851639 X75346	Hs.75584 Hs.75074	polymyositis/scieroderma autoantigen 2 (mitogen-activated protein kinase-activat	1.7
_	105355	AL031447	Hs.26938	Homo sapians, clone IMAGE:4053044, mRNA	1.7 1.7
5	129601	AB032964	Hs.115726	KIAA1138 protein	1.7
	113739	AA356599	Hs.173904	ESTs	1.7
	100840 122878	U04816 AAB47744	Hs.183418 Hs.99640	cell division cycle 2-like 1 (PITSLRE pr ESTs	1.7
••	119495	BE144608	Hs.55533	ESTs	1.7 1,7
10	125669	R51308	Hs.333256	ESTs, Wealty similar to ALUS_HUMAN ALU	1.7
	109891	HD4757	Hs.323176	ESTS	1.7
	126884 132977	U49436 AA093322	Hs.288238 Hs.301404	KIAA1856 protein RNA binding motif protein 3	1.7
	101396	BE267931	Hs.78996	profilerating cell nuclear antigen	1.7 1.7
15	104730	AW139789	Hs.16370	Homo saplens cDNA FLJ11652 fis, clone HE	1.7
	102205	BE242291	Hs.197540	hypoxia-inducible factor 1, alpha subuni	1.7
	112945 129902	AW138458 AA076278	Hs.20787 Hs.13277	Homo sapiens cDNA: FLJ21686 fis, clone C	1.7
	107157	AW853745	Hs.286035	hypothetical protein FLJ22054 hypothetical protein FLJ22686	1.7 1.7
20	133229	AL137480	Hs.6834	KIAA1014 protein	1.7
	129912	AF155098	Hs.107213	hypothetical protein FLJ20585	1.7
	119811 126323	AW137640 N77584	Hs.231444 Hs.68644	Homo sapiens, Similar to hypothetical pr	1.7
	133134	AF198620	Hs.65648	Homo septens microsomal signal peptidase RNA binding motif protein 8A	1.7
25	115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.7 1.7
	133817	AW578718	Hs.7644	H1 histone family, member 2	1.7
	130753	AA205223	Hs.189	phosphodiasterase 4C, cAMP-specific (dun	1,7
	107463 121009	AW952022 NM_001533	Hs.315164 Hs.2730	hypothetical protein similar to actin re	1.7
30	125546	H09950	ris.2730	heterogeneous nuclear ribonucteoprotein gb:ym01d12.r1 Soares infant brain 1NIB H	1.7
	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7 1.7
	119015	N95490	Hs.29700	hypothetical protein FLJ20094	1.7
	100058 116655	AC074720	II- 00000	3214-14 4 6	1.7
35	119898	AF271732 R93325	Hs.68090 Hs.58690	bridging integrator-3 ESTs	1.7
	105021	H07960	Hs.306044	CGI-05 protein	1.7 1.7
	102098	N25485	Hs.330310	maternal G10 transcript	1.7
	126730	AA442429		gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_	1.7
40	113427 122317	T85105	Hs.15471	ESTs	1.7
-10	130503	T85253 BE208491	Hs.290874 Hs.295112	ESTs, Weakly similar to ALUS_HUMAN ALU S KIAA0818 gene product	1.7
	117348	N24157		gb:yx96b12.s1 Soares melanocyte 2NbHM Ho	1.7 1.7
	127033	AF169301	Hs.9098	sulfate transporter 1	1.7
45	128554	AW972147	Hs.101395	hypothetical protein MGC11352	1.7
73	124733 106310	R20547 R98185	Hs.100830 Hs.17240	ESTs ESTs	1.7
	122638	AL137476	Hs.123609	ESTs Homo sapiens mRNA; cDNA DKFZp43410623 (f	1.7 1.7
	101075	L03532	Hs.79024	haterogeneous nuclear ribonucleoprotein	1.7
50	126659	T16245		gb:NIB1005R Normalized Infant brain, Ben	1.7
50	127717 105441	F12209 N28522	Hs.1733B0	CK2 interacting protein 1; HQ0024c prote	1.7
	104188	AA478423	Hs.8935 Hs.300870	quinolinate phosphoribosyltransferase (n Homo sapiens mRNA; cDNA DKFZp547M072 (fr	1.7
	134750	L29073	Hs.1139	cold shock domain protein A	1.7 1.7
55	106826	BE253927	Hs.24983	hypothetical protein from EUROIMAGE 2021	1.7
33	113511	T89578	Hs.189740	ESTs	1.7
	111070 129091	AA056483	Hs.171834 Hs.301463	PCTAIRE protein kinase 1	1.7
	129710	AJ277841	Hs.120963	Human Chromosome 16 BAC clone CIT987SK-A ELG protein	1.7 1.7
60	132833	U78525	Hs.57783	eukaryotic translation initiation factor	1.7
60	125775	AW514585	Hs.29205	alpha integrin binding protein 63	1.7
	113675 100487	T81034 AU076640	Hs.14841 Hs.15243	ESTs	1.7
	119302	T25725	HS.13243	nucleolar protein 1 (120kD) gb:ESTDIR162 CD34+DIRECTIONAL Homo sapla	1.7
	128245	AA993101	Hs.170486	ESTs	1.7 1.7
65	130322		Hs.154545	PDZ domain containing guarrine nucleotide	1.7
	135363	AW589601	Hs.119	Wilms' turnour 1-associating protein	1.7
	125181 132347	R40815 BE271016	Hs.12396 Hs.169850	ESTs, Weakly similar to 2004399A chromos	1.7
	127206	AW816490	Hs.337508	ESTs, Weakly similar to T21554 hypotheti ESTs	1.7 1.7
70	121880	AW946155	Hs.7750	hypothetical protein AL133206	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	114601 126278	AA075568	U= 62040	gb:zm88f06.s1 Stratagene ovarian cancer	1.7
	120276	AA417302 AA398085	Hs.63042 Hs.142390	DKFZp564J157 protein ESTs	1.7
75	133634	AL035071	Hs.234279	microtubule-associated protein, RP/EB fa	1.7 1.7
	107025	AA825523	Hs.21255	ESTs. Weakly similar to 138022 hypotheti	1.7
•	105538	AA493453	Hs.247817	H2B histone family, member A	1.7
	135398 115794	M16029 AA424900	Hs.287270	ret proto-oncogene (multiple endocrine	1.7
80	102083	T35901	Hs.112227 Hs.75117	membrane-associated nucleic acid blinding interleukin enhancer binding factor 2. 4	1.7
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.7 1.7
	130868	AB037855	Hs.171917	hypothetical protein FLJ11085	1.7
	110493	A1247707	Hs.36915	ESTs	1.7

		AA252457 Hs.86543	ESTs, Moderately similar to T00256 hypot 1.7
		AW024282 Hs.104938	hypothetical protein MGC15908 1.7
		X78992 Hs.78909	butyrate response factor 2 (EGF-response 1.7
5		BE616731 Hs.80645	Interferon regulatory factor 1 1.7
5		U20582 Hs.2149	actin like protein 1.7
		AI817130 Hs.9195 AI073373 Hs.326923	Homo saplens cDNA FLJ13698 fis, clone PL 1.7
		AL390127 Hs.7104	EST, Weakly similar to 138022 hypothetic 1.7 Kruppel-like factor 13 1.7
		TB1309 Hs.251664	Kruppel-like factor 13 1.7 Insuffin-like growth factor 2 (somatomedi 1.7
10		AA281959 Hs.5210	glia maturation factor, gamma 1.7
		AA742596 Hs.91216	ESTs, Wealthy similar to 2004399A chromos 1.7
		Al125867 Hs.20734	EST6 1.7
	104570	AW978870 Hs.131828	ESTs 1.7
• ~	134752	BE246762 Hs.89499	arachidonate 5-lipoxygenase 1.7
15	130430	WZ7893 Hs.150580	putative translation initiation factor 1.7
	119244	AW407564 Hs.275865	ribosomel protein S18 1.7
	131152	NM_004380 Hs.23598	CREB binding protein (Rubinstein-Taybi s 1.7
	133419	BE242676 Hs.73172	growth factor independent 1 1.7
20		AA339541 Hs.24956	hypothetical protein FLJ22056 1.7
20	116482 132555		Homo sapiens cDNA FLJ12936 fis, clone NT 1.7
	125840	AW500131 Hs.171763 AB028986 Hs.12064	CD22 antigen 1,7 ubiquitin specific protease 22 1,7
	115416		ublquitin specific protease 22 1.7 ESTs 1.7
	120041	AA830882 Hs.59368	ESTs 1.7
25	126295	Al281459 Hs.270114	ESTS 1.7
	122528	AA449804 Hs.292154	strumal cell protein . 1.7
		101110001	The production of the producti
	Table 28:	;	
	Pkey:	Unique Ecs pr	obeset Identifier number
30	CAT num		
	Accessio	n: Genbank acce	ssion numbers
	_		
	Pkey	CAT number	Accession
35	108451	13766_27	AA079195 AA0B4955 AA126308 AA084956
33	124236	46919_1	AF086006 H64722 H65212 H66282
	115982	173_2	W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353
			AW088477 AI887846 AW502824 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA577404 AA831618
	116665	1394292_1	A1124782 AA889402 AA765804 AA765530 AA055698 AA594019 A1267368 AA456946 R93354 AF264624 AW668618 AA601493
40	125165	1852047_1	F04405 BE173130 W45350 W45406
-10	125324	1692163_1	R07785 T85948 T86972
	126053	1601238_1	H64450 H64464
	125499	1562851_1	H10543 R11878
	126127	1205826_1	N95428 W24040 AW751366 H81987
45	125546	356478_1	H09950 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	125761	1744008_1	R68351 R68364
	127155	200358_1	AA284993 AA478122 AA477923
	125957	1583542_1	H41694 H45213
50	125982	1766315_1	R98091 W92898
	127245	226662_1	AA323958 AA370268
	127248	227560_1	AA364195 AA325029 AW962050
	127262	231725_1	AA828125 AA834883 AA330555
55	126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
55	127303	258778_1	AA366951 AA470999 AA469425
	127315	37938_1	AF116622 AI114507 AA840834 AA377999
	126730	297653_1	AA442429 T19477
	103898	187213_3	AA248884
60	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
-	112540	1605263_1	BE011368 BE011362 BE011215 BE011365 BE011363 R69751 R70467 H69771 H80879 H80878
	127705	966283_2	AJ003322 AJ003324
	121335		AA404418 AI217248
•	120734		AA29948 AA299949
65	114620		AA642974 AA084223
• -	122652		AA454641
	123636		AA609263
	100842	tigr_HT4398	U05597
~ ^	116548	genbank_D20433	D20433
70	123783	genbank_AA610112	AA610112
	125032	genbank_T74884	T74884
	123808		AA620552
	102316		U34301
75	102406		U43177
75	134076		AF086215 W02702 AA284288 W25655
	104542		R29657
	113119		T47910
	104799		AA029703
80	127984		F06298 R18057
30	120809 113610		AA346495
		. umumuk 1332/3	T93279·
	113947 101045	genbank_W84768	

	129959	genbank_N57818	
	117031	genbank H88353	
	101447	entrez_M21305	
_	124540	genbank_N63232	
5	124554	genbank N65961	
-	117348	genbank_N24157	
	117357	genbank_N24829	
	124677	genbank_R01073	
	124694	genbank_R06108	
10	103138	entrez X65965	
	103305	entrez_X82279	
	103392		
	103392	entrez_X94563	
	119229	entrez_X95406	
15		genbank_T03229	
IJ	119302	genbank_T25725	
	126825	430458_1	AA100230 AA100274
	105225	genbank_AA211777	
	121292	genbank_AA401807	1
20	112853	genbank_T02843	T02843
20	121387	genbank_AA405854	
	114601	genbank_AA075566	
	100221	entrez_D28383	D28383
	123197	genbank AA489250	AA489250
~-	114740	379876_1	N70103 N70020 AW383189 AI207469 W00935 W00906 AA551569 AI343837 AA135199
25	123331	genbank_AA497013	100 100 100 100 100 100 100 100 100 100
	107794	genbank_AA019255	
	100554	Upr_HT2241	M95923
	123423	genbank_AA598484	
	123474	genbank AA599209	
30	109061	genbank_AA160898	
		\$	

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hernatopoletic Tissues

Table 3A lists about 1346 Genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hernatopoletic tissues. These were selected from 35403 probesets on the Affymethy/Eos Hut01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult hernatopoletic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 65% percentile amongst various ALL samples. The "average" normal adult hernatopoletic tissue was set to the 75% percentile amongst various non-both the numerator and the denominator before the ratio was evaluated.

Piey:

Unique Eos probeset Identifier number

ExAcc:

Examplar Accession number, Genbank accession number

Unigene Dit:

Unique Gene title:

Unique Gene title

Unique Gene title

R1:

Ratio of leukemia to hernatopoletic tissues

40

35

45	Pkey	ExAcon	11-110	distriction	
	129498	AA449789	UnigenelD Hs.75511	Unigene Title	R1
	100458	S74019	Hs.247979	connective tissue growth factor	57.88
	133774	X54079		pre-8 lymphocyle gene 1	49.45
	102564	U59423	Hs.76067	heat shock 27kO protein 1	48.42
50	130650	AB040951	Hs.79067 Hs.284208	MAD (mothers against decapentaplegic, Dr	41.49
	132922	AF249745		DKFZP434N161 protein	35.88
	112254	AA852097	Hs.6066	Rho guanine nucleotide exchange factor	35.74
	106706	AB037810	Hs.25829	ras-related protein	33.28
	101050	AU077324	Hs.18760	KIAA1389 protein	32.39
55	102455	U48705	Hs.1832	nauropeptide Y	30.68
~~	101838	BE243845	Hs.75562	discoldin domain receptor family, member	26.81
	113374	T79925	Hs.75511	connective tissue growth factor	25.46
	134125	NM_014781	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	24.69
	106943	AW888222	Hs.50421	KIAA0203 gene product	24.63
60	130069	AV000222 AI754813	Hs.9973	tensin	23.14
00	119073		Hs.146428	collagen, type V, alpha 1	23.06
	130444	BE245360 M12125	Hs.279477	ESTs	22.53
	100420	M12125 D86983	Hs.300772	tropomyosin 2 (beta)	21.96
	114324	AF084481	Hs.118893	Melanoma associated gene	21.05
65	101400		Hs.26077	Wolfram syndrome 1 (wolframin)	18.95
05	102759	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	18.46
	100893	NM_005100	Hs.788	A kise (PRKA) anchor protein (gravin)	17.88
	131689	BE245294	Hs.180789	S164 protein	16.75
		AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.60
70	106410	AB037787	Hs.26229	neuroligin 2	16.51
70	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8	15.60
	131524	AB040927	Hs.301804	KIAA1494 protein	15.01
	107794	AA019255		gb:ze56e10.s1 Soares reti N2b4HR Homo	14.78
	129213	AJ148494	Hs.109525	ESTs, Weakly stmilar to IRX2, HUMAN IROQU	14.76
75	116068	AA328041	Hs.194329	hypothetical protein FLJ21174	14.24
15	134416	X68264	Hs.211579	melanoma cell adhesion molecule	14.06
	134545	Al902899	Hs.85155	butyrate response factor 1 (EGF-response	14.03
	114009	A1248544	Hs.103000	KIAA0831 protein	13.93
	115110	AK001671	Hs.11387	KIAA1453 protein	13.75
80	130107	AF112977	Hs.172887	phytanoyl-CoA hydroxylase (Refsum diseas	13.60
οU	133558	X66945	Hs.748	fibroblast growth factor receptor 1 (fms	13.60
	100871	T85231	Hs.179661	tubulin, beta 5	13.50
	101462	AL035668	Hs.73853	bone morphogenetic protein 2	13.48
	120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens	13.33
				6 APONT I CHOI INCHIEN HILLING ORDINGIA	13.33

	4500.00				
	123340 103460	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	13.25
	102460	Al021993 U48959	Hs.14331	S100 calcium-binding protein A13	13.25
_	100168	H73444	Hs.211582 Hs.394	myosin, light polypeptide kise adrenomeduttin	13.14
5	115844	Al373062	Hs.332938	hypothetical protein MGC5370	13.09
	130103	Y13492	Hs.149098	Smoothelin	13.00 12.92
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	12.03
	113632	T94907	Hs.188572	ESTs	11,85
10	118951 100305	NM_000448 NM_004941	Hs.73958	recombition activating gene 1	11.73
	109737	AA055415	Hs.171872 Hs.13233	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	11.63
	122577	AA829725	Hs.334437	ESTs, Moderately similar to A47582 B-cel hypothetical protein MGC4248	11.55
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	11.49 11.40
15	132303	BE177330	Hs.325093	Homo saplens cD: FLJ21210 ffs, clone C	11.37
13	103176	AL021154	Hs.76884	inhibitor of D binding 3, domint neg	11.17
	108358 104584	MB1933 AA704538	Hs.1634	cell division cycle 25A	11.15
	106777	AF037261	Hs.193777 Hs.33787	ESTs	11.12
	121054	AW976570	Hs.97387	vinexin beta (SH3-containing adaptor mol ESTs	11.08
20	119400	T92767	1001001	gb:ye27d06.s1 Stratagene kung (937210) H	10.90
	126610	AI911353	Hs.191391	ESTs	10.83 10.83
	134555	U34879	Hs.85279	hydroxysterold (17-beta) dehydrogese 1	10.80
	131555	T47384	Hs.278613	Interferon, alpha-inducible protein 27	10.79
25	130979 113783	NM_012446 AL359588	Hs.169833	single-stranded-D-binding protein	10.70
	123503	AW975051	Hs.7041 Hs.293156	hypothetical protein DKFZp762B226	10.65
	117031	H88353	115.253150	ESTs, Weakly similar to 178885 serine/th	10.60
	100752	T81309	Hs.251664	gb:yw21s02.s1 Morton Fetal Cochlea Horno insufin-like growth factor 2 (somatomedi	10.45
20	102618	AL037672	Hs.81071	extraceBular matrix protein 1	10.44 10.36
30	113089	T40707	Hs.270862	ESTs	10.33
	132089	W22007	Hs.39122	hypothetical protein MGC15737	10.29
	101663 104876	NM_003528	Hs.2178	H2B histone family, member Q	10.23
	106370	Al933128 AF039843	Hs.25220	ike-glycosyltransferase	10.23
35	129406	AB018255	Hs.18676 Hs.111138	sprouty (Orosophila) homolog 2	10.18
	115354	AA281636	Hs.334827	KIAA0712 gene product ESTs	10.18
	123077	AA485229	Hs.105649	ESTs	10.13 10.05
	131273	AW206008	Hs.283378	Homo sapiens cD: FLJ21778 fis, clone H	9.95
40	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	9.83
40	133699 110855	BE501689	Hs.75617	collagen, type IV, alpha 2	9.80
	111826	AB007928 R35975	Hs.28169	KIAA0459 protein	9.65
	126947	Z40778	Hs.191837	gb:yh91b07.s1 Soares placenta Nb2HP Homo ESTs	9.58
	116674	AI768015	Hs.92127	ESTs	9.50
45	129087	Al348027	Hs.108557	hypothetical protein PP1057	9.48 9.46
	114837	BE244930	Hs.166895	ESTs	9.45
	120009	Al080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	9.45
	112483 103487	AW989785	Hs.285885	Homo sapiens cD FLJ11321 fis, clone PL	9.40
50	105675	AA743603 AL390083	Hs.172108	nucleoporin 88kD	9.30
• •	129158	NM_004413	Hs.271277 Hs.109	hypothetical protein from EUROIMAGE 3636 dipeptidase 1 (rel)	9.28
	114394	T34462	Hs.103291	nemin .	9.23
	133331	Y14487	Hs.738	ribosomal protein L14	9.17 9.11
55	114787	AA156509	Hs.231892	ESTs, Wealdy similar to S65657 alpha-1C-	9.10
75	125502 132325	AW977181	Hs.194718	zinc finger protein 265	9.03
	127968	N37085 AA830201	Hs.44856	hypothetical protein FLJ12116	9.01
	114605	AL157423	Hs.124347 Hs.306478	ESTs Homo sapiens mR; cD DKFZo76100511 (f	9.00
~	114875	AA235609	Hs.236443	Homo saplans mR; cD OKFZp564N1063 (i	8.93
60	129898	AI672731	Hs.13256	ESTs	8.93 8.89
	108283	W21493	Hs.28329	hypothetical protein FLJ14005	8.89
	117130 105553	AA748850	Hs.125830	bladder cancer overexpressed protein	8.88
	103657	AA256756 273677	Hs.31178	ESTS	8.85
65	105831	AA329449	Hs.247302	gb:H.sapiens gene encoding plakophilin 1	8.83
	106375	AW872878	Hs.289072	twisted gastrulation hypothetical protein FLJ22175	8.82
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	8.80 8.75
	123433	AW450922	Hs.112478	ESTe	8.67
70	134558	NM_001773	Hs.85289	CD34 antigen	8.67
70	115893 128621	Al652127 AA032197	Hs.48419	EST8	8.67
	122798	AW366286	Hs.102558	Homo sapiens, clone MGC:5352, mR, comp	8.60
	112554	R71489	Hs.145696 Hs.29198	splicing factor (CC1.3) EST	8.58
75	129989	N57818	110120100	gb:yv59d07.s1 Soares fetal liver spieen	8.55
75	131558	AA453208	Hs.28726	RAB9, member RAS oncogene family	8.53 8.45
	134027	Z97630	Hs.226117	H1 histone family, member 0	8.45 8.45
	134138	AB023169	Hs.7935	KIAA0952 protein	8.43
	120030 101005	AI076355	Hs.58694	ESTs	8.43
80	115423	NM_005239 AI499516	Hs.85146	v-ets avian erythrobiastosis virus E26 o	8.33
•	104948	AW242407	Hs.89303 Hs.73848	ESTs carcinoembryonic antigen-related cell ad	8.33
	131965	W79283	Hs.35962	ESTs	8.30 9.30
	126426	AA125984		gb:zn27h06.rl Stratagene neuroepithelium	8.30 8.28
				^^	u.e.

	480000	*******			
	108886 107985	AW248434	Hs.91521	hypothetical protein	8.26
	114239	T40064 AL137667	Hs.71968	Homo sapiens mR; cD DKFZp564F053 (fr	8.25
	124281	A1333756	Hs.267445 Hs.111801	Homo seplens mR; cD DKFZp434B231 (fr	8.23
5	117099	H93699	F13.111001	arsete resistance protein AR\$2	8.23
	119432	AL120247	Hs.40109	gb:;v16a11.s1 Soares fetzi liver spieen KIAA0872 protein	8.20
	115967	AI745379	Hs.42911	ESTS	8.15
	132355	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	8.15 8.13
10	108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.10
10	131694	NM_000246	Hs.3076	MHC class II transactivator	8.05
	104897 120266	N33937	Hs.10336	ESTs	8.03
	130404	A1807264 A1672727	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	8.03
	115729	AA417812	Hs.76753 Hs.38775	endoglin (Osler-Rendu-Weber syndrome 1)	8.00
15	127216	AI798703	Hs.143702	ESTS	8.00
	131693	AW983776	Hs.110796	ESTs, Wealdy similar to S70029 probable SAR1 protein	7.95
	113107	AI821027	Hs.8429	ESTs	7.93
	122282	BE246331	Hs.98401	Homo sapiens mR full length insert cON	7.90 7.90
20	111040	Al435502	Hs.14931	ESTs	7.90
20	127987 125317	Al022103	Hs.124511	ESTs	7.90
	105242	Z99348 Al564857	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	7.88
	100421	D86985	Hs.27888 Hs.79276	ESTs, Weakly similar to serine/threonine	7.75
	114359	NM_016929	Hs.283021	KIAA0232 gene product chloride Intracellular channel 5	7.71
25	119772	AJ250839	Hs.58241	gene for serine/fireonine protein kise	7.70
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.70 7.65
	134361	BE549343	Hs.82208	acyl-Coenzyme A dehydrogese, very long	7.57
	105476	AL117352	Hs.120828	Human D sequence from clone RP5-876B10	7.55
30	113289 122707	T66900	Hs.188446	ESTs	7.50
	130055	NM_002039 AJ568248	Hs.239706	GRB2-associated binding protein 1	7.50
	108766	AF145713	Hs.146355 Hs.61490	v-abl Abelson murine leukemia viral onco	7.49
	107957	Z36842	Hs.57548	schwannomin-interacting protein 1 ESTs	7.45
26	123116	AW190412	Hs.183738	FERM, RhoGEF (ARHGEF) and pleckstrin dom	7.45
35	123190	AA489212	Hs.105228	EST	7.38 7.38
	129574	AA026815	Hs.11463	UMP-CMP kise	7.38
	115274	C01566	Hs.86671	ESTs	7.35
	102571 116845	U60115 AA649530	Hs.239069	four and a half LIM domains 1	7.34
40	134851	AB011124	Hs.90232	gb:ns44f05.81 NCI_CGAP_Alv1 Homo septens	7.33
	101780	M82882	Hs.154365	KIAA0552 gene product	7.33
	125042	T78906	Hs.269432	E74-like factor 1 (ets domain transcript ESTs. Moderately similar to ALU1_HUMAN A	7.28
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	7.28
45	108700	AA121518	Hs.193540	ESTs. Moderately similar to 2109260A B c	7.25 7.23
43	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	7.20
	1 <i>2</i> 7692 128501	Al021912	Hs.187983	ESTs	7.18
	107727	AL133572 AA149707	Hs.199009	protein containing CXXC domain 2	7.18
	118089	AI762507	Hs.173091 Hs.47878	ubiquitin-like 3 ESTs	7.14
50	106025	AV653785	Hs.173334		7.12
	122111	AW593206	Hs.98785	ELL-RELATED R POLYMERASE II, ELONGATIO Ksp37 protein	7.10
	119674	W60379	Hs.57773	ESTs	7,08 7.05
	126607	W87425	Hs.114688	ESTs	7.05
55	121545 113287	AA412442 T66847	Hs.98132	ESTs	7.05
55	126672	AA255592	Hs.194040	ESTs. Wealty similar to I38022 hypotheti	7.03
	132087	H14486	Hs.203631 Hs.3903	ESTs. Weakly similar to altertively sp	7.00
	118697	N22706	Hs.43234	Cdc42 effector protein 4; binder of Rho ESTs	6.97
60	100295	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	6.97
60	101188	L20320	Hs.184298	cyclin-dependent kise 7 (homolog of Xe	6.95 6.95
	121481 113003	AA411931		gb:zu03g05.s1 Soares_testis_NHT Homo sap	6.95
	101851	AW292315 BE260964	Hs.7215	ESTs	6.93
	113529	AJ190741	Hs.82045 Hs.177415	middine (neurite growth-promoting factor	6.91
65	132887	AA195831	Hs.273385	Finkel-Biskis-Rellly murine sarcoma viru	6.90
	113560	T91015	Hs.268626	guanine nucleotide binding protein (G pr ESTs	6.90
	123440	AI733692	Hs.112488	ESTs	6.85
	130390	AA490770	Hs.182382	ESTs	6.83 6.83
70	133889	U48959	Hs.211582	myosin, light polypeptide kise	6.83
70	113573	R89379	Hs.15990	ESTs	6.80
	112453 125221	R63899 AA236115	Hs.28455	ESTs	6.78
	134081	AL034349	Hs.120785 Hs.79005	ESTs	6.78
75	127610	AA960867	Hs.150271	protein tyrosine phosphalese, receptor t	6.77
75	105486	AW449258	Hs.6187	ESTs, Highly similar to unmed protein ESTs	6.75
	107796	AA058848	Hs.60797	ESTs	6.75
	132754	AJ752244	Hs.75309	eukaryotic translation elongation factor	6.71 6.71
	105806	AF206019	Hs.110347	REV1 (yeast homolog)- like	6.70
80	110837 117698	H03109 N82293	Hs.108920	HT018 protein	6.65
	128994	N52293 AF205849	Hs.45107	ESTs	6.65
	129131	AB026436	Hs.107740 Hs.177534	Kruppel-like factor 2 (lung)	6.65
	108528	AA650558	Hs.325202	dual specificity phosphatase 10 ESTs, Highly straigt to GBAS_HUMAN GUANI	6.65
					6.62

	131009	AF169802	Hs.22142	e-deal-man hE majurano hET D	
	129389	NM_012445	Hs.288126	cytochrome b5 reductase b5R.2 spondin 2, extracellular matrix protein	6.61 6.60
	125278	AJ218439	Hs.129998	enhancer of polycomb 1	6.59
_	124667	W24320	Hs.102941	Homo sepiens cD: FLJ21531 fis, clone C	6.59
5	105640	AA001021	Hs.6685	thyroid hormone receptor interactor 8	6.58
	106474 105808	BE383668	Hs.42484	hypothetical protein FLJ 10618	6.58
	120087	AI133161 AF186780	Hs.286131 Hs.79219	CGI-101 protein	6.53
	100514	AU076887	Hs.28491	RalGDS-like gene; KIAA0959 protein spermidine/spermine N1-acety/trans/erase	6.52
10	108378	A1368460	Hs.74615	platelet-derived growth factor receptor.	6.50 6.50
	133350	A1499220	Hs.71573	hypothetical protein FLJ 10074	6.50
	115673	AA406341	Hs.269908	Homo saplens cD FLJ11991 fis, clone HE	6.48
	133410	Y07847	Hs.73088	RAS-related on chromsome 22	6.48
15	131281 105510	AA251716 Z42047	Hs.25227	ESTs	6.46
10	128766	AW160432	Hs.283978 Hs.296460	Homo sapiens PRO2751 mR, complete cds crantofacial development protein 1	6.45
	114530	AA60103B	Hs.191797	ESTs, Weakly similar to S65657 alpha-1C-	6.45 6.43
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	6.40
20	120593	AA748355	Hs.193522	ESTs	6.40
20	125832	AA628600	Hs.117587	ESTs	6.38
	129637 115302	NM_004606 AL109719	Hs.1179	TATA box binding protein (TBP)-associate	6.38
	126137	AA312594	Hs.47578 Hs.99115	ESTs	6.33
	114465	BE621056	Hs.131731	hypothetical protein FLJ 20689 hypothetical protein FLJ 11099	6.30 6.29
25	125562	A1494372	Hs.98968	hypothetical protein FL123058	6.29
	127380	AF070554	Hs.15535	Homo sapiens clone 24582 mR sequence	6.26
	106956	R06428	Hs.226351	ESTs	6.25
	105962 109416	AW880358 BE268388	Hs.339808	hypothetical protein FLJ 10120	6.25
30	111116	AK002039	Hs.86945 Hs.26243	ESTs, Weakly similar to A45010 X-linked	. 6.23
	127282	AA347158	Hs.185780	Hamo sepiens cD FLJ11177 fis, done PL ESTs	6.23 6.23
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	6.21
	101664	AA436989	Hs.121017	H2A histone family, member A	6.20
35	103317	X83441	Hs.166091	ligase IV, D, ATP-dependent	6.20
33	133894 109260	AW021236 AW976515	Hs.180433	rTS beta protein	6.19
	112772	A1992283	Hs.131915 Hs.35437	KIAA0863 protein	6.18
	132050	Al267615	Hs.38022	ESTs, Moderately similar to 138026 MLN 6 ESTs	6.18
40	113009	T23699	Hs.7246	ESTs	6.18 6.17
40	118835	AA535246	Hs.50852	ESTs	6.16
	125626	A1038854	Hs.180789	\$164 protein	6.15
	117086 101960	AA581602 AL036287	Hs.41840	ESTs	6.14
	104488	N58191	Hs.194662 Hs.106511	caiponin 3, ecidic protocadherin 17	6.13
45	127695	AA714731	Hs.291457	ESTs, Wealdy similar to heterogeneous ri	6.13
	127894	AL121053	Hs.5534	Homo sapiens co FLJ12961 fis, clone NT	6.13 6.13
	113595	T92056	Hs.290240	ESTs, Moderately similar to ALU2_HUMAN A	6.10
	120784	AW752101	Hs.16580	hypothetical protein FLJ11026	6.10
50	115004 129740	AA329340 BE165866	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	6.08
50	117483	N72185	Hs.83623 Hs.44189	nuclear receptor subfamily 1, group I, m	6.05
	103815	BE245294	Hs.180789	ESTs S164 protein	6.04
	122040	AA847758	Hs.111030	ESTs	6.03 6.03
55	109638	AW977747	Hs.119120	E3 ubiquitin ligase SMURF1	6.02
55	112727	T91029	Hs.15069	ESTs	6.01
	120273 122127	AA176688	Hs.269284	ESTs	6.00
	126046	AW207175 AA8049 5 7	Hs.106771 Hs.119840	ESTs ESTs	6.00
	119774	AB032977	Hs.6298	KIAA1151 protein	5.99
60	106265	AA412176	Hs.236463	Homo sapiens mR; cD DKFZp586I0521 (I	5.98 5.98
	111987	NM_015310	Hs.6763	KIAA0942 protein	5.98
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sepiens	5.96
	128122 128473	Al267491	Hs.160593	ESTs	5.95
65	102283	178277 AW161552	Hs.100293	O-linked N-acetylgtucosamine (Gicc) tr	5.95
••	122468	AA448172	Hs.83381 Hs.137687	guarine nucleotide binding protein 11 ESTs, Highly similar to K6B1_HUMAN RIBOS	5.94
	101801	M88407	Hs.1216	actinin, sipha 3	5.93 5.93
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) hornolog (E coli Re	5.92
70	108908	AA136569	Hs.10848	KIAA0187 gene product	5.90
70	121470	AA558958	Hs.324751	ESTs	5.90
	131938 109613	AF176085 H47315	Hs.34956	neural polypyrimidine tract binding prot	5.89
	109384	AA219172	Hs.27519 Hs.86849	ESTs ESTs	5.89
	118559	N68456	Hs.49519	ESTs	5.88
75	102010	U02687	Hs.385	fms-related tyrosine kise 3	5.88 5.86
	105921	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	5.85
	124298	H91679		gb:yv04s07.s1 Soares fetal liver spieen	5.85
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.84
80	103331 135052	A1825463 AL136653	Hs.147996	protein kise, X-linked	5.82
	115219	AA262778	Hs.93675 Hs.269314	decidual protein induced by progesterone Homo sapiens cD FLJ14123 fis, clone MA	5.80
	121899	R55341	Hs.50421	KIAA0203 gene product	5.78 6.70
	135217	AA453880	Hs.9658	hypothetical protein FLJ11790	5.78 5.77
				* *****	W. 1

	123973	C14805		t assumer day a site of the control	
	112605	R79374	Hs.29852	gb:C14805 Clontech human aorta polyA+ mR ESTs	5.77
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.76 5. 75
_	129889	AA810932	Hs.131899	ESTs, Weakly similar to T00370 hypotheti	5.75
5	102638	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	5.73
	121501 124921	AA470687	Hs.104772	ESTs	5.73
	109850	R93082 A1150548	Hs.332635 Hs.23155	ESTs ESTs	5.70
	120594	AW136478	Hs.5094	ring finger protein 10	5.70 5.70
10	126433	AA325606	T-0-12-0-1	gb:EST28707 Cerebellum II Horno sapiens c	5.70
	100455	AW888941	Hs.75789	N-myc downstream regulated	5.69
	106565	NM_014892	Hs.227602	KIAA1116 protein	5.68
	120912 127209	AA376690 AA305023	Hs.187650	ESTs	5.68
15	107606	AF207989	Hs.81964 Hs.330425	SEC24 (S. cerevisiae) related gene famil Homo septens, Similar to G protein-coupt	5.68
	106597	AI091277	Hs.302634	frizzled (Orosophila) homolog 8	5.67 5.66
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	5.65
	100064			AFFX control - TrpnX-3	5.63
20	108758 101392	AA127395	Hs.222414	ESTs	5.63
20	102211	NM_002507 BE314524	Hs.1827 Hs.78776	nerve growth factor receptor (TNFR super	5.61
	107427	W26975	Hs.46736	putetive transmembrane protein hypothetical protein FLJ23476	5.60 5.60
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	5.60
25	111764	AI420368	Hs.290259	ESTs, Weakly similar to 138022 hypotheti	5.58
25	119405	T93865	Hs.91085	ESTs	5.58
	126464 133865	Al990046 AB011155	Hs.54780 Hs.170290	transcription termition factor, R po	5.58
	123255	AA830335	Hs.105273	discs, large (Drosophila) homolog 5 ESTs	5.58 5.57
20	122861	AA335721	Hs.119394	ESTs	5.56
30	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	5.55
	132906	BE613337	Hs.234896	geminin	5.55
	109001 115816	AI056548 BE042915	Hs.72116 Hs.287588	hypothetical protein FLJ20992 similar to	5.55
	128401	R01865	Hs.268586	Homo sapiens cD FLJ13676 fis, clone PL ESTs	5.55
35	129298	AI051967	Hs.110122	ESTs	5.53 5.53
	120314	T10013	Hs.221040	HBS1 (S. cerevisiae)-like	5.51
	132815	AJ815189	Hs.57475	sex comb on midleg homolog 1	5.50
	113983 105002	W87415 - AA224244	Hs.55296 Hs.182704	HLA-B associated transcript-1	5.50
40	132025	AA011117	Hs.3745	ESTs, Moderately similar to altertivel milk fat globule-EGF factor 8 protein	5.49 5.49
	110732	AW070838	Hs.174174	KIAA0601 protein	5.49 5.48
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	5.48
	126758 129426	AI559444	Hs.293960	ESTs	5.48
45	103217	AF077953 NM_001841	Hs.111323 Hs.73037	Protein inhibitor of activated STAT X	5.47
	132261	U80743	Hs.306094	canbinoid receptor 2 (macrophage) trinuclectide repeat containing 12	5.48 5.45
	105586	AA865118	Hs.191538	ESTs	5.43
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-lin	5.43
50	113063 134092	W15573 AA218558	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	5.43
90	119316	A)114630	Hs.7905 Hs.208334	sorting nexin 9 Homo saptens cD: FLJ21874 fis, clone H	5.41
	108019	AI017773	Hs.249159	adrenergic, alpha-2A-, receptor	5.38 5.38
	109421	AW604652	Hs.332442	ESTS	5.38
55	111929	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
23	119718 106154	W69216 BE540255	Hs.92848	ESTs	5.38
	108544	W39433	Hs.6994 Hs.23971	Homo saplens cD: FLJ22044 fis, clone H hypothetical protein DKFZp547N043	5.35 5.35
	119580	AL079310	Hs.92260	high-mobility group protein 2-like 1	5.35 5.35
60	126777	AL157491	Hs.145211	Homo saplens mR; cD DKFZp434K1111 (f	5.35
OO	112944	H18083	Hs.13254	ESTs	5.34
	103149 132437	NM_006201 AA152106	Hs.171834 Hs.4859	PCTAIRE protein kise 1	5.34
	103860	AW976877	Hs.38057	cyclin L ania-6a ESTs	5.33 5.33
~-	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member 8 (zinc fi	5.33
65	129914	NM_012421	Hs.13321	rearranged L-myc fusion sequence	5.33
	130309	AF067804	Hs.15423	hypothetical protein HDCMC04P	5.31
	116312 124191	BE379794 T96509	Hs.65403 Hs.248549	hypothetical protein	5.30
	125583	AA195667	Hs.86022	ESTs, Moderately similar to S65657 alpha ESTs	5.28 5.28
70	130591	N59646	Hs.169745	crumbs (Orosophila) homotog 1	5.28
	116355	AA789133	Hs.88650	ESTs	5.26
	115553	AJ275988	Hs.71414	transcription factor (SMIF gene)	5.26
	122802 128495	A1687303 NM_005904	Hs.285529 Hs.100602	G protein-coupled receptor 49	5.25
75	117667	U59305	Hs.44708	MAD (mothers against decapenteplegic, Dr Ser-Thr protein kise related to the my	5.24
	127890	AA294934	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	5.23 5.22
	134843	AA428520	Hs.90061	progesterone binding protein	5.21
	120958	AA528283	Hs.292737	ESTs	5.21
80	102076 100934	BE299197 J03019	Hs.179665 He 00013	cyclin-dependent kise Inhibitor 1A (p2	5,20
- •	112667	BE538516	Hs.99913 Hs.1 542 3	adrenergic, beta-1-, receptor hypothetical protein HDCMC04P	5.20 6.20
	119304	AW249266	Hs.98493	X-ray repair complementing defective rep	5.20 5.20
	131868	AW408296	Hs.33532	zinc finger protein 151 (pHZ-67)	5.20
				102	
				102	

	105914	AW245680	N. ozna		
	102258	NM_001546	Hs.9701 Hs.34853	growth arrest and O-damage-inducible,	5.18
	103850	AA187101	Hs.213194	inhibitor of D binding 4, domint neg hypothetical protein MGC10895	5.18 5.18
_	112516	T83909		gb:yd67/10.r1 Soares fetal liver spieen	5.18
5	133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homoto	5.18
	135180 135309	D90070 Al564123	Hs.96 Hs.42500	phorbol-12-myristate-13-acetate-induced	5.18
	134801	S76825	Hs.89595	ADP-ribosylation factor-like 5 insulin receptor	5.18
10	133362	AK001519	Hs.7194	CGI-74 protein	5.17 5.17
10	135206	AB024703	Hs.98334	ring finger protein 11	5.15
	111480	R06453	Hs.19706	ESTs	5.15
	118466 125757	N66741 Al274908	Hs.166835	gb:yz33g08.s1 Morton Fetal Cochlea Homo	5.15
	127140	AI273507	Hs.303966	ESTs, Highly similar to 1814460A p53-ass ESTs	5.15
15	109223	AW000714	Hs.65818	ESTs	5.15 5.14
	103656	273497	Hs.247802	Human D sequence from clone U240C2 on	5.14
	133388 100511	AW245631	Hs.182447	heterogeneous nuclear ribonucleoprotein	5.12
	101941	M76676 S77583	Hs.116840	ESTs	5.10
20	109937	AI084066	Hs.20072	gb:HERVK10/HUMMTV reverse transcriptase myosin regulatory light chain interactin	5.10
	122996	Al436216	Hs.191715	ESTs, Weakly similar to ZN91_HUMAN ZINC	5.10 5.10
	128242	AA992626	Hs.269755	ESTs, Moderately similar to ALUS HUMAN A	5.10
	112374	NM_016323	Hs.26663	cyclin-E binding protein 1	5.10
25	124506 104216	BE273688 AB002313	Hs.182447 Hs.3989	helerogeneous nuclear ribonucleoprotein	5.10
	135051	AI272141	Hs.83484	plexin B2 SRY (sex determining region Y)-box 4	5.09
	131629	Z45794	Hs.238809	ESTs	5.08 5.08
	111722	R23924	Hs.23596	EST	5.07
30	107034 110243	AF257770	Hs.20930	poly(rC)-binding protein 4	5.06
50	125837	H26683 AW968123	Hs.333513	gb:yl14g03.s1 Soares breast 2NbHBst Homo	5.05
	130300	X58288	Hs.154151	small inducible cytokine subfamily E., me protein tyrosine phosphatase, receptor t	5.05 5.05
	103967	AL120051	Hs.144700	ephrin-B1	5.04
35	112678	AI418466	Hs.33665	ESTs	5.03
33	124963 131379	F06600 AK001123	Hs.101375	Homo sapiens mR; cD DKFZp434H205 (fr	5.03
	109451	N32264	Hs.26176 Hs.44330	hypothelical protein FLJ10261 ESTs	5.03
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	5.02 5.02
40	131038	W87778	Hs.169388	hypothetical protein DKFZp761H2024	5.01
40	101208	L25081	Hs.179735	ras homolog gene family, member C	5.01
	104973 103141	NM_015310 X66113	Hs.6763	KIAA0942 protein	4.99
	111260	AB033035	Hs.75584 Hs.51965	polymyositis/scleroderma autoantigen 2 (KIAA1209 protein	4.98
4.0	128142	T67162	Hs.135127	ESTs. Wealdy similar to unmed protein	4.98 4.98
45	113857	AW243158	Hs.5297	DKFZP564A2416 protein	4.95
	105292 114341	AF128542	Hs.166846	polymerase (D directed), epsilon	4.96
	100615	AF270491 W32474	Hs.28249 Hs.301746	hepatocellular carcinoma-associated anti	4.95
	103208	AW411340	Hs.31314	RAP2A, member of RAS oncogene family retinoblastoma-binding protein 7	4.95
50	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.95 4.95
	125321	T86652	Hs.178294	ESTs	4.95
	101145 100551	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	4.95
	126182	M73980 AA721331	Hs.129053 Hs.293771	Homo sapiens NOTCH 1 (N1) mR, complete ESTs	4.93
55	127925	AA805151	Hs.3628	mitogen-activated protein kise kise	4.93 4.93
	133969	AA669112	Hs.78	GA-binding protein transcription factor,	4.93
	120873	AA358015		gb:EST66864 Fetal lung III Homo sapiens	4.92
	125219 102790	AI804331 BE245277	Hs.99423	ATP-dependent R helicase	4.91
60	129486	NM_005754	Hs.154196 Hs.220689	E4F transcription factor 1	4.90
	130381	L47345	Hs.155202	Ras-GTPase-activating protein SH3-domain transcription elongation factor B (SIII)	4.90 4.89
	132389	AA310393	Hs.190044	ESTs	4.88
	100260	D38491	Hs.322478	KIAA0117 protein	4.88
65	109585 111603	N59650 R11529	Hs.27252	EST8	4.88
00	120514	AA258335	Hs.20634	EST gb:zr59b02.s1 Soæres_NhHMPu_S1 Homo sapi	4.88
	130314	NM_014874	Hs.154332	KIAA0212 gene product	4.88 4.86
	108958	AF142482	Hs.203846	TEA domain family member 3	4.86
70	126603	W86610	Hs.185738	ESTs	4.85
/0	100406 116238	Al962060 AV660717	Hs.118397	AE-binding protein 1	4.85
	105288	N99673	Hs.47144 Hs.3585	DKFZP586N0819 protein ESTs, Wealdy similar to AF126743 1 DJ	4.84
	118753	AA346206	Hs.50471	ESTs, Weakly similar to T14267 Xin prote	4.83 4.82
75	113070	AB032977	Hs.6298	KIAA1151 protein	4.81
13	107908	AF087999	Hs.42826	ESTs	4.80
	119678 100415	A1658666 D86970	Hs.6106 Hs.75822	R binding motif protein 4	4.80
	128360	F12374	LI2-1 0055	TGFB1-induced anti-apoptotic factor 1 gb:HSC39B101 normalized infant brain cDN	4.79
٥٨	133101	AK000299	Hs.180952	dyctin 4 (p62)	4.78 4.78
80	103507	AJ000512	Hs.295323	serum/glucocorticold regulated kise	4.78
	107666 108030	AA010611 Al378523	Hs.60418	EST	4.78
	131479	D86181	Hs.62011 Hs.273	ESTs	4.78
			110.613	galactosylceramidase (Krabbe disease)	4.78
				· 103	

	133140	AF180581	Hs.6582	Rho guanine exchange factor (GEF) 12	4.78
	134654	AK001741	Hs.8739	hypothetical protein FLJ 10879	4.78
	106288	AB037742	Hs.24336	KIAA1321 protein	4.76
5	101524	NM_000448	Hs.73958	recombition activating gene 1	4.75
,	113095 114924	AA828380	Hs.126733	ESTs	4.75
	127543	A1338053 AK000787	Hs.87329	HSPC072 protein	4.75
	115866	AW062629	Hs.157392 Hs.52081	Homo sepiens cD FLJ20780 fis, clone CO	4.75
	101382	AU076772	Hs.1279	KIAA0867 protein complement component 1, r subcomponent	4.75
10	126509	R47400	Hs.23850	ESTs	4.74 4.74
	127930	AA809572	Hs.123304	ESTa	4.73
	127824	AI911516	Hs.127811	ESTs	4.73
	110049	H12449	Hs.31159	EST, Weakly similar to ALUB_HUMAN IIII A	4.73
15	127115	H77859	Hs.65450	reticulon 4	4.73
13	104727	N81203	Hs.20047	zinc finger protein, subfamily 2A (FYVE	4.72
	127532 127304	AJ003429 AI741577	H- noorn	gb:AJ003429 Selected chromosome 21 cD	4.71
	105409	AW505076	Hs.99962 Hs.301855	proteoglycan 2, bone marrow (tural kil	4.70
	114969	AW162998	Hs.24684	DiGeorge syndrome critical region gene 8 KIAA1376 protein	4.70
20	115125	AA193588	Hs.85888	ESTs	4.70
	118348	AW408586	Hs.91052	ESTs, Moderately similar to ALUS_HUMAN A	4.70 4.70
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	4.70
	130881	AA809875	Hs.25933	ESTs	4.70
25	132074	AA478486	Hs.3852	KIAA0368 protein	4.70
23	106897	AF039023	Hs.167496	RAN binding protein 6	4.69
	131121 116046	AA120865 BE395293	Hs.23136	ESTs	4.69
	112868	AW388359	Hs.94491 Hs.10667	hypothetical protein FLJ20297	4.68
	116877	AA70895B	Hs.168732	ESTs ESTs	4.68
30	131241	BE501914	Hs.24654	Homo sapiens cD FLJ11640 fis, clone HE	· 4.68
	132027	AF151020	Hs.181444	hypothetical protein	4.68 4.68
	133323	BE336654	Hs.70937	H3 histone family, member A	4.68
	114269	AA176769	Hs.23450	mitochondrial ribosomal protein S25	4.67
35	122713	AI089443	Hs.99436	ESTs	4.67
22	133571	BE515037	Hs.177556	melanoma entigen, family D, 1	4.66
	134453 115510	AJ272141 BE299339	Hs.83484	SRY (sex determining region Y)-box 4	4.66
	115322	L08895	Hs.72249 Hs.78995	three-POZ containing protein similar to	4.66
	129315	NM 014563	Hs.174038	MADS box transcription enhancer factor 2 spondyloepiphyseal dysplasia, tate	4.66
40	104674	Al935962	Hs.26289	ESTs	4.65 4.65
	106276	AA625947	Hs.25750	ESTs	4.65
	108216	AA524743	Hs.44883	ESTs	4.65
	120376	AA227469		gb:zr18a07.s1 Stratagene NT2 neurol pr	4.65
45	121743	AA397636		gb:zi79e09.r1 Soares_testis_NHT Homo sap	4.65
43	128011 123454	Al347067	Hs.124636	ESTs	4.65
	103409	AA868510 NM_004454	Hs.112496	ESTs	4.64
	120484	AA253170	Hs.43697 Hs.96473	ets variant gene 5 (ets-related molecule EST	4.64
	127046	AA321948	Hs.293968	ESTs	4.63
50	133184	AA001021	Hs.6685	thyroid hormone receptor interactor 8	4.63 4.63
	123184	BE247767	Hs.18166	KIAA0870 protein	4.62
	106627	AK000708	Hs.15125	hypothetical protein FLJ20699	4.61
	115475	AB033085	Hs.40193	hypothetical protein KIAA1259	4.61
55	119468 133662	AI911535	Hs.6657	hypothetical protein bK1048E9.5	4.59
55	113941	BE409053 AA531016	Hs.299629 Hs.22399	peroxisomal long-chain acyl-coA thioeste	4.58
	131590	R46277	Hs.250638	hypothetical protein FLJ14924	4.58
	128795	AA531287	Hs.105805	Homo saplens mR full length Insert cDN ESTs	4.58
	116480	C14088	Hs.169476	glyceraldehyde-3-phosphate dehydrogese	4.58 4.58
60	111713	C75253	Hs.220950	ESTs	4.58
	113721	AF143885	Hs.18190	EST	4.57
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	102009 135242	8E245149	Hs.82643	protein tyrosine kise 9	4.55
65	127580	AI583187 BE548749	Hs.9700	cyclin E1	4.55
•••	109785	AB011131	Hs.148016 Hs.12376	ESTs piccolo (presyptic cytomatrix protein)	4.55
	109700	F09809	15.12570	gb:HSC33H092 normalized infant brain cDN	4.53
	124882	AI698652	Hs.101539	ESTs	4.53 4.53
70	131765	AW381270	Hs.194110	hypothetical protein PRO2730	4.53 4.53
70	115684	NM_006577	Hs.284284	ESTs, Highly similar to bela-1,3-N-acety	4.52
	102034	AJ903474	Hs.230	fibromodulin	4.52
	109776 111650	R43665	Hs.12257	ESTs	4.50
	132993	R16722 AB023154	Hs.124248	ESTs	4.50
75	129017	AB023154 AA115333	Hs.62264 Hs.107968	KIAA0937 protein	4.49
. •	132902	A1936442	Hs.59838	ESTs hypothetical protein FLJ10808	4.49
	114814	AB006622	Hs.182536	KIAA0284 protein	4.48
	120839	AA348913		gb:EST55442 Infant adrel gland II Homo	4.48 4.48
00	101434	AV650068	Hs.1430	coagulation factor XI (plasma thrombopla	4.48 4.48
80	102018	U03398	Hs.1524	tumor necrosis factor (figand) superfami	4.48
	104619	AA001635	Hs.287414	transcriptiol Intermediary factor 1 ga	4.48
	105716 126020	AA931198	Hs.238928	HT002 protein; hypertension-related calc	4.48
	120020	H79863	Hs.114243	ESTs	4.48

	119899	Al057404	Hs.58698	EŞTs	4.47
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated turn	4.48
	125695	W22529	Hs.30942	ephrin-B2	4.46
5	105715 117169	BE621800	Hs.29444	putative small membrane protein NID67	4.45
,	102757	R87866 AW955454	Hs.95120 Hs.30942	ESTs, Weakly similar to HZHU hemoglobin	4.45
	120637	AA811804	118.30342	ephrin-B2 gb:bb39a05.s1 NCI_CGAP_GCB1 Homo saplens	4.45 4.45
	131579	N62922	Hs.29088	ESTs	4.45 4.45
	135287	U82670	Hs.9786	zinc linger protein 275	4.45
10	112540	R69751		gb:yi40a10.s1 Scares placenta Nb2HP Homo	4.45
	125724	AL360190	Hs.295978	Homo sepiens mR full length Insert cDN	4.44
	115498	AA291070		gb:zs46a08.s1 NCL_CGAP_GCB1 Homo sapiens	4.43
	102263	U29171	Hs.75852	casein kise 1, delta	4.43
16	124312	H94647	Hs.102329	ESTs	4.43
15	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mR sequence	4.43
	115955	AF283813	Hs.44198	Intracellular membrane-associated calciu	4.43
	103562 100169	NM_002702	Hs.2815	POU domain, class 6, transcription facto	4.42
	108928	AL037228 AA143802	Hs.82043 Hs.71781	D123 gene product	4.40
20	125908	AF265555	Hs.250646	ESTs baculoviral IAP repeat-containing 6	4.40
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.40 4.40
	129512	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.40
	134570	U66815	Hs.172280	SW/SNF related, matrix associated, acti	4.40
	135073	W55956	Hs.94030	Homo sapiens mR; cD DKFZp586E1624 (f	4.40
25	105011	BE091926	Hs.16244	mitotic spindle colled-coil related prot	4.40
	128793	AB011125	Hs.105749	KIAA0553 protein	4.40
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	4.38
	126144	H84455	Hs.40639	ESTs	4.38
30	130783	X07282	Hs.171495	refinoic acid receptor, beta	4.38
30	135192	U83993	Hs.321709	purinergic receptor P2X, ligand-gated to	4.38
	100284 117269	D43767	Hs.66742	small inducible cytokine subtemily A (Cy	4.37
	104261	N21621 AW248364	Hs.91142 Hs.5409	KH-type splicing regulatory protein (FUS	4.36
	108609	BE409857	Hs.69499	R polymerase I subunit hypothetical protein	4.35
35	126319	D81689	113.03433	gb:HUM184E05B Human fetal brain (TFujiwa	4.35 4.35
••	127445	AA906286	Hs.193942	ESTs CENTRAL TELEVISION OF THE PROPERTY OF THE	4.35
	130772	BE270640	Hs.19192	cyclin-dependent kise 2	4.35
	134625	AA977638	Hs.184389	ESTs	4.35
40	135397	L14922	Hs.166563	replication factor C (activator 1) 1 (14	4.35
40	128070	AA886944	Hs.303908	ESTs	4.35
	135046	Al494054	Hs.93589	hypothetical protein DKFZp564B1162	4.33
	101881	NM_004957	Hs.754	folytpolyglutamate synthase	4.33
	129838	AB007863	Hs.185140	KIAA0403 protein	4.33
45	130974	NM_003528	Hs.2178	H2B histone family, member Q	4.33
73	107763 129818	AA018220 T71092	Hs.106730	chromosome 22 open reading frame 3	4.32
	129407	AL137597	Hs.172572 Hs.11114	hypothetical protein FLJ20093 hypothetical protein dJ1181N3.1	4.31
	110846	BE277343	Hs.297875	endoplasmic reliculum chaperone SIL1, ho	4.30
	111433	R01452	Hs.40193	hypothetical protein KIAA1259	4.30 4.30
50	114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.30
	115853	AW978561	Hs.191548	ESTs	4.30
	116165	Al184751	Hs.75874	pregncy-associated plasma protein A	4.30
	126911	AA428049	Hs.1501	syndecan 2 (heparan sulfate proteoglycan	4.30
55	131230	NM_005865	Hs.274407	protease, serine, 16 (thymus)	4.30
23	100349	D64110	Hs.77311	BTG family, member 3	4.29
	100175 105335	BE258769	Hs.32500	acetyl-Coenzyme A acyltransferase 2 (mit	4.29
	122507	AW291165 BE567620	Hs.25447	ESTs	4.29
	105397	AA814807	Hs.99210 Hs.7395	ESTs hypothe@cal protein FLJ23182	4.28
60	133674	AW851121	Hs.75497	Homo sapiens cD: FLJ22139 fis, clone H	4.28 4.28
	102826	NM_007274	Hs.8679	cytosolic acyl coerzyme A thioester hydr	4.26 4.28
	103272	NM_006680	Hs.2838	matic enzyme 3, DP(+)-dependent, mitoc	4.28
	111887	R38635	Hs.12328	KIAA 1005 protein	4.28
~~	120336	N85785	Hs.181165	eukaryotic translation elongation factor	4.28
65	133736	D49958	Hs.75819	glycoprotein M6A	4.28
	130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	4.27
	119830	AW054922	Hs.53478	Homo sapiens cD FLJ12366 fis, clone MA	4.27
	106758	AB014564	Hs.22616	KIAA0664 protein	4.25
70	109709	F09749	Hs.187405	ESTs	4.25
, 0	110463 124472	H52931	Hs.165067	ESTs	4.25
	109770	N52517 R40322	Hs.102670	EST	4.25
	131487	F13036	Hs.248420 Hs.27373	ESTs, Moderately similar to A47582 B-cel	4.24
	107216	D51069	Hs.211579	Homo sapiens mR; cO DKFZp564O1763 (f melanoma cell adhesion molecule	4.23
75	123562	AA177088	Hs.190085	ESTs	4.23
	125986	W02410	Hs.205555	ESTs	4.23 4.23
	126221	N20514	Hs.172965	ESTs	4.23 4.23
	127092	T26985		gb:NIBT065H01R Infant brain, LLNL array	4.23
00	132349	AW975654	Hs.181286	serine protease inhibitor, Kazal type 1	4.23
80	118946	N92834		gb:zb67f03.s1 Soares_fetal_lung_NbHL19W	4.22
	101531	Al199711	Hs.576	fucosidase, alpha-L- 1, tissue	4.21
	105322	T87179	Hs.16346	ESTs, Weakly similar to \$57447 HPBRII-7	4.21
	104219	AB002323	Hs.7720	dynein, cytopiasmic, heavy polypeptide 1	4.20

	102825	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	4.20
	103571 106942	A1675749	Hs.21,1608	nucleoporin 153kD	4.20
	112685	AA995351 R87650	Hs.31314 Hs.33439	relinoblastoma-binding protein 7	4.20
5	123107	AA225048	Hs.104207	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	4.20
_	132659	275190	Hs.54481	low density (Ipoprotein receptor-related	4.20 4.20
	130084	AI929377	Hs.173724	creatine kise, brain	4.19
	114553	BE219860	Hs.22505	hypothetical protein FLJ 10159	4.18
10	129628	U3B945	Hs.1174	cyclin-dependent kise inhibitor 2A (me	4.18
10	102266	U29725	Hs.3080	mitogen-activated protein kise 7	4.18
	110637	Al241470	Hs.268982	ESTs	4.18
	127520 130322	T51239 NM_014247	Vo 454545	gb:yb20d12.s1 Stratagene fetal spieen (9	4.18
	104768	D82319	Hs.154545 Hs.11056	POZ domain containing guanine nucleotide RALBP1 protein	4.17
15	123360	AA532718	Hs.178604	ESTs	4.17 4.17
	133110	AA808177	Hs.65228	ESTs	4.16
	130923	H96115	Hs.21293	UDP-N-actey/glucosamine pyrophosphorylas	4.16
	109878	BE620775	Hs.4866	Homo saptens cD FLJ14387 fis, clone HE	4.16
20	119265	BE539706	Hs.285363	ESTs	4.16
20	124214	H58608	Hs.151323	ESTs	4.15
	106193 105169	AA057478	Hs.23272	ESTs	4.15
	132304	BE245294 AA610002	Hs.180789 Hs.44296	S164 protein	4.15
	131600	NM_004377	Hs.29331	hypothetical protein FLJ22324 camitine palmitoyitransferase I, muscle	4.15 4.14
25	131365	M93415	Hs.26014	activin A receptor, type II	4.14
	121993	AW297880	Hs.98661	ESTs	4.14
	110779	Al391472	Hs.12561	ESTs, Highly similar to C212_HUMAN 28.3	4.13
	126383	AB032977	Hs.6298	KIAA1151 protein	4.13
30	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	4.13
30	131475 128933	AA992841	Hs.27263	KIAA1458 protein	4.13
	113141	NM_002050 AJ493276	Hs.334695 Hs.9187	GATA-binding protein 2	4.12
	134833	L20965	Hs.89901	ESTs phosphodiesterese 4A, cAMP-specific (dun	4.11
	106461	Al630759	Hs.17481	Homo sapiens clone 24606 mR sequence	4.11 4.10
35	128058	Al990131	Hs.276973	potassium large conductance calcium-acti	4.10
	114757	AW970579	Hs.291031	ESTs	4.10
	134653	Al765883	Hs.87385	ESTs	4.09
	100472	D90084	Hs.1023	pyruvate dehydrogese (lipoamide) alpha	4.08
40	103102 106779	X61177 BE276013	Hs.68876	interleukin 5 receptor, alpha	4.08
40	133815	M62843	Hs.172364 Hs.75236	Homo sepiens mR for FLJ00086 protein,	4.08
	130178	U20982	Hs.1516	ELAV (embryonic lethal, abnormal vision, insulin-like growth factor-binding prote	4.08 4.07
	124659	AI680737	Hs.289068	Homo saplens cD FLJ11918 fls, clone HE	4.07
	127861	AW295020	Hs.198529	ESTs	4.07
45	112129	AB037715	Hs.183639	hypothetical protein FLJ10210	4.07
	100918	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.06
	124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	4.05
	102722 111117	F13271	Hs.79981	Human clone 23560 mR sequence	4.05
50	122506	AB037721 AA449120	Hs.173871 Hs.99209	KIAA1300 protein ESTs	4.05
••	126392	Al356294	Hs.3280	caspase 6, apoptosis-related cysteine pr	4.05 4.05
	130760	AW379130	Hs.18953	phosphodieslerase 9A	4.05
	104220	AB002324	Hs.301094	KIAA0326 protein	4.05
55	112774	R95770	Hs.35455	ESTs	4.04
55	111128	AW505364	Hs.19074	LATS (large turnor suppressor, Drosophila	4.04
	113146 124940	BE151985 AF068846	Hs.5722	hypothetical protein FLJ23316	4.04
	105498	H68279	Hs.103804 Hs.24937	heterogeneous nuclear ribonucleoprotein	4.03
	112631	R82040	110.24007	transformer-2 alpha (htra-2 alpha) gb:yj06b06.s1 Soares placenta Nb2HP Homo	4.03 4.03
60	118244	N62516	Hs.48556	ESTs	4.03
	118720	N73515		gb:za49d07.s1 Soares fetal liver spieen	4.03
	129232	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	4.03
	134192	H01345	Hs.24139	Homo sapiens cD: FLJ23137 fis, clone L	4.03
65	131893 116793	BE336886	Hs.3416	adiposa differentiation-related protein	4.02
UJ	125674	T77781 AL036166	U- 222270	gb:yd20a11.s1 Soares fetal liver spieen	4.02
	116640	X89984	Hs.323378 Hs.211563	coated vesicle membrane protein B-cell CLL/lymphoma 7A	. 4.01
	105057	AA134233	Hs.336942	Homo sepiens cD: FLJ21488 fts, clone C	4.01 4.00
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	4.00
70	116245	AB033107	Hs.42796	KIAA1281 protein	4.00
	119946	AA932283	Hs.58925	ESTs	4.00
	121975	AA740679	Hs.98631	ESTs	4.00
	132037 133669	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cD 2700	4.00
75	109468	NM_006925 NM_015310	Hs.166975	splicing factor, arginine/serine-rich 5	4.00
. 5	106829	AW959893	Hs.6763 Hs.27099	KIAA0942 protein	3.99
	134682	AW882645	Hs.88044	hypothetical protein FLJ23293 simitar to sprouty (Drosophila) homolog 1 (antagoni	3.99 3.98
	105966	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.98
00	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	3.98
80	102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	3.98
	104148	AW880614	Hs.146381	R binding motif protein, X chromosome	3.98
	111465 126499	AI968256 AK001779	Hs.15470	putative ring zinc finger protein NY-REN	3.98
	140403	CHANILLS.	Hs.110445	CGI-97 protein	3.98

	134388	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.98
	105564 115208	BE616694 AW183695	Hs.288042	hypothetical protein FLJ14299	3.97
	103853	AF272390	Hs.186572	ESTs	3.96
5	110542	H58373	Hs.111782 Hs.332938	myosin 5C	3.96
	106797	Al768801	Hs.169943	hypothetical protein MGCS370	3.96
	130589	AL110226	Hs.16441	Homo sapiens cD FLJ13569 fis, clone PL DKFZP434H204 protein	3.96
	122788	AI828638	Hs.99514	hypothetical protein FLJ20574	3.95
10	104518	H20816	Hs.112423	Homo sapiens mR; cD OKFZp586I1420 (I	3.95 3.95
10	130640	NM_004753	Hs.17144	short-chain dehydrogese/reductase 1	3.95
	110847 116156	N30169	Hs.279807	ESTs, Wealthy similar to 2004399A chromos	3.95
	122096	AA461045 AA431162	Hs.50701	ESTS	3.95
	122160	AI769281	Hs.98690 Hs.97439	ESTs	3.95
15	123930	AA740878	Hs.112982	ESTs ESTs	3.95
	126280	Z19417	113.112302		3.95
	126547	U47732	Hs.84072	gb:HSB26B122 STRATAGENE Human skeletal m transmembrane 4 superfamily member 3	3.95
	134757	AA913267	Hs.211576	IL2-inducible T-cell kise	3.95 3.95
20	117296	AL133427	Hs.42506	Homo sapiens mR full length insert cDN	3.95
20	112261 112268	AL050297	Hs.300861	ESTs, Highly similar to T08701 hypotheti	3.95
	131844	W39609 AJ419294	Hs.22003	solute carrier family 6 (neurotransmitte	3.94
	101607	X60111	Hs.324342 Hs.1244	ESTs	3.94
0.5	121613	AA416879	Hs. 193195	CD9 antigen (p24)	3.94
25	115815	AW905328	Hs.180842	ESTs, Wealdy similar to 2109260A B cett ribosomal protein L13	3.93
	125684	AW589427	Hs. 158849	Homo sapiens cD: FLJ21663 ffs, clone C	3.93
	126783	AA083531		gb:zn09d10.s1 Stratagene hNT neuron (937	3.93 3.93
	129201 128954	H18359	Hs.109390	ESIS	3.93
30	122939	AA346839 AA477141	Hs.209100	DKFZP434C171 protein	3.92
	130348	AB032957	Hs.210850	gb:zu37g08.s1 Soares overy tumor NbHOT H	3.92
	125847	AW161885	Hs.249034	KIAA1131 prolein	3.92
	120452	AL022328	Hs.104335	ESTs hypothetical protein IMAGE3510317	3.91
35	123143	AA487595		gb:aa95e02.s1 Stratagene felal reti 93	3.91
33	105729	H46612	Hs.293815	Homo saplens HSPC285 mR, partial cds	3.91 3.91
	106605 126714	AW772298	Hs.21103	Homo saplens mR; cD DKFZp564B076 (fr	3.90
	121611	AF114491 M31669	Hs.137354	egf-like module containing, mucin-like,	3.90
	120468	AW967675	Hs. 1735 Hs. 964B7	inhibin, beta B (activin AB beta polypeg	3.90
40	101356	AW878229	Hs.80842	ESTs, Highly similar to S08228 ribosomal	3.90
	133668	L77984	Hs.271980	sigl transducer and activator of trans mitogen-activated protein kise 6	3.89
	109114	BE622787	Hs.84045	hypothetical protein FLJ20288	3.89
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol	3.88
45	107850	AA022910	Hs.295446	ESTs, Moderately similar to 810024C cyto	3.88 3.88
7,5	130907 101879	AA322866 AA176374	Hs.21107	neuroligin	3.88
	104267	AF043244	Hs.243886	nuclear autoantigenic sperm protein (his	3.88
	112232	BE253927	Hs.278439 Hs.24983	nucleolar prolein 3 (apoptosis repressor	3.88
	113248	T63857	113-24303	hypothetical protein from EUROIMAGE 2021	3.88
50	114044	BE327427	Hs.79953	gb:yc16e01.s1 Stratagene lung (937210) H ESTs	3.88
	115414	AA662240	Hs.283099	AF15q14 protein	3.88
	129598	N30436	Hs.11656	Homo sapiens cD FLJ12566 fis, clone NT	3.88 3.68
	102134 106310	AL036967	Hs.2324	protamine 2	3.87
55	116470	R98185 AL272141	Hs.17240	ESTs	3.87
	110947	AW298410	Hs.83484 Hs.21475	SRY (sex determining region Y)-box 4	3.86
	115839	BE300266	Hs.28935	ESTs	3.85
	103534	AW970672	Hs.9247	transducin-like enhancer of split 1, hom protein kise, AMP-activated, alpha 1 c	3.85
60	105209	AB023197	Hs.227743	KIAA0980 protein	3.85
00	108749	AA127017	Hs.71052	ESTs	3.85 3.85
	110565 110799	A1884970	Hs.4983	ESTs	3.85
	117068	Al089660 H91257	Hs.323401	dpy-30-like protein	3.85
	130956	NM_001135	Hs.41391 Hs.2159	EST	3.85
65	102273	BE391815	Hs.75981	aggrecan 1 (chondrollin sulfate proteogl	3.85
	112980	AL110209	Hs.6770	ubiquilin specific protease 14 (tik-gua LCAT-like lysophospholipase	3.85
	114414	AW152166	Hs.182113	ESTs	3.84
	109885	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	3.84
70	106208	AK001674	Hs.22630	cofector required for Sp1 transcriptio	3.84 3.84
, 0	122311 124271	NM_014913	Hs.131915	KIAA0863 protein	3.84
	106650	AW293223 AL049951	Hs.8928	hypothelical protein FLJ20291	3.83
	112167	N99591	Hs.22370 Hs.25587	Homo sepiens mR; cD DKFZp56400122 (f	3.83
75	122354	AL157579	Hs.153610	ESTs, Weakly similar to T00329 hypotheti KIAA0751 gene product	3.83
75	111462	R05296	***************************************	gb:ye91e08.s1 Soares fetal liver spleen	3.83
	128109	AW269421	Hs.128093	ESIS	3.81
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	3.81 3.81
	109210 132543	AA669722	Hs.272137	ESTS	3.81 3.81
80	106827	BE568452 AA457456	Hs.5101	protein regulator of cytokinesis 1	3.80
	124232	H63391	Hs.11408 Hs.339677	hypothetical protein FLJ20435	3.80
	126039	AL137523	Hs.181102	ESTs, Weatdy similar to 138022 hypotheti	3.80
	128022	AW195569	Hs.125906	p30 DBC protein ESTs	3.80
					3.80

	132005	AA149707	Hs.173091	ubiquitin-like 3	3.79
	131392	AA235153	Hs.26320	TRABID protein	3.79
	131775	AB014548	Hs.31921	KIAA0648 protein	3.79
_	126257	N99838	12.0.04.	gbtzp39g11.r1 Soares fetal liver spisen	3.79
5	121950	AA429515		gb:zw75c05.s1 Soares_testis_NHT Homo sap	3.79
	116067	AA454827	Hs.293637	ESTs	3.78
	104658	AA360954	Hs.27268	Homo sapiens cD; FLJ21933 fis, clone H	3.78
	104493	AW960427	Hs.79059	transforming growth factor, beta recepto	3.77
10	100163	W44671	Hs.124	gene predicted from cD with a complete	3.77
10	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kise 1	3.77
	120588	AL031778	Hs.797	nuclear transcription factor Y, sipha	3.76
	128764	AW024282	Hs.104938	hypothetical protein MGC15906	3.75 3.75
	111574 117396	AI024145 W20128	Hs.188526 Hs.296039	ESTs ESTs	3.75
15	119052	R10889	118.290033	gb:yf38d02.s1 Soares feiat liver spicen	3.75
1.5	121806	AA424313	Hs.98402	ESTs	3.75
	122410	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	3.75
	126638	AA649257	Hs.188602	ESTs .	3.75
	127879	AA768098	Hs.189079	ESTs	3.75
20	121095	AA320134	Hs.196029	Homo sapiens mR for KIAA1657 protein,	3.75
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr	3.74
	101230	AW504300	Hs.295605	mannosidase, elpha, class 2A, member 2	3.74
	100200	H94688	Hs.173737	ras-related C3 botulinum toxin substrate	3.73
25	106913	Al219346	Hs.86178	M-phase phosphoprotein 9	3.73
25	110975	H17012	Hs.14633	ESTs	3.73
	117314	N32498	Hs.42829	ESTs	3.73 3.73
	118737 124169	AA199686 BE079334	Hs.271630	gb:zq75g09.r1 Stratagene hNT neuron (937 ESTs	3.73
	124580	N68420	Hs.107992	EST8	. 3.73
30	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	3.73
	124879	R73588	Hs.101533	ESTs	3.72
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.72
	103644	M13305	Hs.247787	opsin 1 (cone pigments), long-wave-sensi	3.72
~ ~	106044	N90344	Hs.149436	kinesin family member 58	3.71
35	127867	C18530		gb:C18530 Human placenta cD (TFujiwara	3.71
	133828	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	3.71
	107387	D86983	Hs.118893	Melanoma associated gene	3.71
	104160	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.71
40	106098	BE278344	Hs.7970	DKFZP434B027 protein	3.70 3.70
40	133891 120717	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perfecan	3.70
	119263	AA904681 T15977	Hs.154434	ESTs, Weakly similar to unknown (H.sapie gb:182328 Infant brain, Bento Soares Hom	3.70
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.70
	106566	8E298210	13.00010	gb:601118016F1 NIH_MGC_17 Homo saplens c	3.70
45	110708	N33878	Hs.306117	KIAA0306 protein	3.70
	114357	R41677	Hs.6107	Homo saplens cD FLJ14839 fis, clone OV	3.70
	115285	AW972872	Hs.293736	ESTs	3.70
	123034	AL359571	Hs.44054	ninein (GSK3B interacting protein)	3.70
60	126396	T06298	Hs.153326	EST	3.70
50	132597	Y11192	Hs.5299	aldahyda dehydrogese 5 family, member	3.70
	105823	AI559444	Hs.293960	ESTs	3.70
	102644	T59816	Hs.173311	C18B11 homolog (44.9kD)	3.70
	133513 116450	AF136407 A1654450	Hs.7446	chromosome 6 open reading frame 5	3.70 3.69
55	104596	AF067804	Hs.47274 Hs.15423	Homo saplens mR; cD DKFZp564B176 (fr hypothetical protein HDCMC04P	3.69
55	133579	X75346	Hs.75074	miliogen-activated protein kise-activat	3.68
	124556	N29317	Hs.236463	Homo sapiens mR; cD DKFZp586i0521 (f	3.68
	120534	AI635113	Hs.270368	ESTs, Weakly similar to 178885 serine/th	3.68
	103156	BE259039	Hs.129953	Ewing sercome breakpoint region 1	3.68
60	134992	AA464444	Hs.5831	tissue inhibitor of metalloproteise 1	3.68
	106730	BE467313	Hs.260707	ESTs	3.68
	120880	AA360240	Hs.97019	EST	3,68
	123731	AA609839		gb:ee62f01.s1 Stratagene lung carcinoma	3.68
65	126973	W48653	Hs.251928	nuclear pore complex interacting protein	3.67
0.5	103646	AW248439	Hs.2340	junction plakoglobin	3.67
	116333 120922	AF155827	Hs.203963	hypothetical protein FLJ 10339	3.67
	127407	AA481003 AW089514	Hs.97128	ESTs heterogeneous nuclear ribonucleoprotein	3.67 3.67
	106578	AA836381	Hs.279681 Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.67
70	123000	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mR.	3.87
	101464	AA852431	Hs.51299	DH dehydrogese (ubiquinone) flavogro	3.67
	101397	M26380	Hs.180878	Epoprotein lipase	3.67
	131135	NM_016569	Hs.267182	TBX3-iso protein	3.66
	106112	AL117518	Hs.3686	KIAA0978 protein	3.66
75	123974	NM_015678	Hs.3821	neurobeachin	3.66
	127742	AW293496	Hs.180138	ESTs	3.66
	112908	BE281000	Hs.3530	TLS-essociated serine-arginine protein 2	3.66
	131802	AL137406	Hs.296358	Homo septens mR; cD DKFZp434M162 (fr	3.65
80	135162	A)187925	Hs.95667	F-box protein 30	3.65
٥U	124984	BE313210	Hs.223241	eukaryotic translation elongation factor	3.65
	118844 125429	AL035364 Al023654	Hs.50891	hypothetical protein ESTs	3.65 3.65
	125425		Hs.114191	gb:yg44h11.r2 Soares Infant brain 1NiB H	3.65 3.65
	,2000	145000		Solfator in a Society quant or one true Li	3.03

	40000				
	125792	AA496205	Hs.193700	Homo sapiens mR; cD DKFZp58610324 (f	3.65
	126965	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.65
	130776	AF167706	Hs.19280	cysteine-rich motor neuron 1	3,65
5	131949	AK000010	Hs.258798	hypothetical protein FLJ20003	3.65
,	116612	C14904	Hs.45184	Homo sapiens cD FLJ12284 ffs, clone MA	3.65
	123749 134203	AA609949	Hs.112790	EST	3.65
	133605	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi	3.64
	109235	AL038165	Hs.75187	translocase of outer mitochondrial membr	3.64
10	125447	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	3.64
10	122942	Al582222 Al277829	Hs.128686	ESTs	3.63
	122748	AA458822	Hs.111862	KIAA0590 gene product	3.63
	103840	AW975861	Hs.193815	ESTs	3.63
	105333	AA234831	Hs.47367 Hs.246112	KIAA1785 protein	3.63
15	108807	Al652236	Hs.49376	KIAA0788 protein	3.63
	114699	AA127386	ris.49376	hypothetical protein FLJ20644	3.63
	126040	Z28444	Hs.24119	gb:zn90d09.r1 Stratagene lung carcinoma	3.63
	131028	AI879165	Hs.2227	Homo saplens mR; cD DKFZp588G2222 (f	3.63
	131710	NM_015368	Hs.30985	CCAAT/enhancer binding protein (C/EBP), pannexin 1	3.63
20	100164	AW372032	Hs.173714	MORF-related gene X	3.63
	120837	BE149656	Hs.306621	Homo sapiens cD FLJ11963 fis, clone HE	3.62
	131089	Z42645	Hs.22870	Homo saplens mR full langth insert cDN	3.62
	126428	AA412436	Hs.301985	ESTs	3.62
0.5	129148	AW501216	Hs. 108945	KIAA0515 protein	3.62
25	102337	AJ814663	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	3.61
	104520	AI702384	Hs.76925	hypothetical protein FLJ14981	3.81 3.60
	112954	AA928953	Hs.6655	Homo saplens EST from clone 208499, full	3.60
	125197	AF086270	Hs.278554	heterochromatin-like protein 1	3.60
20	128124	Al125748	Hs.130194	ESTs	3.60
30	129553	AW015763	Hs.113065	ESTs	3.60
	123998	AA203429	Hs.79474	tyrosine 3-monooxygese/tryptophan 5-mo	3.60
	128835	AK001731	Hs.106390	Homo sapiens mR; cD DKFZp586H0924 (f	3.59
	129226	BE222494	Hs.180919	inhibitor of D binding 2, domint neg	3.59
35	135131	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	3.59
55	128955 100225	AA775076	Hs.185807	Homo seplens, Similar to PRO0478 protein	3.58
	101572	D28539	Hs.167185	glutamate receptor, metabotropic 5	3.58
	102277	AA437199 U31099	Hs.656	cell division cycle 25C	3.58
	103667	ZB0788	Hs.158326 Hs.247815	prostaglandin D2 receptor (DP)	3.58
40	112373	AW963357		H4 histone family, member L	3.58
	119284	AL041224	Hs.7847 Hs.65379	ESTS	3.58
	125422	AA903229	Hs.153717	ESTs ESTs	3.58
	126381	M76665	Hs.275215		3.58
<i>:</i>	129168	Al132988	Hs.109052	hydroxysteroid (11-beta) dehydrogese 1	3.58
45	123133	AA487264	Hs.154974	chromosome 14 open reading frame 2 Homo saplens mR; cD OKFZp667N084 (fr	3.58
	128789	AW368576	Hs.139851	caveolin 2	3.57
	104172	AA476418		gb:zx02a12.s1 Soares_total_fetus_Nb2HF8_	3.57
	134263	AW973443	Hs.8086	R (guanine-7-) methyltransferase	3.57
50	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	3.57
50	104942	NM_016348	Hs.10235	chromosome 5 open reading frame 4	3.57 3.56
	123443	BE244537	Hs.167382	triuretic peptide receptor A/guanylate	3.56
	110707	AI239832	Hs.15617	ESTs, Wealdy similar to ALU4_HUMAN ALU S	3.55
	106787	AJ492261	Hs.32450	ESTs	3.55
55	112940	AK001757	Hs.281348	hypothetical protein FLJ10895	3.55
"	115301	T11832	Hs.127797	Homo saplens cD FLJ11381 fls, clone HE	3.55
	125978 128002	N66843	Hs.35608	ESTs	3.55
	119847	Al985897	Hs.125293	ESTs	3.55
	134595	H81136 NM_002401	Hs.334604	Homo septens mR for KIAA1870 protein,	3.55
60	121309	AA293834	Hs.29282	mitogen-activated protein kise kise	3.55
	122679	AA811286	Hs.97312 Hs.192837	ESTS	3.54
	106061	AA565356	Hs.13250	ESTs. Wealdy strailer to ALUS_HUMAN ALU S	3.54
	127207	AA377165	Hs.44833	ESTs ESTs	3.54
	129563	AF119664	Hs.27299	transcriptiol regulator protein	3.54
65	105951	R48700	Hs.20733	Homo saplens cD: FLJ22356 fis, clone H	3.54
	115643	AA404276	Hs.123253	hypothetical protein FLJ22009	3.53
	130473	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.53
	104246	AF016032	Hs.201377	lysosomal	3.53
70	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	3.53
70	101211	AA355357	Hs.283429	SMC (mouse) homolog, X chromosome	3.53 3.53
	100774	J05581	Hs.89603	mucin 1, transmembrane	3.53 3.53
	108407	AA075519		gb:zm87h09.s1 Strategene overlan cancer	3.53
	113538	A1554947	Hs.15167	ESTs, Weakly similar to 837482 finger or	3.53
75	113876	A)799751	Hs.5635	ESTs	3.53
15	110731	NM_014899	Hs.188006	KIAA0878 protein	3.52
	125845	AK001440	Hs.131840	hypothetical protein FLJ10578	3.51
	112945	AW138458	Hs.20787	Homo septens cD: FLJ21686 fis. clone C	3.51
	131586	NM_012296	Hs.30687	GRB2-associated binding grotein 2	3.51
80	125413 129360	AI887951	Hs.74566	dihydropyrimidise-like 3	3.51
00	128819	AJ000534 R38007	Hs.110708	sercoglycan, epsilon	3.50
	101973	U41514	Hs.77578	ubiquitin specific protease 9, X chromos	3.50
	103616	NM_002647	Hs.80120	UDP-N-acetyl-atpha-D-galactosamine:potyp	3.50
	.03010	MMC002047	Hs.32971	phosphoinosilide-3-kise, class 3	3.50

	105535	Al459519	Hs.297681	serine (or cysteine) proteise inhibito	250
	118767	AI038653	Hs.50500	ESTs	3.50 3.50
	126634	AW361109	Hs.43627	SRY (sex determining region Y)-box 22	3.50
5	130851	R66282	Hs.20247	ESTs, Wealty similar to \$65657 alpha-1C-	3.50
,	134353 111394	AL138201	Hs.82120	nuclear receptor subtamily 4, group A, m	3.50
	102696	AA412227 BE540274	Hs.16131	hypothetical protein FLJ12876	3.50
	113037	R17268	Hs.239	forkhead box M1	3.49
	111028	H59346	Hs.259873 Hs.30151	exol transport of syptic vesicles	3.49
10	131688	AI935413	Hs.30692	ESTs, Weakly similar to I38022 hypotheti	3.49
	115613	AW136951	Hs.173948	p21 (CDKN1A)-activated kise 2 hypothetical protein FLJ 10486	3.49
	116975	H81076	Hs.269001	ESTs	3.48
	100210	D26381	Hs.3104	KIAA0042 gene product	3.48
15	110147	H18700	Hs.268799	ESTS	3.48 3.48
13	115600	AA081395	Hs.42173	Homo sapiens cD FLJ10366 fis, clone NT	3.48
	119088	R39261	Hs.90790	Homo saplens cD: FLJ22930 fis, clone K	3.48
	120347 122702	AA211068	Hs.120247	nuclear fragile X mental retardation pro	3.48
	125552	AI220089 H09701	Hs.99439	ESTs	3.48
20	126461	Al381659	Hs.278366 Hs.267086	ESTs, Weakly similar to 138022 hypotheti	3.48
	128572	AA933022	Hs.256583	ESTs	3.48
	118397	BE139479	Hs.161492	interleukin enhancer binding factor 3, 9 ESTs	3.48
	127999	AW978827	Hs.69851	nucleolar protein family A, member 1 (H/	3.47
25	132066	A1929392	Hs.181195	DJ (Hsp40) homolog, subfamily 8, membe	3.47
25	105693	BE250951	Hs.181368	U5 snRNP-specific protein (220 kD), orth	3.47 3.47
	128874	HD6245	Hs.106801	ESTs, Weakly similar to PC4259 territin	3.46
	119984	AA230228	Hs.59197	ESTs	3.46
	104000 101488	Al146527	Hs.80475	polymerase (R) ii (D directed) polyp	3.46
30	101045	BE547216 J05614	Hs.181128	ELK1, member of ETS oncogene family	3.46
	120149	AA227609	Un 04934	gb:Human proliferating cell nuclear anti	3.46
	107025	AA825523	Hs.94834 Hs.21255	ESTs	3.46
	101716	AF050658	Hs.2563	ESTs, Wealdy similar to I38022 hypotheti	3.45
25	102899	Al815559	Hs.75730	tachykinin, precursor 1 (substance K, su sigl recognition particle receptor (d	3.45
35	123075	AW293133	Hs.101340	ESTs. Weakly similar to A42442 integrin	3.45
	124695	AA594979	Hs.239307	lyrosyl-IR synthetase	3.45
	127669	N28989	Hs.22891	solute carrier family 7 (cationic amino	3.45 3.45
	129793	AW207000	Hs.126857	Homo sapiens cD FLJ12936 fis, clone NT	3.44
40	120095 110915	AA693774	Hs.59601	ESTs	3.44
-10	130542	BE092285	Hs.29724	hypothetical protein FLJ 13187	3.43
	100488	U64675* BE273749	Hs.179825	RAN binding protein 2-like 1	3.43
	115027	AA743331	Hs.752	FK508-binding protein 1A (12kD)	3.43
	119298	NM_001241	Hs.272572 Hs.155478	hemoglobin, elpha 2	3.43
45	126486	AI065133	Hs.152316	cyclin T2	3.43
	130021	M24470	Hs.1435	hypothetical protein PRO0971 guanosine monophosphate reductase	3.43
	127166	AW954605	Hs.283395	sema domain, transmembrane domain (TM).	3.43
	114988	AA251089		gb:zs04f05.s1 NCI_CGAP_GCB1 Homo sapiens	3.42
50	133817	AW578716	Hs.7644	H1 histone family, member 2	3.42 3.41
30	133562	M60721	Hs.74870	H2.0 (Orosophila)-like homeo box 1	3.41
	105610	AA280072	Hs.99872	fetal Alzheimer antigen	3.41
	129007 100662	AK001521	Hs.107882	hypothetical protein FLJ10659	3.41
	120159	Al368680 R60781	Hs.816	SRY (sex determining region Y)-box 2	3.41
55	134966	AW402389	Hs.92927	putative 47 kDa protein	3.41
•	100369	D79988	Hs.920 Hs.115778	modulator recognition factor I	3.41
	104260	AF008192	Hs.194283	KIAA0168 gene product	3.41
	100134	AA305746	Hs.49	pulative GR6 protein macrophage scavenger receptor 1	3.40
60	116015	AA338648	Hs.50334	testes development-related NYD-SP22	3.40
6 0	119251	T15753	Hs.65250	EST	3.40
	127176	BE387162	Hs.280858	ESTs, Highly similar to A35661 D excis	3.40 3.40
	123422	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.39
	123094	AA761073	Hs.146847	TRAF family member-associated NFKB activ	3.39
65	105289 111219	AB020638	Hs.103000	KIAA0831 protein	3.39
UJ	127963	N68836 A1200012	Hs.19247	ESTs, Moderately similar to ALUC_HUMAN I	3.38
	109412	A1299013 BE543313	Hs.87779 Hs.209473	Homo sapiens cD: FLJ23087 fis, clone L	3.38
	118794	AW517051	Hs.118210	hypothelical protein FLJ10520 ESTs	3.38
	112040	R43286	H8.110210		3.38
70	111180	AI798851	Hs.283108	gb.yg17e11.a1 Soares infant brain 1NIB H hemoglobin, gamma G	3.38
	117329	AA524065	Hs.93670	Homo saplens cD: FLJ22664 fis, clone H	3.38
	104371	Al288698	Hs.194081	ESTs, Wealdy similar to 138022 hypotheti	3.38
	109265	AA195285	Hs.85982	ESTs	3.38 3.38
75	109557	AW452405	Hs.6427	ESTs	3.38 3.38
, 5	120753	AA312551	Hs.230157	ESTs	3.38
	120970 127094	AA398118 F13215	Hs.97579	ESTs, Wealthy similar to A46010 X-linked	3.38
	127746	F13215 Al239495	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	3.38
	123553	A1494291	Hs.120189	ESTA	3.38
80	130652	M31689	Hs.111977 Hs.1735	ESTs	3.37
	135101	U82275	Hs.94498	inhibin, beta B (activin AB beta polypep	3.37
	121799	AI885670	Hs.124027	leukocyte immunoglobulin-like receptor, SELENOPHOSPHATE SYNTHETASE; Human selen	3.37
	112278	Z41698	Hs.26039	Homo sepiens co FLJ13937 fis, clone Y7	3.37
				and and an an an analytic COURTY	3.36

	113401	AA610175	Hs.179847	Homo saplens cO FLJ12195 fis, clone MA	3.36
	109292	AW975746	Hs.188662	KIAA1702 protein	3.38
	135026 118210	N92165 N49233	Hs.93231	ESTs	3.36
5	123476	AA384564	Hs.46914 Hs.108829	ESTs, Wealdy similar to A46010 X-linked	3.35
	111076	N59129	Hs.20851	ESTs ESTs	3.35
	111520	A1985369	Hs.301134	ESTs	3.35 3.35
	133383	BE313555	Hs.7252	KIAA1224 protein	3.35
10	103731 110828	AA070545 AK002114	Hs.23495	gb:zm70c03.r1 Stratagene neuroepithelium	3.35
	112520	R68654	Hs.30814	hypothetical protein FLJ11252 ESTs	3.35
	115725	AW899053	Hs.76917	F-box only prolein 8	3.35 3.35
	125867	H13331	Hs.123721	ESTs	3.35
15	127719	AI242163	Hs.22670	chromodomain helicase D binding protei	3.35
13	129863 130816	BE379765 M61877	Hs.129872 Hs.1985	sperm associated antigen 9	3.35
	130888	AL044315	Hs.173094	spectrin, eipha, erythrocytic 1 (ellipto Homo saplens mR for KIAA1750 protein.	3.35
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	3.35 3.35
20	118986	AF148713	Hs.125830	bladder cancer overexpressed protein	3.35
20	101723 134693	U34304 N70361	II- Mes	gb:Human nonmuscle myosin heavy chain II	3.34
	102856	M26150	Hs.8854 Hs.248177	Human transcription unit PVT gene, exons	3.34
	105593	AA279341	Hs.174151	H3 histone family, member L aldehyde oxidase 1	3.34 3.34
25	134748	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retil)	3.34
25	109149	AA831179	Hs.40065	hypothetical protein MGC4825	3.33
	115026 103548	AA251972 Z14244	Hs.188718 Hs.75752	ESTs	3.33
	111189	N67603	Hs.272130	cylochrome c oxidase subunit VIIb ESTs, Weakly similar to S65824 reverse t	3.33
20	127078	Al422951	Hs.146162	ESTs	3.33 3.33
30	124949	AI903210	Hs.336780	tubulin, beta polypeptide	3.33
	111012 113412	A1077389 AW628660	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.33
	116351	AL133623	Hs.44131 Hs.82501	KIAA0974 protein similar to mouse Xm1 / Dhm2 protein	3.33
25	121633	AA417011	Hs.98175	EST	3.33 3.33
35	124591	N59243	Hs.192974	hypothetical protein FLJ12735	3.33
	130225 131945	AB021179	Hs.15299	HMBA-Inducible	3.33
	132581	NM_002916 AK000631	Hs.35120 Hs.52256	replication factor C (activator 1) 4 (37	3.33
40	105726	NM_012068	Hs.9754	hypothetical protein FLJ20624 activating transcription factor 5	3.33 3.32
40	101867	M96132		gb:Human MHC class II HLA-DR-beta-1*0901	3.32
	105004 100288	BE616023	Hs.25298	KIAA1813 protein	3.32
	116349	AL039103 N63786	Hs.153834 Hs.94149	pumilio (Drosophila) homolog 1	3.32
	103352	H09366	Hs.78853	ESTs, Weakly similar to ALU1_HUMAN ALU S uracil-D glycosylase	3.32
45	107436	W27720	Hs.12450	protocedherin 9	3.30 3.30
	109062 110379	AA160941		gb:zq40d12.s1 Stratagene hNT neuron (937	3.30
	111221	Al300505 AB037782	Hs.33130 Hs.15119	Homo saplens cD: FLJ23486 fis, clone L	3.30
	117903	AA768283	Hs.47111	KIAA1381 protein ESTs	3.30
50	123265	AA491209		gb:aa47a08.s1 NCI_CGAP_GCB1 Homo saciens	3.30 3.30
	128226 111945	A1284940	Hs.289082	GM2 ganglioside activator protein	3.30
	126214	R40663 AW748338	Hs.124944 Hs.168052	ESTB	3.30
	121073	H46199	Hs.112184	KIAA0421 protein DKFZP586J0819 protein	3.30 3.30
55	102083	T35901	Hs.75117	interlaukin enhancer binding factor 2, 4	3.30
	100992 134021	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral	3.30
	126452	L13720 R26867	Hs.78501	growth arrest-specific 8	3.30
	117195	AJ798425	Hs.42710	.gb:yh52e01.s1 Soares placenta Nb2HP Homo ESTs	3.29 3.29
60	127663	AK000452	Hs.10340	hypothetical protein FLJ20445	3.29
	113677 132398	Z70200 AA876616	Hs.246112	KIAAD788 protein	3.28
	109533	AL043979	Hs.16979 Hs.259729	ESTs, Weakly similar to A43932 mucin 2 p KIAA0596 protein	3.28
	102915	X07820	Hs.2258	matrix matalloproteisa 10 (stromelysis	3.28 3.28
65	104348	H05405	Hs.19221	hypothetical protein DKFZp566G1424	3.28
	113047 113203	A1571940	Hs.7549	£518	3.28
	114503	AA743563 AL040600	Hs.10305 Hs.188083	ESTs	3.28
~ ^	122100	AA431220	Hs.41086	ESTs pleckstrin homology domain-containing, f	3.28
70	123073	AA485061	Hs.105652	ESTs	3.28 3.28
	130253	AI078570	Hs.167473	phosphoglucomutase 5	3.28
	130365 130762	W56119 D84371	Hs.155103 Hs.1898	eukaryotic translation initiation factor	3.28
7.	132360	AW893660	Hs.46440	paraoxose 1 solute carrier family 21 (organic anion	3.28
75	110763	AJ928445	Hs.92254	syptotagmin-like 2	3.28 3.27
	103437	AV655598	Hs.184211	peptidase (milochondrial processing) bet	3.27
	114840 106888	AA447591 AA020964	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	3.27
00	129896	BE295568	Hs.24734 Hs.13225	cxysterol binding protein UDP-Gal:betaGlcc beta 1,4- galactosylt	3.27
80	113459	T80206	Hs.14716	ESTs	3.26 3.26
	134332	D86962	Hs.81875	growth factor receptor-bound protein 10	3.26
	117048 109249	H89732 AA194730	Hs.230113	EŞT	3.26
	,00473	(47174190	Hs.268189	hypothetical protein FLJ20438	3.26

	424002	1100.400			
	134663 114440	W73428 AL046511	Hs.8750 Hs.106525	uncharacterized bone marrow protein BM04	3.26
	102196	BE266830	Hs.75238	hypothetical protein FLJ 12567	3.25
_	109581	R45584	Hs.23025	chromatin assembly factor 1, subunit B (ESTs, Wealdy similar to ALUS_HUMAN ALU S	3.25 3.25
5	120814	AW887798	Hs.95860	ESTs, Weakly similar to 138022 hypotheti	3.25
	122391	AA446316	Hs.191622	ESTs	3.25
	122553 124755	AA451884	Hs.190121	ESTs	3.25
	130943	R38087 U20760	Hs.267690 Hs.2 7 2429	KIAA1228 protein	3.25
10	115185	BE299677	Hs.105461	calcium-sensing receptor (hypocalciuric hypothetical protein FLJ20357	3.25 3.25
	114297	AA149707	Hs.173091	ubiquitin-like 3	3.25 3.25
	106657	AW854339	Hs.33476	hypothetical protein FLJ11937	3.25
	124320	H95749	Hs.102342	EST	3.25
15	124087 110705	H08773 AB007902	Hs.288590 Hs.32168	Homo sapiens cD FLJ11454 fis, clone HE	3.24
	106508	AI205785	Hs.30348	KIAA0442 protein ESTs	3.24
	112538	AA908813	·	gb:og77h06.s1 NCI_CGAP_Ov8 Homo sapiens	3.24 3.24
	100130	NM_000304	Hs.103724	peripheral myelin protein 22	3.24
20	106017	AA477956	Hs.26268	ESTs 🥱	3.24
20	113921 121520	AW976530 AA412163	Hs.28355 Hs.164785	hypothetical protein FLJ22402	3.23
	129255	AI961727	Hs.109804	ESTs H1 histone family, member X	3.23 3.23
	125069	H81306	Hs.194485	ESTs	3.23 3.23
25	119863	AA081218	Hs.58608	Homo saplens cD FLJ14206 fis, clone NT	3.23
23	111273 102971	N70934	11 40000	gb:za33f06.s1 Soares fetal liver splean	3.23
	103937	X16609 AA934083	Hs.183805 Hs.13836	ankyrin 1, erythrocytic	3.23
	121770	NM_015902	Hs.278428	ESTs, Weakly similar to 138022 hypotheti progestin induced protein	3.23 3.23
20	128972	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.23 3.23
30	132528	T78738	Hs.50758	SMC4 (structural maintence of chromoso	3.23
	134835 103158	L04569	Hs.89925	calcium channel, voltage-dependent, L ty	3.23
	118405	8E242587 AL117518	Hs.118651 Hs.3686	hematopoletically expressed homeobox	3.22
	104631	AA002064	Hs.18920	KIAA0978 protein ESTs	3.22
35	114253	BE149866	Hs.14831	Homo saplens, Similar to zinc finger pro	3.22 3.22
	134607	A1675881	Hs.86538	ESTs	3.22
	135114 120191	AW340493	Hs.175043	ancient conserved domain protein 4	3.22
	105029	BE407106 AI122691	Hs.65907 Hs.13268	Homo sapiens, clone IMAGE:3959816, mR, ESTs	3.22
40	128550	AA418276	Hs.170142	ESTs	3.21
	119873	Al660149	Hs.44865	lysosomal	3.21 3.21
	130115	T47294	Hs.149923	X-box binding protein 1	3.21
	133916 120259	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.21
45	110721	AW014788 H97678	Hs.192742 Hs.31319	hypothetical protein FLJ12785	3.21
	130062	AL049415	Hs.278679	ESTs a disintegrin and metalloproteise doma	3.21
	100265	D38521	Hs.112396	KIAA0077 protein	3.21 3.20
	100624	AB001025	Hs.9349	ryanodine receptor 3	3.20
50	122275 127099	AA437124	Hs.187247	ESTs	3.20
50	134321	AA347668 BE538082	Hs.8172	gb:EST54026 Fetal heart II Homo sapiens	3.20
	132809	AF036144	Hs.5734	ESTs, Moderately similar to A46010 X-lin meningloma expressed antigen 5 (hyaluron	3.20
	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	3.20 3.20
55	128339	AL121087	Hs.296406	KIAA0685 gene product	3.19
33	117121 124760	H95044	Hs.321386	EST	3.19
	132232	AW408586 Al522273	Hs.91052 Hs.42640	ESTs, Moderately similar to ALU5_HUMAN A	3.19
	125919	W26713	Hs.256972	ESTs ESTs	3.19
60	123324	AB018352	Hs.105399	KIAA0809 protein	3.19 3.19
60	100157	D14661	Hs.119	Wilms' tumour 1-associating protein	3.19
	101447 124345	M21305	ht- 400700	gb:Human alpha satellite and satellite 3	3.19
	122583	NM_014487 NM_012447	Hs.120766 Hs.20132	nucleolar cysteine-rich protein	3.18
	128961	AL133014	Hs.107387	stromat entigen 3 CGI-20 protein	3.18 3.18
65	111321	A1569766	Hs.13205	ESTs	3.18
	134977	AL044963	Hs.306121	leukocyta receptor cluster (LRC) encoded	3.18
	131535	N22120	Hs.75277	hypothetical protein FLJ13910	3.18
	109950 129875	H08200 AA181018	Hs.268770 Hs.13056	ESTs, Weakly similar to 2004399A chromos	3.18
70	101654	M60298	Hs.733	hypothetical protein FLJ13920 erythrocyte membrane protein band 4,2	3.18
	104732	AL079294	Hs.29952	Homo sapiens mR full length insert cDN	3.18 3.18
	106867	AB037744	Hs.34892	KIAA1323 protein	3.18
	108301 118042	AA069728	Hs.184582	ribosomal protein L24	3.18
75	120900	AJ432389 AA830712	Hs.161465 Hs.291931	ESTs	3.18
	129312	T97579	Hs.110334	ESTs ESTs, Wealdy similar to 178885 serine/th	3.18
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.18 3.17
	110672	AW612890	Hs.191178	ESTs	3.17
80	115665 127581	BE072425 AK000680	Hs.44579	hypothetical protein FLI20199	3.17
-	127581	AV656017	Hs.266175 Hs.184325	phosphoprotein associated with GEMs	3.17
	108830	AA131743	Hs.193352	CGI-76 protein ESTs	3.16
	124443	AI857519	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.16 3.16
					w.10
				112	

	400000	A145004300	11- 40004	hand all and and the Pt 1400FF	2 40
	106290 122787	AW961393 Al209093	Hs.16364 Hs.99512	hypothetical protein FLJ 10955 ESTs	3.16 3.16
	133112	T15465	Hs.182231	thyrotropin-releasing hormone	3.16
	118435	AA185761	Hs.334812	hypothetical protein DKFZp586K0717	3.16
5	109121	BE389387	Hs.49767	DH dehydrogese (ubiquinone) Fe-S pro	3.16
_	126721	AW579621	Hs.125359	Thy-1 cell surface antigen	3.15
	102526	AA203429	Hs.79474	lyrosine 3-monooxygese/tryptophan 5-mo	3.15
	100512	D13317	Hs.78915	GA-binding protein transcription factor,	3.15
• •	105299	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	3.15
10	117842	AI984505	Hs.161121	ESTs	3.15
	123049	BE047680	Hs.211869	dickkopi (Xenopus lasvis) homolog 2	3.15
	128639	AW582962	Hs.102697	CG1-47 protein	3.15
	130343	AB040914	Hs.278628	KIAA1481 protein	3.15
15	115706	AB004849	Hs.50748	chromosome 21 open reading frame 18	3.15
13	120673 132116	AW968634 AW960474	Hs.105093 Hs.40289	ESTs ESTs	3.15 3.15
	116217	AU076474	Hs.123178	translocase of inner mitochondrial membr	3.15
	104926	BE298808	Hs.33363	DKFZP434N093 protein	3.14
	105297	NM_015905	Hs.183858	transcriptiol intermediary factor 1	3.14
20	125343	A1475495	Hs.304101	ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.14
	115618	H11695	Hs.322901	disrupter of silencing 10	3.14
	124893	AA830185	Hs.269680	ESTS	3.13
	105481	BE539071	Hs.69388	hypothetical protein FLJ20505	3.13
25	126165	AJ741816	Hs.125897	ESTs	3.13
25	105212	AA205334	Hs.324278	Homo sepiens mR; cD DKFZp566M063 (fr	3.13
	101628	M57508	Hs.72918	small inducible cytokine A1 (I-309, homo	3.13
	107951	A1300077	Hs.61590	ESTS	3.13
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.13
30	117299 119694	N75768 AA041350	Hs.57847	gb:yw30b07.r1-Morton Fetal Cochles Homo	3.13 3.13
50	124840	R56146	Hs.164515	ESTs, Moderately similar to ICE4_HUMAN C EST, Weakly similar to AF090930 1 PRO047	3.13
	127433	AW979155	Hs.298275	amino acid transporter 2	3.13
	128337	Al123529	Hs.166592	ESTs	3.13
	134053	AW628686	Hs.78851	KIAA0217 protein	3.13
35	134475	NM_014733	Hs.83790	KIAA0305 gane product	3,13
	128761	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	3.12
	124971	T23800	Hs.151001	hypothetical protein FLJ14728	3.12
	128314	T8747 9	Hs.291797	ESTs	3.12
40	134695	AB036829	Hs.178347	SKIP for skeletal muscle and kidney enri	3.12
40	131333	BE244603	Hs.25726	transposon-derived Buster1 transposase-I	3.12
	119781	AJ278016	Hs.55565	ankyrin repeat domain 3	3.12
	131824	U28838	Hs.32935	TATA box binding protein (TBP)-associate	3.11
	124595	AW194851	Hs.111801	arsete resistance protein ARS2	3.11
45	116115 129415	AL042355 Al907084	Hs.70202 Hs.111243	WD repeat domain 10 MADS box transcription enhancer factor 2	3.11 3.11
72	111552	T97939	Hs.191185	ESTs	3.10
	134861	NM_000937	Hs.171880	polymerase (R) II (D directed) polyp	3.10
	104971	BE311926	Hs.15830	hypothetical protein FLJ 12691	3.10
	126536	AA156151		gh:zo48c06.r1 Stratagene endothelial cel	3.10
50	128246	Al990612	Hs.214818	DMRT-like family C2	3.10
	106412	AA453734	Hs.10198	ESTs	3.10
	107902	AA026827	Hs.61358	ESTs	3.10
	112495	A1346487	Hs.28739	ESTs	3.09
E E	131870	NM_014874	Hs.3363	KIAA0214 gene product	3.09
55	105301	AW352357	Hs.7457	MAGE1 protein	3.09
	123670	AI189844	Hs.112708	ESTs, Moderately similar to ZN91_HUMAN Z	3.09
	116474	AW160774	Hs.159154	tubulin, beta, 4	3.09
	112064	AL049390	Hs.22689	Homo sapiens mR; cD DKFZp58601318 (f	3.09
60	130525 120398	AA361850 AL133649	Hs.322149 Hs.110953	Human clone 137308 mR, partial cds retinoic acid induced 1	3.08 3.08
00	102735	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni	3.08
	124748	R34617	15.5002	gb:yh85h12.e1 Soares placenta Nb2HP Homo	3.08
	120755	AA312934	Hs.190745	Homo sapiens cD: FLJ21326 fis, clone C	3.08
	118895	BE304917	Hs.31097	hypothetical protein FLJ21478	3.08
65	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	3.08
	114290	R51383	Hs.25793	ESTs	3.08
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	3.08
	125876	BE612918	Hs.151973	hypothetical protein FLJ23511	3.08
70	127766	AA723659	Hs.290607	EST	3.08
70	132693	BE244200	Hs.55075	KIAA0410 gene product	3.07
	106812	BE251590	Hs.239370	DKFZP727I051 protein	3.07
	125654	X96753	Hs.9004	chondroitin sulfate protaoglycan 4 (meta	3.07
	111836	R58394	Hs.25119	ESTs, Wealdy similar to YEXQ_YEAST HYPOT	3.06
75	101682 110004	AF043045 H10413	Hs.81008	filamin 8, beta (actin-binding protein-2 ESTs	3.08 3.06
, ,	117591	N64777	Hs.268774 Hs.44656	ESTS	3.06
	110737	AA335609	ris.44030 Hs.7589	ESTs, Weakly similar to A46010 X-linked	3.06
	134337	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famili	3.06
	132450	AA100012	Hs.48827	hypothelical protein FLJ 12085	3.06
80	125556	AB033054	Hs.334B06	KIAA1238 protein	3.06
	101811	NM_002556	Hs.24734	oxysterol binding protein	3.06
	131530	AA574309	Hs.283402	TCR eta	3.06
	105049	AB032945	Hs.172506	myosin VB	3.06

	126614	AA701941	Un 40mmm		
	130960	AF035621	Hs.187555	ESTs	3.05
	105503		Hs.21611	kinesin family member 3C	3.05
		AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	3.05
5	107361	U72513	Hs.159486	Human RPL13-2 pseudogene mR, comptete	3.05
3	107575	D81886	Hs.59908	ESTs	
	116999	H84644	Hs.40707	EST	3.05
	119554	W38188		(NONE)	3.05
	120934	AA226198			3.05
	125805	Al160594	Hs.166656	gb:nc26a07.s1 NCI_CGAP_Pri Homo sapiens	3.05
10	127263	AA331156	113.100030	ESTs, Highly similar to \$49460 glutamate	3.05
	128025	T64877	Un 400470	gb:EST35034 Embryo, 6 week, subtracted (3.05
	131090	Al143139	Hs.108479	ESTs	3.05
	112197		Hs.2288	visinin-like 1	3.05
		NM_003655	Hs.5637	ESTs .	3.05
15	133492	L40397	Hs.74137	transmembrane trafficking protein	3.04
13	118485	AA508515	Hs.291049	ESTs	
	113893	AI373741	Hs.59384	hypothetical protein MGC3047	3.04
	116911	AW205577	Hs.308435	ESTs, Moderately similar to KIAA0745 pro	3.04
	132833	U78525	Hs.57783	cutoscalle tenselation intitution for	3.04
	124724	H20816	Hs.112423	eukaryotic translation initiation factor	3.04
20	105894	Al904740		Homo sapiens mR; cD DKFZp586I1420 (f	3.04
	129991		Hs.25691	receptor (calcitonin) activity modifying	3.04
		R28386	Hs.179925	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.04
	128714	T85231	Hs.179661	tubulin, beta 5	3.04
	134650	U76376	Hs.87247	harakiri, BCL2-Interacting protein (cont	3.04
25	106851	Al458623		gb:lk04g09.x1 NCI_CGAP_Lu24 Homo saplens	
23	133445	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.04
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.04
	127542	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	3.04
	113043	Al528789	Hs.7483	ESTS, MODELANDY SITTERED TO ALUS_MUMAN A	3.03
	134710	Al433797	Hs.8889	ESTs	3.03
30	119245	Al815733		serine hydroxymeihyltransferase 1 (solub	3.03
	106391	AW959538	Hs.114360	transforming growth factor beta-stimutat	3.03
	114607		Hs.321214	hypothetical protein DKFZp564D0478	3.03
		AF041260	Hs.129057	breast cardinoma amplified sequence 1	3.03
	116083	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.03
25	132079	AJ701457	Hs.38694	ESTs	
35	103825	Al571835	Hs.55468	ESTs	3.03
	106438	AJ141031	Hs.21342	ESTs	3.03
	124359	N22508	Hs.139315		3.03
	126384	AW090198	Hs.4779	Homo sepiens cD: FLJ21479 fis, clone C	3.03
	127995	AA970953		KIAA1150 protein	3.03
40	127981	AA837029	Hs.128709	ESTs	3.03
	124417		Hs.157463	ESTs	3.02
		N34059		gb:yv28h09.s1 Soares fetzt liver spleen	3.02
	124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Homo	3.02
	105437	AF151076	Hs.25199	hypothetical protein	3.02
45	101158	AW327723	Hs.76122	splicing factor, arginine/serine-rich 4	
43	113897	R91601	Hs.4947	hypothetical protein FLJ22584	3.02
	100159	AA285268	Hs.23488	KIAA0107 gene product	3.02
	108487	A1697340	Hs. 135265	Homo septens clone FLB8436 PRO2277 mR	3.02
	124977	F04819	Hs.190452	VIAA0365 aaaa aaa baraa PROZZ// MR	3.02
	131631	AA022569	Hs.29802	KIAA0365 gene product	3.02
50	102259	AL041219		slit (Drosophila) homotog 2	3.01
	104399	AL022316	Hs.82222	sema domain, immunoglobulin domain ((g),	3.01
	116536		Hs_301947	kraken-like	3.01
		8E218027	Hs.89969	ESTs	3.00
	125889	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.00
55	102233	AW163045	Hs.79334	nuclear factor, Interleukin 3 regulated	3.00
23	102628	U90322	Hs.27812	G protein-coupled receptor 23	
	112812	H55977	Hs.35810	EST8	3.00
	114654	AA101840	Hs.103679	ESTs	3.00
	118555	N68372			3.00
~ ^	120005	W90105	Hs.94942	gb:ze68c10.s1 Soares_fetal_lung_NbHt_19W EST	3.00
60	123596	AA421130	Hs.112640		3.00
	126134	AL133033	Hs.4084	EST	3.00
	126194	H98755		KIAA1025 protein	3.00
	129778	AK001676	Hs.302975	ESTs, Weakly similar to Z195_HUMAN ZINC	3.00
	123110	WV001010	Hs.12457	hypothetical protein FLJ10814	3.00
65	T-11- 20.			· ·	••••
03	Table 38:				
	Pkey:	Unique Eos proi	beset identifier number		
	CAT number	 Gene cluster nu 	mber		
	Accession:	Genbank acces	sion numbers		
70	Pkey	CAT number	Accession		
	123619	371681_1	AA602964 AA609	2000	
	124417	1642364_1		7440	
	117299	1632586_1	N34059 N46979		
			N75768 N22543		
75	116845	393481_1	AA649530 AA659	316 H84973	
, ,	124748	17150801	R34617		
	125596	1708455_1	R25698 R56582 (R56018	
	126257	182217_1	N99638 AW9737	50 AA328271 H90994 AA558020 AA234435 N59599 R94815	
	126280	1572221_1	Z19417 H20866	21846N 6666GU CC64607NATC04400 NO3009 KO4812	
00	126319	1528523_1	D81689 D81802		
80	104172	273499_1	AA47641R AA202	3338 AA398747 AA476518	
	126426	110687_1	AA12600A AA422	MACCOTO A ACCOTO A AC	•
	·		PATE 40 4 400	7189 AA065075 AA070377 AA100017 AA079891 AA113255 AA0	075168 AA082764 AA083380 NB4829 AA084752
	126433	127143_1			
	- 20700		AA325608 AA099	1517 N89423	

	127092	1779998 1	T26985 Z44165
	127099	244301_1	AA347668 AW956810 Z44271 F07065 F07064 R13506
	126536	149206_1	AA156151 Z25109 C05177
5	103731	112052_1	AA070545 AA131490 AA131373
,	127283 126783	232161_1 113388_1	AA331159 AA331157 AA331155
	118946	1683457_1	AA083531 AA126047 AA074915 AA148649 N92834 W25061
	127520	6561701	T51239
10	127532	353907_1	AJ003429 AJ003367 AA564825
10	112518	1744223_1	T83909 R68586
	112538 112540	504579_1	AA908813 R70255
	113248	1605263_1 328626_1	R69751 R70467 H69771 H80879 H80878
	112631	1746257_1	T63857 AW971220 AA493459 T63699 R82040 R70934
15	128360	1540098_1	F12374 T74059
	120514	25532_3	AA258335 AA258499
	127887	1511945_1	C18530 T63953
	120637 121481	200885_1 123001_1	AA811804 AA809404 AA286907 AW977624
20	120934	177521_1	AA411931 AA411930 AA226198 AA226513 AA383773
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AJ333584 AJ369742
			AND39658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
	121743	274582_1	AND 3 / 000 AND 2 144
25	114699 106851	135322_1	AA127386 R15644 AA127404
2.5	123731	322947_1 genbank_AA609839	Al458623 AA639708 AA485409 R22065 AA485570 AA609839
	123973	5063691	C14805
	116793	74964_1	777781 AW014157 D12422 AI918246 AA452599 AA628404 N35886 AA464593 AW201739 T77780 AI042200 AI045900 AI045900
30	400000		AWS 103/6 H3/614 W61360 AI3/3286 AI/02287 AA152465 AW169067 AW169012 AW340355 AI289311
30	109700 118466	genbank_F09609	rusous
	111273	genbank_N88741 genbank_N70934	N56741
	118555	genbank N68372	N70934 N68372
36	111462	genbank_R05296	R05296
35	118720	genbank_N73515	N73515
	118737 111826	382979_1	AA199686 N73861
	120376	genbank_R35975 genbank_AA227469	- R35975 AA227469
4.0	120809	genbank_AA346495	AA346495
40	120839	genbank_AA348913	AA348913
	120873	genbank_AA358015	AA358015
	115498 101045	genbank_AA291070	A2291070
	129969	entrez_J05614 genbank_N57818	J05614
45	108407	genbank_AA075519	N57818 AA075519
	122939	genbank_AA477141	AA477141
	117031	genbank_H88353	H88353
	124298	genbank_H91679	H91879
50	117099 101447	321871_1 entrez_M21305	H93699 H97976 H80036
	124357	genbank_N22401	M21305 N22401
	101723	2603_1	134304 AA355800 M69181 AA375523 AA093590 AA365595 S87247 AI371761 AW351920 AW181991 H28934 W79172 AA653543
		-	^^144V-> 1133314 MEVOOJUS UUZ948 NYS/608 111988 WY5465 AAA75170 FRE72A E122AE ERE20E E1422A TEE222 EROE4E
55			FV/400 AA 100340 R03204 100//U N38306 AA337253 H12001 H82800 H60305 D60300 M20064 M20020 T07206 T06040
33			MMQJQU/ MLU/300U 1138/ AA3USIX8 AA149133 TR7R13 AA02QGGG AA03G100 AA440199 AA946907 AA994466 MAG400
			MIDDIDA MATADIDA CIDAZO CIDADA CIBERT CIBERT CIRTA MADATRA CERRAN MANATA DERRES DENGES MALESSA ALLASSOS
			AW519024 AA490700 N20575 AW298747 C16068 D58331 C16518 A1141214 N57221 C16423 C16537 C16094 C16152 H28935 T66152 C16586 AW022425 AA602899 AA60240 H22255 W74368 C16356 A1129361 A1917988 A1682253 A1923898 A1038907
60			
60			AYYUSU/01 AUUDSUZ 116084 AWUZZ915 C16558 AWA73979 T98820 AAA78898 N78448 E02576 N60208 700000 AA027402
			1976/3 PV 1301U/ TH 1/30 AUDUZDO MX/SHI BIA74575 NEE71R EDADIA A AEREATO A A0022/0 E0/022 A1/02/27 CO 4700 CA 6226
			7000 0 190 700 200 74 7000 000 127 D57-339 AAA90A77 AIREGRIS AIGOOGE AAA3EEA7 AI 110773 AI 12EA30 AAAEA73E
			AL079521 N40299 Al630191 N86148 AA341165 T28492 N83749 Al382123 Al066033 Al950411 Al9335653 AL276551 AW027482 AW197337 Al168323 Al336530 Al094099 Al351490 AA258563 Al634763 Al492374 AA983970 Al123565 T72559 F09890
65			AA669531 AI445824 T07180 AW084799 AA306254 R60606 W28367 R55928 WZ7995 AL044845 AA501890 N84045 T97274
	101033	1 1	NO 7532 AL 135219 AA 116056 106000 AA 116057 TO 7181 R08126
	124677 110243	genbank_R01073	R01073
	101867	genbank_H26683 entrez_M96132	H26683 M98132
70	101941	entrez_\$77583	S77583
	119052	149538_1	R10889 R10888
	126452	209811_1	R26867 R27438
	119263 112040	genbank_T15977	T15977
75	103657	genbank_R43286 entrez_Z73677	R43286 273877
-	119400	genbank_T92767	T92767
	119554	NOT_FOUND_entrez_W38188	W38188
	123130	genbank_AA487200	AA487200
80	123143 121950	genbank_AA487595 genbank_AA429515	AA487595
- •	123265	genbank_AA491209	AA429515 AA491209
	114988	genbank AA251089	AA251089
	107794	genbank_AA019255	AA019256
			116

	109062	genbank_AA160941	AA598484 AA160941
5	TARI F 4A	· AROUT 1164 CENICS LIDDES	THATEOUR SHOW A COLOR

5	TABLE 4A	ABOUT 1164	GENES UPRE	GULATED IN GLIOBLASTOMA		
	PMSY;	umq	ue Los probes	at identifier number		
	ExAcon:	Exen	nplar Accessio	n number, Genbank accession number		
	UnigenelD Unigene Ti	unig	eue umupet			
10	R1:		ene gene litle	e la bad, alle		
	R2:	Ratio	of brain tumo	r to body atlas r to normal brain		
	Pkey	ExAccn				
	412719	AW016610	UnigenelD Hs.129911	Unigene Title ESTs	Ri	R2
15	428321	AI699994	Hs.301347	EST8	117.8	3.3
	455601	AL368680	Hs.816	SRY (sex determining region Y)-box 2	108.9	19
	431917	D16181	Hs.2868	peripheral myelin protein 2	107.5	9.9
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	99.0 72.0	11.8 11.3
20	449494 439285	AW237014	Hs.288650	aquaporin 4	60.0	2.2
. 20	447072	AL133916 D61594	Hs.298998	ESTs	58.2	2.2
	456759	BE259150	Hs.17279 Hs.127792	tyrosylprotein sulfotransferase 1	54.2	7.1
	427343	AI880044	Hs.176977	delta (Drosophila)-like 3 protein kinase C binding protein 2	53.5	2.5
25	425088	AA663372	Hs.169395	Homo saplens cDNA FLJ12015 fls, clone HE	49.6	2.2
25	412959	D87458	Hs.75090	KIAA0282 protein	49.5 46.3	3.1 3.0
	447004 436878	AW296968	Hs.157539	EST8	43.7	3.2
	433551	BE465204 Al985544	Hs.47448	ESTs	39.8	10.8
	425842	AI587490	Hs.289048 Hs.159823	ESTs	39.7	4.3
30	407034	UB4540	18.150025	NK-2 (Drosophila) homolog B gb:Human dystrobrevin Isoform DTN-3 (DTN	39.3	26.2 .
	431725	X65724	Hs.2839	Nome disease (pseudoglioma)	39.1	39.1
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	38.4 37.5	3.7
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	37.5 37.5	22.1 13.9
35	439415 40 93 95	F05538	Hs.12825	EST8	35.4	3.1
	449539	U46745 W80363	Hs.54435	dystrobrevin, alpha	34.3	3,0
	408582	A1436323	Hs.58446 Hs.31141	ESTS	33.6	33.6
	431019	NM_005249	Hs.2714	Homo sapiens mRNA for KIAA1568 protein, forkhead box G18	32.8	5.9
40	427540	R12014	Hs.20976	ESTs	32.4	17,0
40	425057	AA826434	Hs.96944	ESTs	32.1 31.0	2.0
	431941	AK000106	Hs.272227	Homo saplens cDNA FLJ20099 fis, clone CO	30.8	2.3 30.8
	41682 9 420807	AB013805	Hs.80220	catenin (cadherin-associated protein), d	30.4	2.2
	444190	AA280627 Al878918	Hs.57846 Hs.10526	ESTs	30.4	30.4
45	429466	M85835	Hs.12827	cysteine and glycine-rich protein 2 ESTs	30.4	30.4
	444471	AB020684	Hs.11217	KIAA0877 protein	30.2	7.2
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	29.5	29.5
	439979	AW600291	Hs.6823	hypothetical protein FLJ 10430	28.8 27.7	3.0 3.2
50	433800 440435	AI034361	Hs.135150	lung type-I cell membrane-associated gly	27.1	3.2 27.1
-	411078	AL042201 Al222020	Hs.21273 Hs.182384	ESTs	26.9	26.9
	407808	AA683559	Hs.289109	ESTs, Weakly similar to 25 kDa trypsin i	26.0	26.0
	416155	A1807264	Hs.205442	dimethylarginine dimethylaminohydrolase ESTs, Wealdy similar to AF117610 1 inner	25.8	2.2
55	421659	NM_014459	Hs.106511	protocadherin 17	25.5 25.0	25.5
22	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	25.0 24,7	3.3 24.7
	433332 452744	Al367347 Al267652	Hs.127809	ESTs	24.6	24.6
	419271	N34901	Hs.30504 Hs.238532	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	23.8	23.8
	447397	BE247676	Hs.18442	ESTs E-1 enzyme	23.6	5.5
60	439039	AI656707	Hs.48713	ESTs	23.1	3.2
	414175	Al308876	Hs.103849	ESTs	23.0 22.2	7.2
	451099 410102	R52795	Hs.25954	interleukin 13 receptor, alpha 2	22.0	2.0 7.6
	415910	AW248508 U20350	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	21.6	2.3
65	451468	AW503398	Hs.78913 Hs.210047	chemokine (C-X3-C) receptor 1 ESTs	21.2	3.0
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	21.0	4.7
	443850	AW014723	Hs.134719	ESTs	20.8	20.8
	418738	AW388633	Hs.6682	ESTs	20.4 20.2	38.5
70	449433 435706	Al672096	Hs.9012	ESTs	19.9	2.2 16.6
, ,	407192	W31254	Hs.7045	GL004 protein	19.7	19.7
	416892	AA609200 L24498	Hs.80409	gb:af12e02.s1 Soares_testis_NHT Home sap	19.7	19.7
	442562	BE379584	Hs.34789	growth arrest and DNA-damage-inducible, ESTs	19.6	19.6
75	439451	AF086270	Hs.278554	haterochromatin-like protein 1	19.4	19.4
75	426320	W47595	Hs.169300	transforming growth factor, beta 2	19.1	17.4
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	18.7 18.6	5.4 19.5
	452106 431173	AJ141031	Hs.21342	ESTs	18.6	18.6 10.3
•	422583	AW971198 AA410506	Hs.294068 Hs.118578	ESTS	18.6	18.6
80	419088	AI538323	Hs.77496	H.sapiens mRNA for ribosomal protein L18 small nuclear ribonucleoprotein polypept	18.5	18.5
	443547	AW271273	Hs.23767	Homo seplens cDNA FLJ12666 fis, clone NT	18.5	18.5
	451592	A1805416	Hs.213897	ESTs	18.5 18.4	5.1 19.4
	450313	A1038989	Hs.24809	hypothetical protein FLJ 10826	18.3	18.4 18.3

	422544	AB018259	Hs.118140	KIAA0716 gene product	18.2	4.7
	408096	BE250162	Hs.83765	dihydrofolate reductase	18.0	18.0
	418027 414117	AB037807 W88559	Hs.83293	hypothetical protein	18.0	8.2
5	429418	Al381028	Hs.1787 Hs.99283	proteolipid protein (Pelizaeus-Merzbache ESTs	18.0	18.0
	432527	AW975028	Hs.102754	ESTS	17,8 17,7	17.8 4.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to phosphodiesteras	17.5	4.3
	419704	AA429104	Hs.45057	ESTs	17.4	4.6
10	436476 445133	AA326108 AW157648	Hs.53631 Hs.153506	ESTs, Wealthy similar to enhancer-of-spii	17.4	2.1
	446859	Al335361	Hs.226376	ESTs, Weakly similar to AF150755 1 micro ESTs	17.3	18.8
	409049	AJ423132	Hs.146343	ESTs	17.2 17.2	2.8 3.8
	443672	AA323362	Hs.9657	butyrobetaine (gamma), 2-oxoglutarate di	17.2	11.0
15	407748	AL079409	Hs.38178	KIAA0606 protein; SCN Circadian Oscillat	17.0	6.3
13	438527 417791	Al969251 AW965339	Hs.143237 Hs.111471	ESTs ESTs	16.9	16.9
	417355	D13168	Hs.82002	endothelin receptor type B	16.8 16.4	10.5
	427897	NM_017413		spellin; peptide ligand for APJ receptor	16.3	16.4 4.2
20	419721	NM_001650	Hs.288650	equaporin 4	16.2	4.4
20	427701	AA411101	Hs.221750	ESTs	16.1	3.9
	432435 426809	BE218886 BE313114	Hs.282070 Hs.29706	ESTs	16.1	5.7
	407881	AW072003	Hs.40968	ESTs heparan sulfate (glucosamine) 3-O-sulfot	16.0 15.9	10.0
0.5	400859	***************************************	110.10000	maper an administry (graces an interfer	15.7	15.9 15.7
25	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	15.6	15.6
	420092	AA814043	Hs.88045	ESTs	15.6	5.4
	449605 422365	AW138581 AF035537	Hs.198416 Hs.115521	ESTS	15.5	3.0
	449611	A1970394	Hs.197075	REV3 (yeast homolog)-like, catalytic sub ESTs	15.3 15.2	4.6 15.2
30	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	15.2	5.6
	405238				15.1	2.8
	429007 409638	D80642	11- 04005	gb:HUM092E09B Human fetal brain (TFujiwa	15.0	3.5
	445888	AW450420 AF070564	Hs.21335 Hs.13415	ESTs Homo saptens clone 24571 mRNA sequence	14.9	7.1
35	416737	AF154335	Hs.79691	LIM domain protein	14.8 14.7	5.7 4.2
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	14.6	3.0
	436870	AW204219	Hs.43879	E515	14.6	2.6
	443181 435281	Al039201 AW411194	Hs.54548 Hs.120051	ESTS	14.6	3.5
40	449448	D60730	Hs.57471	ESTS ESTs	14.5 14.4	8.5 4.8
	422564	AI148006	Hs.222120	ESTs	14.4	14.4
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	14.3	2.4
	428748	AW593206	Hs.98785	ESTB .	14.2	14.2
45	452578 452461	AB023177 N78223	Hs.29900 Hs.108106	KIAA0980 protein transcription factor	14.1	8.1
	449670	F07693	Hs.23869	Homo saplens mRNA; cDNA DKFZp434K2172 (f	14.1 14.1	12.8 14.1
	436837	AI783629	Hs.26768	ESTs	14.0	2.3
	429597	NM_003816		a disintegrin and metalloproteinase doma	13.9	13.9
50	419078 410889	M93119 X91662	Hs.89584 Hs.66744	Insulinoma-associated 1	13.9	29
	452355	N54926	Hs.29202	twist (Drosophila) homolog (acrocephalos G protein-coupled receptor 34	13.9 13.9	4.1
	421452	AJ925946	Hs.104530	fetal hypothetical protein	13.9	13.9 13.9
	430290	AI734110	Hs.136355	ESTS	13.8	13.8
55	430387 415875	AW372884 AA894876	Hs.240770	nuclear cap binding protein subunit 2, 2	13.6	13.6
-	416795	AM97778	Hs.5687 Hs.168053	protein phosphatase 18 (formerty 2C), ma ESTs, Highly similar to AF227948 1 HBV p	13.5	13.5
	422025	BE348774	Hs.122554	ESTs	13.5 13.3	13.5 13.3
	400992				13.3	5.5
60	413174 425187	AA723564 AW014486	Hs.191343	ESTs	13.2	2.5
00	456965	AW131888	Hs.22509 Hs.172792	ESTs ESTs, Weakly similar to hypothetical pro	13.1	8.2
	419852	AW503756	Hs.286184	hypothetical protein d.1551D2.5	13.1 13.0	27 24
	409327	L41182	Hs.53563	collagen, type IX, alpha 3	12.9	4.0
65	439519	AA837118	Hs.118366	EST8	12.9	7.6
05	436299 446657	AK000767 Al335191	Hs.5111	hypothetical protein FLJ20729 ESTs, Moderately similar to ALU7_HUMAN A	12.7	3.1
	423073	BE252922	Hs.260702 Hs.123119	MAD (mothers against decapentaplagic, Dr	12.6 12.6	12.6 12.6
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	12.6	12.6
70	451996	AW514021	Hs.245510	ESTs	12.6	7.0
70	400860 439579	AE006400		abiliana ancies 6.81	12.5	23.1
	408312	AF086400 AF263813	Hs.44198	gb:Homo saplens full length insert cDNA Intracellular membrane-associated calciu	12.4	12.4
	419948	AB041035	Hs.93847	NADPH coddase 4	12.4 12.4	12.4 2.4
75	427304	AA761526	Hs.163853	ESTs	12.3	12.3
75	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	12.2	12.2
	428137 432683	AA421792 AW995441	Hs.170999 Hs.10475	ESTs ESTs	12.2	12.2
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	12.2 12.1	2.0 12.1
00	453884	AA355925	Hs.38232	KIAAD188 gene product	12.0	12.1 5.2
80	441440	AJ807981	Hs.30495	ESTs	12.0	3.6
	414217 410227	Al309298 AB009284	Hs.279898		12.0	62.7
	439444	AI277652	Hs.61152 Hs.54578	exostoses (multiple)-like 2 ESTs	11.9	2.9
				·-	11.9	16.5

			15. 400000			
	433309			ESTs	11.7 11.6	9.0 9.7
	439170 417160	N76497	Hs.165539 Hs.1787	ESTs proteolipid protein (Pelizaeus-Merzbache	11.5	7.2
_	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	11.5	5.8
5	410811	AW954134	Hs.20924	KIAA1628 protein	11.5	28.2
	437124	AA554458	Hs.204200	ESTs	11.5	11.5
	418858	AW961605	Hs.21145	Homo saplens cDNA: FLJ22489 fis, clone H	11.3	11.3
	423600 429393	A1633559 AA383024	Hs.29076 Hs.201603	Homo saplens cDNA: FLJ21841 fis, clone H ESTs, Highly similar to hypothetical pro	11.3 11.3	2.8 11.3
10	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	11.3	3.4
10	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	11.3	11.7
	431701	AVV935490	Hs.14658	ESTs	11.3	26
	429399	AA452244	Hs.16727	ESTs	11.2	2.2
15	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	11.2 11.1	27.8
IJ	442671 402524	Al005668	Hs.134779	EST	11.1	11.1 11.1
	415558	AA885143	Hs.125719	ESTs	11.1	11.1
	422390	AW450893	Hs.121830	ESTs, Weakly similar to KIAA0924 protein	11.0	8.8
00	418475	A1858732	Hs.30443	sentrin/SUMO-specific protease	11.0	6.1
20	458809	AW972512	Hs.20985	sin3-essociated polypeptide, 30kD	11.0	5.6
	410297	AA148710	Hs.159441	ESTS	11.0	3.3
	444017 437814	U04840 Al088192	Hs.214 Hs.135474	neuro-oncological ventral antigen 1 ESTs, Weakly similar to DDX9_HUMAN ATP-D	11.0 10.9	11.0 3.3
	427194	AA399018	Hs.250835	ESTs	10.8	8.0
25	432060	AW971364		gb:EST383453 MAGE resequences, MAGL Horno	10.8	10.0
	453861	AI026838	Hs.30120	ESTs	10.8	10.8
	408829	NM_006042	Hs.48384	heparan sullate (glucosamine) 3-O-sulfot	10.6	3.3
	416913 418049	AW934714	U= 100400	gb:RC1-DT0001-031299-011-e11 DT0001 Homo	10.6 10.6	3.4 10.6
30	413063	AA211467 AL035737	Hs.1904B8 Hs.751B4	hypothetical protein FLJ10120 chitinase 3-like 1 (cartilage glycoprote	10.6	27.2
20	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	10.5	20
	434408	AI031771	Hs.132586	ESTs	10.5	10.5
	451697	AW449774	Hs.257208	ESTs	10.5	6.2
35	436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin	10.3	10.3
33	410298 412766	A1693821 BE544475	Hs.182185 Hs.54347	ESTs ESTs	10.3 10.3	2.9 10.3
	450689	Al369275	Hs.243010	ESTs, Moderately similar to RTCO_HUMAN G	10.3	10.3
	408331		Hs.44229	dual specificity phosphatase 12	10.3	4.5
40	442007	AA301116	Hs.142838	Homo sapiens cDNA: FLJ23444 fis, clone H	10.3	10.3
40	410386	W26187	Hs.3327	Home saplens cDNA: FLJ22219 fis, clone H	10.2	2.1
	440684	AI253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI	10.1 10.0	10.1 10.0
	420892 419594	AW975076 AA013051	Hs.172589 Hs.91417	nuclear phosphoprotein similar to S, cer topoisomerase (DNA) il binding protein	9.9	15.8
	419972	AL041465	Hs.294038	ESTs, Moderately similar to ALU2_HUMAN A	9.7	23.2
45	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	9.6	6.5
	434851	AA806164	Hs.116502	ESTs	9.6	6.5
	438306	AA805939	Hs.117927	ESTS	9.5	4.7
	453331 414429	AI240665 R51494	Hs.8895 Hs.71818	ESTs ESTs	9.2 9.0	5.8 6.2
50	424998	U58515	Hs.154138	chitinase 3-like 2	8.9	18.1
	446936	H10207	Hs.47314	ESTs	8.9	3.6
	410276	A1554545	Hs.68301	ESTs	8.8	3.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	8.8	3.8
55	448321 414783	AW069569	3 Hs.20912 Hs.75839	adenomatous polyposis coli like zinc finger protein 6 (CMPX1)	8.8 8.7	20 3.0
JJ	441079	AW150697			8.7	2.2
	437517	A1927675	Hs.99858	ribosomai protein L7a	8.6	4.5
	409062	AL157488	Hs.50150	Homo sepiens mRNA; cDNA DKFZp564B182 (fr	8.6	12.2
60	429630	AL133101	Hs.99508	Homo saplens mRNA; cONA DKFZp43400921 (f	8.6	10.4
00	409260 442343	AW242407 AA992480		ESTs ESTs	8.5 8.4	11.6 4.6
	416439	AA180363			8.4	7.2
	428054	Al948688	Hs.266619		8.2	9.2
	421633	AF121860	Hs.108260	sorting nexin 10	8.2	26
65	433285	AW975944		EST8	8.1	3.3
	433226 424800	AW503733 AL035588		KIAA1488 protein	8.0 8.0	13.4 2.5
	425681	AB018297			7.9	4.8
	445034	AW29337			7.9	3.7
70	435020	AW50507	6 Hs.301854	5 DiGeorge syndrome critical region gene 8	7.6	6.4
	446985	AL038704			7.5	7.8
	446619	AU076643		secreted phosphoprotein 1 (osleopontin,	7.5	3.9 2.2
	418522 439864	AA605038 AI720078		Homo sapiens cDNA: FLJ21950 fis, clone H 7 ESTs	7.5 7.4	6.9
75	419723	AL120193			7.4	3.5
	447896	Al436124			7.3	22.1
	404210				7.3	40.8
	436671	AW13715			7.2	11.8
80.	439231 418030	AW58193 BE207573			7.2 7.1	2.5 6.4
U.	459290	NM_0015			7.1 7.0	6.7
	423869	BE40930		2 C1q-related factor	7.0	4.9
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4

	400040					
	420018 428600	U56387 AW863261	Hs.94376	proprotein convertase subtilisin/kexin t	6.9	8.6
	438380	T06430	Hs.15036 Hs.6194	ESTs, Highly similar to AF161358 1 HSPC0 chondrollin sulfate proteoglycan BEHAB/b	6.9 6.9	7.7
	402504	.00.00	113.015-	CHANGE SEED PROBUBLICATI DELIVORD	6.8	3.1 7.0
5	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.8	2.5
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	6.8	29
	433577	AW007080	Hs.8817	ESTs	6.6	26
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	6.6	13.9
10	413888 451460	AW958264	Hs.103832	ESTs, Wealthy similar to TRHY_HUMAN TRICH ESTs	6.6	2.2
10	442145	A1797550 A1022650	Hs.209652 Hs.8117	erbb2-interacting protein ERBIN	6.5 6.5	13.7 15.6
	437273	AL137451	Hs.120873	ESTs, Highly similar to hypothetical pro	6.5	24
	418365	AW014345	Hs.161690	ESTs	6.4	12.8
	421684	BE281591	Hs.106768	hypothetical protein FLI10511	6.4	4.3
15	449458	A1805078	Hs.208261	ESTs	6.4	23
	426413	AA377823	11- 400000	gb:EST90805 Synovial sarcoma Homo sapien	6.3	13.2
	426423 417709	NM_012446 D87434	Hs.169833 Hs.82426	single-stranded-DNA-binding protein	6.3	10.9
	448499	BE613280	Hs.250655	KIAA0247 gene product prothymosin, alpha (gene sequence 28)	6.3 6.2	23.3 2.9
20	444880	AW118683	Hs.154150	ESTs	6.2	19.4
	432715	AA247152	Hs.200483	ESTs, Wealthy similar to KIAA1074 protein	6.2	12.7
	444864	AW965446	Hs.46637	ESTs, Weakly similar to cONA EST yk289g5	6.2	4.1
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	6.2	3.4
25	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	6.1	2.6
23	424232 436443	AB015982 AW138211	Hs.143460 Hs.128746	protein kinase C, nu ESTs	6.1	14.6
	433647	AA603367	Hs.222294	ESTs	6.1 6.1	2.8 15.0
	449961	AW265634	Hs.133100	ESTs	6.1	3.4
20	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	6.1	6,1
30	408393	AW015318	Hs.23165	ESTs	6.1	21.6
	450693	AW450461	Hs.203965	ESTs	6.1	2.2
	407846 445817	AA426202 NM_003642	Hs.40403 Hs.13340	Cbp/p300-interacting transactivator, wit	6.0	24
	440650	R44692	Hs.6640	histone acetyltransferase 1 ESTs	6.0 6.0	10.9 2.1
35	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	6.0	2.4
	411083	N41340	Hs.68318	hypothetical protein FLJ20344	6.0	3.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	• 6.0	6.0
	402855	411/050460			6.0	2.6
40	445594 418791	AW058463 AA935633	Hs.12940 Hs.194628	zinc-fingers and homeoboxes 1	6.0	11.6
40	409262	AK000631	Hs.52256	ESTs hypothetical protein FLJ20624	5.9 5.9	6.7 2.3
	435677	AA694142	Hs.293726	ESTs	5.9	11.8
	430334	AI824719	Hs.47557	ESTs	5.9	7.5
45	452834	AI638627	Hs.105685	ESTs	5.9	26
45	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	5.8	3.1
	428250	AWB09208	Hs.183297	DKFZP566F2124 protein	5.8	2.0
	418506 417115	AA084248 AW962792	Hs.85339 Hs.1066	G protein-coupled receptor 39 small nuclear ribonucleoprotein polypept	5.8	25
	436758	AW977167	Hs.155272	ESTs	5.8 5.B	16.0 3.8
50	446332	AK001635	Hs.14838	hypothetical protein FLI10773	5.7	5.1
	423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	5.7	11.1
	428180	Al129767	Hs.182874	Homo sapiens cDNA: FLJ21929 fis, clone H	5.6	7.1
	424343	AW956360	Hs.4748	ESTs, Highly similar to JN0902 pitultary	5.6	2.2
55	417318 423582	AW953937 BE000831	Hs.12891 Hs.23837	ESTs Homo sepiens cDNA FLJ11812 fis, clone HE	5.6 5.6	25.0
	427472	AA522539	Hs,131250	transposon-derived Buster3 transposase-I	5.6 5.4	4.1 3.5
	434701	AA460479	Hs.4096	KIAA0742 protein	5.4	21.2
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	5,3	2.7
60	41,1019	AW993097	Ha.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	5.3	4.1
60	424939	AK000059	Hs.153881	Homo saplens NY-REN-62 antigen mRNA, par	5.3	24
	424028 444534	AF055084 AW271626	Hs.153692 Hs.42294	KIAA0688 protein	5.3	2.7
	426171	Al128606	Hs.301454	ESTs ESTs	5.3 5.2	2.1 3.8
	431843	AA516420	Hs.183526	ESTs	5.2	6.2
65	438204	Al589845	Hs.128690	ESTs	5.2	5.8
	424635	AA420687	Hs.115455	Homo seplens cDNA FLJ14259 fis, clone PL	5.2	8.4
	436223	AK001884	Hs.23799	ESTs	5.2	2.4
	450649	NM_00142	9 Hs.297722		5.2	15.3
70	441689 443392	Al123705 Al055821	Hs.106932 Hs.293420		5.2	2.2
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	5.1 5.1	3.3 16.7
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	5.1	18.7
	434001	AW950905	Hs.3897	serine (or cystelne) proteinase inhibito	5.0	2.4
75	458435	Al418718	Hs.144121	ESTs, Wealdy similar to dJ37E16.2 [H.sep	5.0	3.9
75	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	5.0	2.8
	452040	AW973242	Hs.293690	ESTS	5.0	4.5
	404029 421141	AW117281	Hs.125914	ESTs	5.0	4.3
	402605	A-F11720	113.123319	Colo	5.0 4.9	2.1 4.2
80	435839	AF249744	Hs.25951	Rho guardne nucleotide exchange factor (4.9	2.5
	416404	AA180138	Hs.107924	ESTS	4.9	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KOT-lik	4.9	7.2
	448425	A1500359	Hs.233401	ESTS	4.9	4.9

	445770	1				
	445773	H73456 AW015994	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.9	2.9
	448451 444838	AV651680	Hs.208558	gb:UI-H-BIOp-ebh-g-09-0-UI.s1 NCI_CGAP_S	4.9	22
	452438	BE514230	Hs.29595	ESTs JM4 protein	4.8	6.7
5	443898	AW804296	Hs.9950	Sec61 gamma	4.8 4.8	2.7 7.2
•	452776	AA194540	Hs.13522	ESTs	4.8	3.4
	426108	AA622037	Hs.166458	programmed cell death 5	4.8	16.7
	416774	Al005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.8	3.2
• •	427704	AW971083	Hs.292882	ESTs	4.8	23.8
10	433588	Al056872	Hs.133386	ESTs	4.8	12.8
	410108	AA081659	Hs.191098	KIAA1479 protein	4.7	2.1
	433556	W56321	Hs.111460	Homo saptens cDNA: FLJ21715 fis, clone C	4.7	11.2
	418962	AA714835	Hs.271863	ESTs	4.7	2.2
15	404049	A1000707	U- 42204A	Management of the Management of the Land	4.7	3.0
13	436222 425234	A1208737 AW152225	Hs.122810	Home sapiens cDNA FLJ11489 fis, clone HE	4.7	3.3
	426490	NM_001621	Hs.165909 Hs.170087	ESTs anyl hydrocarbon receptor	4.7	3.1
	426514	BE616833	Hs.301122	bone morphogenetic protein 7 (osteogenic	4.7 4.7	9.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.6	2.7 6.7
20	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	4.6	13.4
	412490	AW803564	Hs.288850	Homo sepiens cDNA: FLJ22528 fts, clone H	4.6	18.4
	422488	AI679968	Hs.152060	ESTs	4.6	7.7
	428862	NM_000346		SRY (sex-determining region Y)-box 9 (ca	4.6	4.6
25	413724	AA131466	Hs.23767	Homo sepiens cONA FLJ12666 fis, clone NT	4.5	11.9
25	442495	AJ184717		gb:qd64b01.x1 Soares_testis_NHT Homo sap	4.5	4.6
	403549				4.5	11.6
	456209	W60633	Hs.297792	ESTs	4.5	5.1
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.5	10.6
30	439566 446329	AF086387 NM_013272	Un 1400E	gb:Homo sapiens full length insert cDNA	4.4	2.6
50	446488	AB037782	Hs.15119	solute carrier family 21 (organic anion KIAA1361 protein	4.4	17.2
	426110		Hs.166563	replication factor C (activator 1) 1 (14	4.4 4.4	8.4 2.5
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	4.4	14.3
	424340	AA339038	Hs.7033	ESTs	4.4	3.9
35	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.3	31.1
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	4.3	6.1
	434476	AW858520	Hs.271825	ESTS	4.3	4,5
	420582	BE047878	Hs.99093	Homo saplens chromosome 19, cosmid R2837	4.3	3.6
40	419904	AA974411	Hs.18672	ESTs .	4.3	17.1
40	407939	W05608	11-04040	gb:za85e07.r1 Soares_fetal_lung_NbHt.19W	4.3	9.0
	425836 426304	AW955696	Hs.94842 Hs.297985	ESTs	4.3	3.2
	439653	AA374532 AW021103	Hs.6631	ESTs	4.3	6.6
	424723	BE409813	Hs.152337	hypothetical protein FLJ20373	4.3	23
45	426064	BE387014	Hs.166146	protein arginine N-methyltransferase 3(h Homer, neuronal immediata early gena, 3	4.3 4.2	2.5 4.1
	409509	AL036923	Hs.127006	ESTs	4.2	16.4
	424391	B£550112	Hs.112712	ESTs	4.2	3.8
	425248	AW957442	Hs.252766	ESTs	4.2	11.1
CO	418259	AA215404	Hs.137289	ESTs	4.2	19.3
50	445525	BE149866	Hs.14831	ESTs	4.2	3.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	4.2	34.8
	430935	AW072916	Hs.115654	ESTs	4.2	3.0
	442233	AW967149	Hs.28439	ESTs, Wealty similar to ORF2 (M.musculus	4.2	2.4
55	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	4.1	15.3
"	437097 428189	N45312 AA424030	Hs.46506 Hs.46627	ESTs ESTs	4.1	15.6
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.1	3.6
	425500	AB011541	Hs.158200	EGF-like-domain, multiple 4	4.1 4.1	12.2 2.8
	435177	Al018174	Hs.42936	ESTs	4.1	2.1
60	418357	Z44718	Hs.301010	ESTs, Highly similar to AF159851 1 Rho G	4.1	4.1
	419086		Ha.89591	Kalimann syndrome 1 sequence	4.1	4.1
	436557	W15573	Hs.5027	ESTs	4.0	2.1
	425588	F07396	Hs.48751	ESTs .	4.0	2.2
65	423905	AW579960	Hs.135150		4.0	3.6
03	437095	D14661	Hs.119	Wilms' tumour 1-associating protein	4.0	10.0
	425332	AA633306	Hs.127279	ESTs	4.0	10.9
	431558	AF016028	Hs.260039		4.0	3.8
	427209 435468	H06509 AW362803	Hs.92423	KIAA1566 protein	4.0	3.1
70	416773	AK000340	Hs.166271 Hs.79828		4.0	2.2
	440483	A1200836	Hs.150386	hypothetical protein FLJ20333 ESTs	4.0 4.0	26
	444821	AA053564	Hs.12040	STE20-like kinase	4.0	2.5 10.4
	433873	AW156913			4.0	2.3
~-	420028	AB014680	Hs.8786	carbohydrate (chondroitin 6/keratan) sul	3.9	28 28
75	446706	AW807631	Hs.190488		3.9	3.8
	424530	AI632083	Hs.28511	ESTs	. 3.9	2.2
	446851	AW007332	Hs.16261	Homo sapiens cONA: FLJ22063 fis, clone H	3.9	16.0
	424720	M89907	Hs.152292		3.9	4.5
80	409456	U34962	Hs.54473	cardiac-specific homeo box	3.9	8.0
οv	420439 447340	AW270041			· 3.9	7.9
	430887	AW981327 N66801			3.9	2.1
	409381	NM_00598	Hs.260287 2 Hs.54416	ESTs, Wealdy similar to ALU7_HUMAN ALU S sine oculis homeobox (Drosophila) homoto	3.9	2.5
	.50001		• 11a-34410	енто осина импросом (отозорина) полною	3.9	4.6

	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.9	4.0
	410079	U94362	Hs.58589	glycogenin 2	3.9	18.3
	426818 435232	AA554827	Hs.124841	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.9	3.0
5	427228	NM_001262 AA115770	Hs.174051	Cyclin-dependent kinese inhibitor 2C (p1	3.8	4.0
•	443801	AW206942	Hs.253594	small nuclear ribonucleoprotein 70kD pol ESTs	3.8	7.9
	450746	D82673	Hs. 169921	general transcription factor II, i, pseu	3.8	3.4
	443837	AI984625	Hs.9884	spindle pole body protein	3.8 3.8	2.2
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	3.8	6.5 2.2
10	426757	AW205640	Hs.158206	ESTs	3.7	3.1
	443101	Al 268936	Hs.129872	sperm surface protein	3.7	24
	440118	AB040893	Hs.6968	KIAA1460 protein	3.7	3.5
	410812	AW502698	Hs.118152	ESTs	3.7	22.5
15	435869	AF255910	Hs.54650	vascular endothelial junction-associated	3.7	4.2
IJ	433208 432357	AW002834 AA452506	Hs.24095	ESTs	3.7	16.0
	413916	N49813	Hs.274412 Hs.75615	similar to yeast Upf3, variant A	3.7	26
	429766	AA612710	Hs.146140	apolipoprotein C-II ESTs	3.7	5.4
	437470	AL390147	Hs.134742	hypothetical protein OKFZp547D065	3.7	3.2
20	438459	T49300	Hs.35304	Homo saplens cDNA FLJ13655 fis, clone PL	3.7 3.7	6.4
	420361	N92054	Hs.206910	ESTs	3.7	10.7 18.7
	408819	AW163483	Hs.48320	DKFZP56681346 protein	3.7	8.8
	411960	R77776	Hs.18103	ESTs	3.7	23
25	435923	BE301930	Hs.5010	Homo saplens clone 24672 mRNA sequence	3.7	2.2
23	440145	AW021433	Hs.250863	ESTs	3.7	3.8
	453740 440975	AL120295	11- 7070	gb:DKFZp781M067_s1 761 (synonym; harry2)	3.6	3.0
	443135	AW499914 Al376331	Hs.7579 Hs.156103	hypothetical protein FLI 10402	3.6	20
	419687	Al638859	Hs.227699	ESTS Weekly of The to Visit To 10 and	3.6	12,4
30	451029	AA852097	Hs.25829	ESTs, Weakly statist to Yhr217cp (S.cere res-retated protein	3.6	2.7
	414512	AL044336	Hs.6831	golgi resident protein GCP60	3.6	29
	410853	H04588	Hs.30469	ESTS	3.6 3.6	10.5
	419900	Al469960	Hs.170698	ESTs	3.6	23.9 3.6
26	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.6	7.5
35	428290	Al932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	3.6	9.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	3.6	4.9
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.6	2.1
	441269 447961	AW015208	Hs.178784	ESTs	3.6	2.8
40	447735	W32791	Hs.170405	ESTS	3.5	4.6
10	437580	AA775268 AA761075	Hs.6127 Hs.293567	Homo sapiens cDNA: FLJ23020 fis, clone L	3.5	2.1
	447710	Al420523	Hs.161282	ESTs ESTs	3.5	3.5
	436446	AW016809	Hs.119021	ESTs	3.5	3.5
4.=	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.5 3.5	2.2
45	409712	AA167385	Hs.13583	ESTs	3.5 3.5	4.1 3.8
	404048				3.5	3.2
	440516	642303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	3.5	10.6
50	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.5	3.8
50	426101 436252	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	3.5	32.2
	430252	Al539519 AA610649	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	3.5	4.6
	408495	W68796	Hs.237731	gb:np95c03.s1 NCI_CGAP_Thy1 Homo saplens	3.5	3.5
	418801	AA228366	Hs.115122	ESTs ESTs	3.5	6.1
55	422493	AW474183	Hs.233816	ESTB	3.5	5.1
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	3.5	15.2
	414591	AI888490	Hs.55902	ESTs	3.5 3.5	2.4 8.3
	439627	BE621702	Hs.29076	Homo saplens cDNA: FLJ21841 fis, clone H	3.5	30.2
4 Λ	444969	Al203334	Hs.160628	ESTS	3.5	3.1
60	435370	AI964074	Hs.225838	ESTs	3.5	3.0
	443228	W24781	Hs.293798	ESTs	3.4	4.6
	414612 437410	BE274552	Hs.76578	protein inhibitor of activated STAT3	3.4	5.0
	444172	AW023340 BE147740	Hs.14880 Hs.1045 5 8	ESTs ESTs	3.4	2.7
65	428484	AF104032	Hs.184601		3.4	129
••	437860	AA333083	Hs.279898	solute certier family 7 (cationic amino	3.4	2.8
	428776	AW016638	Hs.155847	Homo sapiens cDNA: FLJ 23165 fis, clone L ESTs, Highly similar to R29144 1 (H.sapi	3.4	4.0
	409493	AA386192	Hs.193482	ESTs	3.4 3.4	2.5
70	432559	AW452948	Hs.257631	ESTs	3.4	3.4 6.3
70	451455	A1937227	Hs.8821	liver-expressed antimicrobial peptide	3.4	6.1
	444153	AK001610	Hs.10414	hypothetical protein FU 10748	3.4	2.6
	422872	BE326786	Hs.187646	ESTA	3.4	2.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.4	26
75	416131 408576	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	3.4	9.5
, 5	408576 431770	NM_003542		H4 histone family, member G	3.4	3.4
	426030	BE221880 BE243933	Hs.268555	5-3' exoribonuclease 2	3.4	21.2
	422573	AW297985	Hs.108642 Hs.28777	zinc finger protein 22 (KOX 15) H2A histone family, member L	3.4	2.1
••	436865	AW880358	Hs.190488	hypothetical protein FLJ10120	3.4	3.7
80	442091	AW770493	Hs.195904	guanine nucleotide binding protein (G pr	3.4	7.6
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.4 3.4	2.9
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.4	5.5 3.9
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.4	16.8
				101		••••

	447279	AA325308	Hs.18016	Homo sapiens mRNA; cONA DKFZp586H0324 (I	3.3	3.0
	410020 447272	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver,	3.3	5.8
	407656	NM_014827 AW747986	Hs.17969 Hs.37443	KIAA0663 gene product	3.3	13.4
5	435354	AA678267	Hs.117115	Homo saplens mRNA; cDNA DKFZp434B2119 (f ESTs	3.3	2.3
_	443884	N20617	Hs.226627	leptin receptor	3.3 3.3	5.5
	444984	H15474	Hs.12214	Homo sepiens clone 23716 mRNA sequence	3.3	8.6 2.0
	431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	2.4
	424682	AW604804	Hs.151717	KIAA0437 protein	3.3	13.7
10	457972	AJ419060	Hs.47448	ESTs	3.3	4.2
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	3.3	3.2
	438666	AW014493	Hs.126727	ESTs	3.3	10.8
	447796	AW953822	Hs.223025	RAB31, member RAS oncogene family	3.3	4.2
15	426751	W92744	Hs.22664	EST8	3.3	2.6
13	438251 452688	BE515065	Hs.5092 Hs.49930	nucleolar protein (KKE/D repeat)	3.3	3.9
	416359	AA721140 AL042210	Hs.16493	ESTs, Weakly similar to 834087 hypotheti	3.3	4.9
	424090	X99699	Hs.139262	hypothetical protein DKFZp762N2316 XIAP associated factor-1	3.3 3.3	4.2
	434987	AW975114	Hs.293273	ESTs	3.3 3.3	2.9 2.2
20	428642	NM_014899		KIAA0878 protein	3.3	5.7
	420372	AW960049	Hs.293660	ESTs, Weakly similar to A49618 probable	3.3	5.5
	422224	NM_013982	Hs.113264	neuregulin 2	3.2	3.0
	432482	L19267	Hs.275924	dystrophia myotonica-containing WD repea	3.2	27
25	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrota	3.2	2.0
23	428418	A1368826	Hs.30654	EST8	3.2	2.4
	416728 416224	AB024597	Hs.79658	caseln kinase 1, epsilon	3.2	28
	429803	NM_002902 W81489	Hs.223025	reticulocalbin 2. EF-hand calcium bindin	3.2	2.2
	431387	A1878854	Hs.252229	RAB31, member RAS oncogene family v-maf musculoaponeurotic fibrosarcoma (a	3.2	4.3
30	404171	74070004	110.232223	A-ura umecanaharianiotic maasarcansi (a	3.2	2.8
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.2 3.2	35.8 2.6
	426421	AW367884	Hs.169832	zinc finger protein 42 (myeloid-specific	3.2	3.8
	445070	NM_000677	Hs.258	adenosine A3 receptor	3.2	7.6
25	407047	X65965		gb:H.sapiens SOO-2 gene for manganese su	3.2	82.0
35	446006	NM_004403		deafness, autosomal dominant 5	3.2	2.2
	430890	X54232	Hs.2699	glypican 1	3.2	4.3
	439807	AA376417	Hs.173501	Homo sapiens mRNA for FLJ00008 protein,	3.2	23
	430412 442807	AW341754 AL049274	Hs.189305	ESTS	3.2	20
40	420253	AL049214 Al656055	Hs.8736 Hs.96200	Homo saplens mRNA; cDNA DKFZp564H203 (fr	3.2	2.7
	436042	AF284422	Hs.119178	neighbor of A-kinase anchoring protein 9 cation-chloride cotransporter-interactin	3.2	29
	423422	AC005175	Hs.128425	NY-REN-24 antigen	3.2 3.2	4.B
	413020	R98736	,	gb.yr31h09.r1 Soares fetal liver spleen	3.2	4.0 4.1
4.5	452877	Al250789	Hs.32478	ESTs	3.2	4.0
45	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.1	9.0
	421097	Al280112	Hs.125232	Homo saplans cDNA FLJ13266 fis, clone OV	3.1	2.0
	450219	A1826999	Hs.224624	ESTs	3.1	23,7
	434256	AJ378817	Hs.191847	ESTs	3.1	3.4
50	421407 451198	T82331	Hs.127453	ESTs	3,1	3.9
50	445664	AW964541 AW968638	Hs.11500 Hs.237691	Homo seplens cDNA: FLJ21127 fls, clone C ESTs	3.1	3.9
	411089	AA456454	Hs.118637	Homo sapiens cDNA FLJ13365 fis, clone PL	3.1	7.9
	458050	AA834708	113.110001	gb:od99d04.s1 NCI_CGAP_Ov2 Homo saplens	3.1 3.1	6.0 4.4
	454140	AB040888	Hs.41793	hypothetical protein FLJ 10474	3.1	2.7
55	417270	AA429615	Hs.98593	Homo sapians cDNA: FLJ23233 fis, clone C	3.1	24
	427951	AI826125	Hs.43546	ESTs	3.1	23
	443693	A1344782	Hs.9683	protein-kinase, interferon-inducible dou	3.1	7.2
	413367	NM_006517		solute carrier family 16 (monocarboxylic	3.1	26
60	429402 447752	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	3.1	6.5
00	408949	M73700 AF189011	Hs.347 Hs.49163	lactotransferrin	3.1	19.4
	418039	R06859	Hs.193172	putative ribonuclease III ESTs	3.1	3.7
	447343	AA256641	Hs.236894		3.1	3.B
	424441	X14850	Hs.147097	H2A histone family, member X	3.1 3.1	2.2 3.2
65	435163	AA668884	Hs.19155	ESTs	3.1	21
	428712	AW085131	Hs.190452	KIAA0365 gene product	3.1	27
	434542	AA769310	Hs.61260	hypothetical protein FL 13164	3.1	14.3
	428147	AW629965	Hs.234983	ESTs	3.1	2.7
70	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase 8	3.1	25
70	422170	Al791849	Hs.112432		3.1	8.1
	448801 413542	N57423	Hs.179898	HSPC055 protein	3.0	20
	431562	8E295928	Hs.75424	Inhibitor of DNA binding 1, dominant neg	3.0	18.3
_	410274	AI884334 AA381807	Hs.11637 Hs.61762	ESTs hypoxla-inducible protein 2	3.0	3.9
75	458962	NM_005859			3.0	3.0
	436277	R88520	Hs.120917	purine-rich eternent binding protein A ESTs	3.0	3.0
	453288	AW583292			3.0 3.0	2.7
	447471	AF039843	Hs.18676	sprouty (Drosophila) homotog 2	3.0	3.0 4.1
90	442554	AW487378	Hs.129640		3.0	4.7
80	441466	AW873081	Hs.54828	ESTs	3.0	3.0
	420297	AJ628272	Hs.88323	EST6	3.0	8.1
	445101 453406	T75202	Hs.12314	Homo sepiens mRNA; cDNA DKFZp586C1019 (f	3.0	18.7
	453405	Al567972	Hs.49918	ESTs	3.0	9.6

	434521	NM_002267	He 3886	humanahasin alaha 2 (Impantla alaha 4)		
	447948	AI620923	Hs.46679	karyopherin alpha 3 (Importin alpha 4) ESTs	3.0	9.3
	445756	AA290690	Hs.288493	ESTs	3.0 3.0	10.1
_	413243	AA769266	Hs.193657	ESTB	3.0	3.5 5.9
5	422845	AA317841	Hs.301838	ESTs, Wealty similar to ALU1_HUMAN ALU S	3.0	2.2
	419409	AW297831	Hs.143792	ESTs	3.0	21
	446441	AK001782	Hs.15093	hypothetical protein	3.0	2.1
	427150 421043	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate	3.0	4.1
10	427239	BE379455	Hs.89072	ESTs	3.0	3.0
10	433312	BE270447 Al241331	Hs.174070 Hs.131765	ubiquitin carrier protein	3.0	4.1
	415102	M31899	Hs.77929	ESTs excision repair cross-complementing rode	3.0	11.0
	414702	1.22005	Hs.76932	cell division cycle 34	3.0	6.0
	428673	AW601325	Hs.274472	high-mobility group (nonhistone chromoso	3.0 3.0	3.3
15	422676	D28481	Hs.1570	histamine receptor H1	3.0	15.8 2.1
	451693	BE220445	Hs.279635	ESTs	3.0	2.3
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.0	10.5
	424005	AB033041	Hs.137507	KIAA1215 protein	3.0	3.9
20	440769 428832	8E561793		gb:601346842F1 NIH_MGC_8 Homo septens cD	3.0	5.1
20	430293	AA578229 Al416988	LI» 920070	gbtnl22b12s1 NCI_CGAP_HSC1 Homo sepiens	3.0	2.3
	450883	NM_001348	Hs.238272 Hs.25619	inositol 1,4,5-triphosphate receptor, ty	3.0	6.3
	407879	AA045464	Hs.6557	death-essociated protein kinase 3 ESTs	3.0	5.6
	426167	AF039023	Hs.167496	Homo sapiens cDNA FLJ11120 fis, clone PL	29 29	7.0
25	435281	AB020699	Hs.4864	KIAA0892 protein	29	26 39
	432339	AW411259	Hs.25945	ESTs	2.9	2.9
	440524	R71264	Hs.16798	ESTs	2.9	9.7
	408083	BE383668	Hs.42484	hypothetical protein FLJ10618	2.9	4.4
30	427729	AB033100	Hs.300646	Homo sapiens cDNA FLJ11744 fis, clone HE	29	3.1
70	422072 435904	AB018255 AF261655	Hs.111138	KIAA0712 gene product	29	29
	440100	BE382685	Hs.8910 Hs.158549	1,2-alpha-mannosidase IC ESTs	29	3.6
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	29	3.6
	428005	AW302245	Hs.181390	casein kinase 1, gamma 2	29 29	13.9
35	403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	2.9	3.7 5.8
	419175	AW270037	Hs.179507	KIAA0779 protein	29	2.3
	433592	NM_004642		deleted in oral cancer (mouse, homolog)	2.9	23
	413922	AJ535895	Hs.221024	ESTs	2.9	28
40	428593 441789	AW207440	Hs.185973	degenerative spermatocyte (hornolog Droso	29	3.3
40	459107	D52059 AA811881	Hs.7972	KIAA0871 protein	2.9	2.1
	448560	BE613183	Hs.28505 Hs.23213	ubiquitin-conjugating enzyme E2H (homolo ESTs	2.9	2.8
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9	3.0
	434846	AW295389	Hs.119768	ESTs	2.9 2.9	3.3
45	408146	R45621	Hs.81057	ESTs, Moderately similar to CL3BC [R,nor	2.9	5.1 5.1
	446644	NM_003272		transmembrane 7 superfamily member 1 (up	2.9	2.8
	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	29	8.5
	433017	Y15067	Hs.279914	zinc finger protein 232	29	2.2
50	429500 444706	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	2.9	4.5
-	407925	AK000398 BE002320	Hs.11747 Hs.287864	hypothetical protein FLI20391	2.9	3.6
	431730	AF208856	Hs.268122	Homo sapiens cDNA FLJ14030 fis, clone HE hypothetical protein	2.9	2.1
	447118	AB014599	Hs.17411	KIAA0699 protein	2.9	2.5
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.8 2.8	2.1 7.4
55	425227	H84455	Hs.40639	ESTs	2.8	2.3
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.8	76.2
	421465	AK001020	Hs.104627	Homo saplens cDNA FLJ 10158 fis, clone HE	2.8	6.1
	409095 424066	AW337272 Z99348	Hs.293656	ESTs	2.8	34,0
60	432945	AL043683	Hs.112461 Hs.271357	ESTS	2.8	2.1
	414079	H19184	Hs.205230	ESTs, Weakly similar to unnamed protein ESTs	2.8	11.9
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.8 2.8	21
	438890	AA827756	Hs.135049	ESTs	2.8	3.9 4.9
65	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble	2.8	5.2
Ų.	458367	AA088470	Hs.83135	p53-responsive gene 6	28	4.4
	412014	A1620650	Hs.43761	ESTs	2.8	4.8
	428727 447942	AF078847	Hs.191356	general transcription factor IIH, polype	2.8	6.7
	426432	F12628 AF001601	Hs.155470	zinc finger protein 38 (KOX 25) persoxonase 2	28	2.2
70	439189	AI951185	Hs.169857 Hs.144630	nuclear receptor subfamily 2, group F, m	2.8	3.5
	446756	AW028485	Hs.26136	ESTs	28	2.5
	432148	AW504912	Hs.81907	ESTs, Moderately similar to ALU4_HUMAN A	28 28	4.1
	405649			,, ental 2 / 121 (3 / 101 / 101 / 1	2.8	26 3.8
75	414473	BE302693		gb:ba74c02.y1 NIH_MGC_20 Homo saplens cD	2.8	2.4
75	443839	AW139834	Hs.143321	ESTs	2.8	21
	448804 426825	AW512213	Hs.42500	ADP-ribosylation factor-like 5	2.8	27
	417528	AL133415 H47315	Hs.2064	vimentin	2.8	25.0
	453657	W23237	Hs.27519 Hs.296162	ESTs ESTs	2.8	11.6
80	432714	Y12059	Hs.278675	bromodomain-containing 4	28	3.2
	441072	AW275480	Hs.39504	E8Ts	28 27	6.7
	441297	AW403084	Hs.7768	ubiquitin-conjugating enzyme EZE 1 (homo	2.7	2.7 2.2
	443849	BE566066	Hs.9893	ASB-3 protein	27	30

	408243	Y00787	Hs.524	interleukin 8	27	3.8
	446243 432238	BE296396 AL133057	Hs.14512 Hs.274135	Homo sepiens cDNA FLJ11761 fis, clone HE	2.7	3.3
	433944	AL117518	Hs.3686	Homo saplens mRNA; cDNA DKFZp434K1815 (f KIAA0978 protein	2.7 2.7	3.0 3.1
5	411400	AA311919	Hs.69851	GAR1 protein	27	16.0
	436840	AW450376	Hs.130803	ESTs, Highly similar to T00367 hypotheti	2.7	4.1
	428281	AA194554	Hs.183434	ATPase, H+ transporting, tysosomal (vacu	2.7	3.2
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.7	2.0
10	408320 422363	AJ125867	Hs.20734 Hs.115474	ESTs	2.7	4.7
10	422363 436440	T55979 Al471862	Hs.196008	replication factor C (activator 1) 3 (38 Homo sapiens cDNA FLJ11723 fis, clone HE	2.7 2.7	22
	408912	AB011084	Hs.48924	KIAA0512 gene product	27	4.7 2.1
	419304	A1271326	Hs.146101	ESTs	27	3.4
1.5	415045	AA321559	Hs.38270	Homo sapiens cDNA: FLJ20984 fis, clone C	2.7	2.3
15	441872	BE567100	Hs.154938	hypothetical protein MDS025	2.7	2.3
	422343	A1628633		gb:ty77d05.x1 NCI_CGAP_Kld11 Homo sapten	2.7	2.5
	415539 443823	AI733881 BE089782	Hs.72472	ESTs	2.7	2.7
	419881	AA329340	Hs.9877 Hs.44649	hypothetical protein ESTs	2.7 2.7	4.7 3.3
20	429165	BE242291	Hs.197540	hypoxia-inducible factor 1, alpha subuni	27	5.5
	431319	AA873350		gb:oh64h02.s1 NCI_CGAP_Kkd5 Homo saplens	27	65.9
	430219	X99209	Hs.235887	HMT1 (hnRNP methyltransferase, S. cerevi	27	3.1
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.7	5.2
25	417259 431747	AW903838	Hs.81800	chondroitin suffate proteoglycan 2 (vers	2.7	10.7
23	408085	AW979134 N25929	Hs.10700 Hs.42500	hypothetical protein	2.7	2.9
	426218	AF119043	Hs.168005	ADP-ribosylation factor-like 5 transcriptional intermediary factor 1 ga	2.7 2.7	7.8 4.5
	434845	BE267057	Hs.4200	hypothetical protein R32184_1	27	4.6
	451644	N23235	Hs.30567	ESTs	2.7	2.3
30	428408	W74437	Hs.188757	Homo sapiens mRNA; cDNA DKFZp564M113 (fr	2.7	5.7
	446627	AJ973016	Hs.15725	hypothetical protein SB8I48	2.7	2.9
	450167 408821	AA446404 AL050385	Hs.24563 Hs.48332	NTF2-related export protein 1	2.7	9.9
	452068	W76412	Hs.57877	NIMA (never in mitosis gene a)-related k ESTs	2.7 2.7	2.1 2.1
35	431129	AL137751	Hs.263671	Homo saplens mRNA; cDNA DKFZp434l0812 (f	2.7	6.2
	429025	Al399910	Hs.4842	ESTs	2.7	2.9
	421114	AW975051	Hs.293156	ESTs	2.7	8.8
	428755 416391	D87454	Hs.192966	KIAA0265 protein	2.7	3.0
40	414283	Al878927 AW960011	Hs.79284 Hs.154993	mesoderm specific transcript (mouse) hom ESTs	2.7	5.7
-10	425262	D87119	Hs.155418	GS3955 protein	2.7 2.7	5.9 3.7
	447726	AL137638	Hs.19368	Homo saplens mRNA; cDNA DKFZp434J065 (fr	27	14.3
	424623	AW963062	Hs.165809	EST8	27	5.6
15	444772	AW450800	Hs.176859	ESTs	2.7	2.7
45	428419	U49436	Hs.286236	eukeryotic translation initiation factor	2.7	4.6
	441049 412758	W88920	Hs.29341	hypothetical protein FLJ22376	27	4.5
	447720	Y07818 AL038765	Hs.74568 Hs.161304	dihydropyrimidinase-like 3 ESTs	2.6 2.6	5.1
	419708	AK000753	Hs.92374	hypothetical protein	2.6 2.6	3.2 3.0
50	445502	AW379160	Hs.12813	DKFZP434J214 protein	2.6	5.0
	437370	AL359567	Hs.161962	Homo saptens mRNA; cDNA DKFZp547D023 (fr	2.6	29
	444147	AB002306	Hs.10351	KIAA0308 protein	2.6	6.8
	433193 445439	AB040881	Hs.32580	Homo saplens cDNA FLJ13122 fis, clone NT	2.6	3.2
55	450309	BE243084 W61348	Hs.12719 Hs.4864	regulator of nonsense transcripts 1 KIAA0892 protein	2.6 2.6	3,9
•	422092	AB007883	Hs.111373	KIAA0423 protein	2.6	3.8 2.3
	424118	BE269041	Hs.140452	cargo selection protein (mannose 6 phosp	26	5.5
	407618	AW054922		Homo sapiens cDNA FLJ12366 fis, clone MA	2.6	2.9
60	446493	AK001389	Hs.15144	hypothetical protein DKFZp5640043	2.6	3.2
UU	442878 448771	A1868648	Hs.22315	ESTs	2.6	4.7
	416611	BE315511 AA568308	Hs.296244 Hs.192789	SNARE protein	26	5.0
	409348	A1401535	Hs.146090	ESTs, Weakly similar to ALU7_HUMAN ALU S ESTs	2.6 2.6	7.7 3.5
	439349	A1660898	Hs.195602	ESTs	26	3.2
65	428433	AA521410	Hs.41371	ESTa	2.6	7.9
	436565	BE547674	Hs.204169	ESTs	2.6	3.0
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	26	2.6
	429362 459035	T25833 AW291109	Hs.200478	ubiquitin-conjugating enzyme E2M (homolo	2.6	23
70	451814	A44231103 AA847992	Hs.208787 Hs.137003		2.6 2.6	2.6
. •	452331	AA598509	Hs.29117	H.sapiens mRNA for pur stpha extended 3*	2.6	19.1 2.2
	438461	AW075485			26	21
	424362	AL137648	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (f	2.6	4.9
75	423599	H41850	Hs.131846	PCAF associated factor 65 alpha	2.6	3.7
13	441226	BE563042	Hs.118820		2.6	2.5
	444940 448731	AK002148 Al522273	Hs.12151 Hs.42640	hypothetical protein FLJ 11286	2.6	3.4
	424250	AF073310		ESTs Insufin receptor substrate 2	26	3.2
	433468	AA832055			26 26	2.5 3.3
80	419925	AA159850		Riporna HMGIC fusion partner	2.6	3.3 4.6
	441384	AW450466	Hs.126830	ESTS	26	2.6
	425922	AL157466	Hs.162751		2.5	2.7
	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	2.5	2.5

			. •			
	408392	U28831	Hs.44566	KIAA1641 protein	2.5	25.4
	432428		Hs.31050	ESTs	25	10.0
	436623	A1417073	Hs.107265	ESTs	2.5	21
5	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.5	2.6
J	410582 441328	AW887197 AI982794	Hs.14562	Homo sapiens cDNA: FLJ21616 fis, clone C	2.5	3.7
	453983	H94997	Hs.159473 Hs.16450	ESTS	2.5	9.2
	438826	R26709	Hs.10095	ESTs hypothetical protein from EUROIMAGE 1669	2.5 2.5	26.1
	427899	AA829286	Hs.181062	serum amyloid A1	25 25	2.3 20.3
10	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	2.5	3.5
- •	458933	Al638429	Hs.24763	RAN binding protein 1	2.5	3.5
	444871	U46386	Hs.12102	sorting nexts 3	2.5	2.3
	411329	AL360265	Hs.69554	hypothetical protein FLJ20552	2.5	29
	424074	AI902456	Hs.210761	ESTs	2.5	4.0
15	438988	H30039	Hs.107674	ESTs	2.5	27
	412836	AA121384	Hs.191446	ESTs	25	5.7
	430189	AI298841	Hs.135133	ESTs, Wealthy similar to ORF YNL310c (S.c	2.5	3.0
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.5	13.4
20	416926	H03109	Hs.108920	HTO18 protein	2.5	2.8
20	451429	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU 6	2.5	3.9
	416388	AJ417358	Hs.73677	ESTs	25	4.2
	421561	Z45399	Hs.105779	protein inhibitor of activated STAT prot	2.5	7.5
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	2.5	26
25	416273	AW575691	Hs.79123	KIAA0084 protein	2.5	2.6
23	427149	H94888	Hs.173737	ras-related C3 botulinum toxin substrate	2.5	2.6
	453041	AI680737	Hs.289068	transcription factor 4	2.5	2.2
	446899 447301	NM_005397		podocalyxin-like	2.5	4.7
	447769	AW958124 AW873704	Hs.142442	HP1-8P74 ESTs	2.5	3.2
30	447754	AW073310	Hs.48764 Hs.163533	Homo saplens cDNA FLJ14142 fis, clone MA	2.5	24
-0	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HTO	2.5	25 25
	440903	AI468079	Hs.126623	ESTs	2.5 2.5	23.6
	432353		Hs.274411	SCAN domain-containing 1	2.5	2.3 4.1
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.5	2.5
35	411373	BE326276	Hs.8861	ESTs	2.5	3.9
	452402	Al138530	Hs.22218	peroxisome proliferative activated recep	2.5	24
	429998	A1458063	Hs.57841	ESTs	2.5	2.6
	421772	Z24958	Hs.108139	zinc finger protein 212	2.5	3.7
40	442573	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	2.5	2.1
40	444677	AL110212	Hs.9242	purine-rich element binding protein B	2.5	3.4
	441887	AW967865	Hs.92145	ESTs	2.5	3.3
	451031	Al360187	Hs.4254	ESTs .	2.5	4.8
	432450	Al990739	Hs.77868	ORF	2.5	2.4
45	415860	D56051	Hs.78888	diazepam binding inhibitor (GABA recepto	2.5	4,8
43	439630	AA313607	Hs.58633	Homo saplens cDNA: FLJ22145 fis, clone H	2.4	2.3
	428607	AB002353	Hs.186840	KIAA0355 gene product	2.4	4.0
	415402 446888	AA164687 AL030996	Hs.297889	ESTS	2.4	2.5
	439208	AK000299	Hs.16411 Hs.180952	hypothetical protein LOC57187	2.4	2.2
50	452900	AA626794	Hs.250655	dynactin p62 subunit prothymosin, alpha (gene sequence 29)	2.4 2.4	2.4 3.4
	408657	AA782601	Hs.173328	protein phosphalase 2, regulatory subuni	2.4	3.6
	439143	AJ359214	Hs.179260	ESTs	24	2.5
	439867	AA847510	Hs.161292	ESTS	2.4	9.3
	40813B	AA535740	Hs.301967		2.4	5.6
55	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	2.4	4.2
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.4	2.2
	405268				2.4	3.1
	439734	AC005013	Hs.149	cAMP response element-binding protein CR	2.4	3.6
60	445378	AV653564	Hs.226946		2.4	2.4
00	454085	D82418	Hs.29626	ESTs, Wealdy similar to unknown [D.melan	24	22.0
•	427354	T57896	Hs.191095		2.4	3.6
	452906 450085	BE207039 AL050107	Hs.75621	serine (or cysteine) proteinase inhibito	2.4	2.2
	451091	AA810932	Hs.301558 Hs.131899		24	3.6
65	414839	X63592	Hs.77462		24	2.7
05	420303	AA258282	Hs.278436	DNA (cytosine-5-)-methyltrensferase 1 KIAA1474 protein	2.4	26 20
	437068	AA743643	Hs.291427		2.4 2.4	2.6
	417446	AL118871	Hs.82163	monoamine oxidase B	24	4.4
	421454	A1660389	Hs.286108		24	3.5
70	434943	Al929819	Hs.320	xeroderma pigmentosum, complementation g	24	6.4
	446342	BE298665	Hs.14848	Homo saplens mRNA; cDNA DKFZp564D016 (fr	2.4	3.0
	452847	AK000857	Hs.30783	hypothetical protein FLJ20850	24	21
	422506	R20909	Hs.117816		24	2.2
75	405204				2.4	4.3
75	419441	AW023731			2.4	11.7
	442293	AW292634			2.4	21
	451484	AV648896		hypothetical protein	2.4	20
	438545	AB032977		KIAA1151 protein	24	21
80	442724	AA355525	Hs.159604	cysteinyl-IRNA synthetase	2.4	2.8
30	405517	R08950	Un 272044	ESTo Mookly similar to At 114 1 10 1244 1 414 -	2.4	6.6
	413822 445879	AJ343868	Hs.272044 Hs.58800	ESTs, Wealdy similar to ALU1_HUMAN ALU S Homo sapiens cDNA FLJ12488 fis, clone NT	24	3.8
	408838	BE294925		CGI-12 protein	24	2.3
			· TOUG	and the formation	2.4	8.1

	409142	AL136877	Hs.50758	chromotomo recondeded a climacilida C	•	
	422043		Hs.110953	chromosome-associated polypeptide C Homo septens mRNA; cDNA DKFZp434A139 (fr	24 24	24 2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	24	26
5	442560	AA365042	Hs.228598	ESTs	24	4.9
5	418126 413313	T91451	Hs.86538	ESTS	24	11,7
	415167	NM_002047 AA160784	Hs.26410	glycyl-iRNA synthetase ESTs	· 24 24	2.1 4.4
	440040	BE219431	Hs.300713	ESTs	24	3.4
10	443595	AF169312	Hs.9613	PPAR(gamma) angiopoletin related protein	24	10.7
10	438977	AA482026	Hs.298625	ESTS	2.4	28
	452066 428500	AA772149 A1815395	Hs.16979 Hs.184641	ESTS	24	5.4
	408503	AW119059	Hs.63163	delta-6 fatty acid desaturase ESTs, Weakly similar to UDP-GalNAc:polyp	24 24	2.2
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	24	2.7 4.8
15	412676	NM_000165		gap junction protein, alpha 1, 43kD (con	24	2.2
	453753	8E252983	Hs.35086	ubiquitin specific protesse 1	2.4	28
	424050 440225	AA211218	Hs.138381	famesyltransferase, CAAX box, elpha	24	3.9
	430512	BE295782 AF182294	Hs.159 Hs.241578	tumor necrosis factor receptor supertami U8 snRNA-associated Sm-like protein LSm8	24	76.7
20	415156	X84908	Hs.78060	phosphorylase kinase, beta	2.4 2.4	12.3 10.4
	435975	AL118990	Hs.41997	alpha-1-8 glycoprotein	24	7.7
	429831	AA564489	Hs.137526	ESTs	2.4	4.1
	407373 422221	AA031576 AA306649	Hs.143812	Homo sapiens cDNA FLJ12956 fis, clone NT	24	3.3
25	451351	AW058261	Hs.168213	gb:EST177656 Jurkat T-cells VI Homo sapi ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4 2.4	3.8
	410082	AA081594	Hs.158311	Museshi (Drosophile) homolog 1	2.4	3.3 2.5
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	24	6.5
	418863	AL135743	Hs.25566	ESTs	2.4	5.2
30	448414	8E391820	Hs.21145	Homo saplens cDNA: FLJ22489 fis, clone H	24	3.7
50	428351 425750	AK001701 AL050276	Hs.183779 Hs.159456	Homo saplens cDNA FLJ 10590 fis, clone NT zinc finger protein 288	2.4	6.2
	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	24 24	5.1 113.6
	408772	W88532	Hs.254562	ESTs	2.4	12.3
25	426307	F24978	Hs.294084	ESTs	2.4	4.0
35	405203	******	11- 000004	FOT-	24	2.5
	453537 431427	AA036755 AK000401	Hs.283681 Hs.252748	ESTs Homo sapiens cDNA FLJ20394 fis, clone KA	2.4	3.6
	458021	AJ885190	Hs.156089	ESTs, Weakly similar to KIAA1339 protein	24 24	6.2 4.3
40	453928	BE222198	Hs.143851	ESTs	24	2.6
40	446853	AV660630	Hs.87627	disrupter of silencing 10	2.3	9.7
	441626 446138	AA281167	Hs.111911	ESTs	23	23.0
	452568	AW504182 AA805634	Hs.13999 Hs.3337	KIAA0700 protein transmembrane 4 superfamily member 1	23	2.2
	417665	AW852858	Hs.22862	ESTs	23 23	22.2 8.0
45	420088	AC006486	Hs.298033	Homo sepiens cDNA: FLJ22286 fls, clone H	2.3	5.1
	421456	AW579842	Hs.104557	hypothetical protein FLJ 10697	2.3	2.5
	412093 428172	BE242691 U09367	Hs.14947	ESTs	2.3	31.4
	450447	AF212223	Hs.182828 Hs.25010	zinc finger protein 136 (clone pHZ-20) hypothetical protein P15-2	23	4.9
50	436001	AW903849	Hs.173840	HUEL (C4or11)-interacting protein	2.3 2.3	2.3 4.1
	414786	AI246482	Hs.249989	ESTs	, 23	2.1
	459284	AF155660	Hs.34401	mitochondrial solute carrier	2.3	2.9
	452701 448320	NM_005110 AF126245		glutamine-fructose-6-phosphate transamin	2.3	2.6
55	446669	AW972832	Hs.14791 Hs.29468	acyl-Coenzyme A dehydrogenase family, me ESTs	23 23	3.9 3.8
	434618	D79338	Hs.239720	CCR4-NOT transcription complex, subunit	2.3	3.6
	452135	AJ492175	Hs.301805	ESTs	23	2.3
	408696 436176	AW958157 AL121422	Hs. 16542	ESTs	2.3	28
60	419713	AW968058	Hs.184013 Hs.92381	ESTs, Highly similar to unnamed protein nudix (nucleoside diphosphate linked mol	23 23	3.2
	414197	W44877	Hs.55501	ESTs	23	17.0 11.8
	445270	Al762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	2.3	4.2
	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.3	5.1
65	426494 405687	AL119528	Hs.170098	KIAA0372 gene product	23	4.4
-	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	23 23	2.2 2.0
	450747	Al064821	Hs.48306	ESTs, Highly similar to EWS_HUMAN RNA-BI	23	3.8
	433680	AI805366	Hs.199945	ESTs .	23	6.7
70	420025	AF184939	Hs.94392	LDL induced EC protein	2.3	24
,0	413407 452908	Al356293 AB001451	Hs.75339 Hs.30965	tnostiol polyphosphate phosphatase-like neuronal Sho adaptor homolog	23	3.1
	424414	Al361002	Hs.94814	Homo sapiens cDNA FLJ12168 fis, clone MA	23 23	3.0
	435791	AA243086	Hs.25204	chondroitin 4-O-sulfoiransferase 2	23 23	20 24
75	457635	AV660976	Hs.3569	hypothetical protein	23	6.9
75	427985	AJ770170	Hs.65583	ESTs	2.3	23
	445488 410310	AV654019 J02931	Hs.180402 Hs.62192	Homo saplens cDNA: FLJ23506 fis, clone L coagulation factor III (thromboplastin,	2.3	2.3
	450388	AU077158	Hs.24930	tubuln-specific chaperone a	23 23	4.1 3.5
90	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	2.3	2.6
80	448607	AL042506	Hs.21599	Homo sapiens cDNA FLJ10107 fis, clone HE	2.3	2.8
	447975 429767	8E378418 AW793022	Hs.127240		23	2.2
	408877	AA479033	Hs.218329 Hs.130315		23	11.5
					2.3	2.3

	448481	W15284	Hs.74832	ESTs		2.3	3.3
	452833	BE559681	Hs.30736	KIAA0124 protein		23	2.8
	421057 408885	T58283 C02741	Hs.42679 Hs.48712	ESTs		23	11.0
5	427615	BE410107	Hs.179817	hypothetical protein FLJ20736 CGI-82 protein		2.3	4.6
	448861	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp56400122 (r		2.3	2.3
	430154	AW583058	Hs_234726	serine (or cysteine) proteinase inhibito		2.3 2.3	6.3
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005		2.3	34.6 10.2
10	422987	AW407887	Hs.301772	serine/threonine kinase 11 (Peutz-Jegher		23	3.2
TO	408216 407862	AA741038 BE548267	Hs.6670	ESTs		2.3	3.3
	432215	AU076609	Hs.50724 Hs.2934	Homo sapiens cDNA FLJ10934 ffs, clone OV		2.3	5.7
	410086	Al268405	Hs.13467	ribonucleotide reductase M1 polypeptide Homo sapiens BAC clone RP11-121A8 from 7		2.3	2.1
	444853	AW576245	Hs.149740	Homo saplens mRNA for FLJ00028 protein,		23 23	2.2
15	413284	AU077055	Hs.289107	baculoviral IAP repeat-containing 2		2.3	4.5
	445547	D86181	Hs.273	galactosylceramidase (Krabbe disease)		23	4.8 2.5
	420258	AA477514	Hs.96247	translin-associated factor X		23	3.5
	437223 437353	C15105	Hs.107884	ESTs		23	27
20	426224	AA749195 BE085860	Hs.143748	ESTs		23	2.6
	402575	Z23024	Hs.168075 Hs.138860	karyopherin (importin) beta 2		2.3	36.1
	430712	AW044647	Hs.196284	Rho GTPase activating protein 1 ESTs		2.3	3.1
	452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat.		23 23	24
25	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote		23	2.4 4.3
25	441848	H05734	Hs.30559	ESTs		2.3	2.1
	424130 414682	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr		23	29
	423814	AL021154 AF105020	Hs.76884	inhibitor of DNA binding 3, dominant neg		2.3	12.2
	421641	AI638184	Hs.132989 Hs.106334	putative protein O-mannosyltransierase		23	3.7
30	427882	AA640987	Hs.193767	Homo sapiens clone 23836 mRNA sequence ESTs		2.3	2.3
	442159	AW163390	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm		2.3 2.3	10.2
	412541	BE009398	Hs.74002	nuclear receptor coactivator 1		23	4.4 2.4
	447217	BE465754	Hs.17778	neuropilin 2		2.3	3.0
35	452338	AA960951	Hs.29147	hypothetical protein FLJ11015		23	4.1
33	423913 411737	NM_016436		hepatocellular carcinoma-associated anti		2.3	3.4
	412276	AW160339 BE262621	Hs.71791 Hs.73798	hypothetical protein		2.2	2.0
	456974	M12529	Hs.169401	macrophage migration inhibitory factor (apolipoprotein E		2.2	2.4
40	416033	NM_012201	Hs.78979	Golgi apparatus protein 1		22	2.6
40	406739	AI566709	Hs.182426	ribosomal protein S2		2.2 2.2	10.4 115.3
	448848	AU077149	Hs.21704	transcription factor 12 (HTF4, helix-loo		22	4.2
	437371	AK000868	Hs.5570	hypothetical protein FLJ 10006		22	3.6
	451413 408665	AA448974 T88845	Hs.26367	PC3-96 protein		2.2	6.2
45	437548	Al701596	Hs.112200 Hs.121592	ESTs, Weakly similar to ALU7_HUMAN ALU S ESTs		2.2	3.2
	452053	Al750575	Hs.173933	nuclear factor I/A		22	3.0
	428303	AW974476	Hs.183601	regulator of G-protein signatting 16		2.2 2.2	3.3
	441376	. H94227	Hs.6592	ESTs, Weakly similar to salivary proline		2.2	3.4 2.5
50	413399	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo		2.2	2.3 2.1
50	448913 439053	AA194422	Hs.22564	myosin VI		2.2	2.4
	428065	BE244588 Al634046	Hs.6456 Hs.157313	chaperonin containing TCP1, subunit 2 (b		2.2	3.1
	425846	AA102174	Hs.159629	ESTs myosin IXB		2.2	3.5
~ ~	426404	AA377607	Hs.273138	ESTS		2.2 2.2	7.1
55	423464	NM_016240	Hs.128856	CSR1 protein		2.2	3.3 2.1
	436135	D85390	Hs.5057	carboxypeptidase D		2.2	9.1
	450478 420798	AL045285	Hs.246849	ESTs, Moderately similar to ALUS_HUMAN A		2.2	2.6
	433530	W93774 BE349534	Hs.99936 Hs.281789	keratin 10 (epklermolytic hyperkeratosis		2.2	2.8
60	436297	A1084582	Hs.5105	ESTs hypothetical protein FLJ 10569		2.2	21
	433058	HB6865	Hs.280668	Homo saplens chromosome 19, cosmid R3218		2.2	2.4
	435924	AW029203	Hs.191952	ESTS		2.2 2.2	2,3 3,2
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein		2.2	2.3
65	449338 446065	H73444	Hs.394	adrenomeduliin		2.2	18.3
42	410668	AA085191 BE379794	Hs.6949 Hs.65403	ESTs, Weakly similar to T2D3_HUMAN TRANS		2.2	3.1
	424992	AW290893	Hs.96918	hypothetical protein Homo sapiens cDNA: FLJ21581 fis, clone C		2.2	2.5
	437801	AA613866	Hs.5848	Homo saplens mRNA; cONA DXFZp564L222 (fr		2.2	10.8
70	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	•	2.2	25
70	446392	AF142419	Hs.15020	homolog of mouse quaking QM (KH domain		2.2 2.2	2.4 3.4
	450503	R35917	Hs.25042	Homo sepiens mRNA full length insert cDN		22	28
	432476 424251	T94344	Un 4.43000	gb:ye31h10.s1 Stratagene lung (937210) H		2.2	26
	456619	AA677466 AV647917	Hs.143696 Hs.107153	coactivator-associated arginine methytir		2.2	5.0
75	433411	A1658666	Hs.49994	inhibitor of growth family, member 1-lik ESTs		2.2	26
	424714	Al114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H		2.2	2.1
	416326	AF186780	Hs.79219	RefGDS-like gene: KIAA0959 omtein		22	2.7
	407698	Al697340	Hs.76549	ATPase, Na+/K+ transporting, sinha 1 not		2.2 2.2	2.2 6.5
80	445939	BE018658	Hs.141003	Homo saplens cDNA: FLJ21691 fis, clone C		22	4.4
50	414765 407138	X07854 T64896	Hs.77269	guanine nucleotide binding orotein (G or		22	6.2
	453865	T64896 AA626250	Hs.287420 Hs.181165	Homo sapiens CDNA FLJ11533 fis, clone HE	•	22	2.8
	433608	AW340005	Hs.164485	eukaryolic translation elongation factor ESTs		2.2	2.3
						22	2.1

	447646	BE619752	Hs.66053	ESTs, Weakly similar to \$22126 finger pr	2.2	4.1
	433139	AB029826	Hs.47649	3-methylcrotonyl-CoA carboxylase blotin-	2.2	11.7
	413433 421535	NM_003199		transcription factor 4	2.2	2.2
5	428591	AB002359 BE313029	Hs.105478 Hs.185807	phosphoribosylformylglycinamidine syntha	2.2	2.2
•	417248	AA329449	Hs.247302	Homo saptens clone 24758 mRNA sequence byisted gastrutation	2.2	4.8
	403966	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	16.247602	CALE DESTRUCTION	22	2.5
	437112	AA744692	Hs.166539	ESTs	22	5.2
• •	414799	AI752416	Hs.77326	Insulin-like growth factor binding prote	2.2 2.2	3.0 4.9
10	431049	AA846576	Hs.103267	hypothetical protein FLJ 22548 similar to	22	4.4
	422100	Al096988	Hs.111554	ADP-ribosylation factor-like 7	2.2	2.5
	426543	AV650198	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.2	2.4
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	2.2	4.2
15	443804	AL135352	Hs.255883	ESTs	2.2	2.2
13	435080	AI831760	Hs.155111	ESTs	2.2	2.5
	452808 433934	AF244135	Hs.30670	hepatocellular carcinoma-associated anti	2.2	7.1
	432004	AW273261 BE018302	Hs.216292 Hs.2894	ESTs	2.2	2.1
	452518	AA280722	Hs.24758	placental growth factor, vascular endoth ESTs	22	4.4
20	409600	AJ011679	Hs.55099	Homo sapiens mRNA; cDNA DKFZp586D2123 (f	22	3.0
	448965	AF092134	Hs.22679	CGI-24 protein	2.2 2.2	2.3
	444954	AW247076	Hs.12163	eukaryolic translation initiation factor	2.2	4.0 5.3
	458894	AW292171	Hs.23978	scaffold attachment factor B	22	2.5
26	402269				22	2.2
25	423798	AF047033	Hs.301617	Homo saplens mRNA full length insert cDN	2.2	4.0
	413836	W92003	Hs.70614	ESTs	2.2	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	21	2.1
	412204 438807	A)125507	Hs.130829	ESTs	2.1	3.0
30	404170	AA848011	Hs.124570	ESTs, Wealdy similar to reverse transcri	21	2.2
	434858	AW979012	Hs.134462	ESTs	2.1	41.6
	426982	AA149707	Hs.173091	ubiquitin-like 3	21	2.2
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	21 21	21
2.0	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.1	26.5 3.7
35	424950	AA602917	Hs.156974	ESTs	2.1	19.9
	418123	AA669830	Hs.83530	hypothetical protein	2.1	4.6
	440467	AK001519	Hs.7194	CGI-74 protein	2.1	5.3
	437092	AA744292	Hs.181244	major histocompatibility complex, class	2.1	3.0
40	421579	NM_002975		stem cell growth factor, lymphocyte secr	21	3.3
70	428953 457313	AA306610	Hs.194676	DKFZP434C013 protein	21	5.0
	420570	AF047002 AI453665	Hs.241520	transcriptional coactivator	<u>2,1</u>	3.5
	446918	AL135125	Hs.290870 Hs.13913	ESTs, Weakly similar to S23650 retroviru	2.1	2.1
	427567	N24236	Hs.179662	KIAA1577 protein nucleosome assembly protein 1-like 1	2.1	2.3
45	448363	AL117440	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	2.1	2.8
	428482	AI290352	Hs.184592	KIAA0344 gene product	2.1 2.1	4.0 2.8
	456559	Al336273	Hs.102548	glucocorticoid receptor DNA binding fact	2.1	2.3
	442819	BE622721	Hs.301766	ESTs, Weakly similar to hypothetical pro	2.1	27.1
50	428808	AA436007	Hs.188780	ESTs	2.1	5.0
20	414893	AA215295	Hs.77578	ubiquilin specific prolease 9, X chromos	21	15.9
	447023	AA356764	Hs.17109	Integral membrane protein 2A	2.1	3.0
	402250 429952	AV655272 AF080158	Hs.20252	novel Ras family protein	2.1	4.2
	420006	H14429	Hs.226573 Hs.94300	inhibitor of kappa light polypeptide gen	21	7.9
55	407316	AA031663	Hs.28802	serologically defined colon cancer antig centaurin-alpha 2 protein	2.1	5.6
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.1 2.1	4.4
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.1	103.2 29.9
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	21	2.1
60	428580	U69199	Hs.90259	ESTs, Wealthy similar to alpha 1 [H.sapie	21	2.5
60	448501	AA332316	Hs.4273	hypothetical protein FLJ 13159	2.1	20
	422552	N39729	Hs.118243	deoxyribonuclease II, lysosomal	2.1	2.9
	419476 408681	AW953030	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	2.1	3.1
	417353	AW953853 AA375752	Hs.292833	ESTS	2.1	3.9
65	422070	AF149785	Hs.76362 Hs.111126	general transcription factor IIA, 2 (12k	21	4.1
	442711	AF151073	Hs.8645	pituitary tumor-transforming 1 Interacti	21	4.9
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ 10976 fis, clone Pi.	21	2.2
	452897	BE066058	Hs.269233	ESTs	2.1 2.1	7.4 4.2
~^	409147	A1889208	Hs.17283	hypothetical protein FLJ 10890	21	4.5
70	433028	Al199144	Hs.283737	AD-017 protein	2.1	2.6
	407831	BE613377	Hs.15580	Homo sapiens cONA: FLJ22276 fis, clone H	2.1	8.5
	417871	AA521368	Hs.24252	ESTs	21	2.9
	428754	A1521102	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	2.1	5.3
75	430127 442622	AA219498 NNA 000435	Hs.233952	proteasome (prosome, macropaln) subunit,	21	4.3
, 5	414242	NM_000435 AA749230		Notch (Drosophila) homolog 3	2.1	8.5
	433323	AA805132	Hs.22666 Hs.30701	ESTs	2.1	2.8
	439022	AA356599	Hs.173904	ESTs	21	5.0
	443357	AW016773	Hs.75615	apolipoprotain C-II	21	6.4
80	449103	T24968	Hs.23038	HSPC071 protein	21	20
	427512	AB018322	Hs.179507	KIAA0779 protein	21 21	27 20
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	21	2.9
	440112	AA099014	Hs.231029	ESTs	2.1	23

	446920	BE397649	Hs.31257	Homo sapiens cDNA FLJ13634 fis, clone PL	21	4.8
	428459	D44850	Hs.184411	gene with multiple splice variants near	2.1	2.9
	432842 438829	AW674093	Hs.279525	hypothetical protein PRO2605	2.1	23
5	411442	AA826926 N25956	Hs.204214	ESTs	21	27
•	409423	A1969783	Hs.43071	Homo sapiens cDNA FLJ14232 fis, clone NT	21	2.2
	456804	Al421645	Hs.139851	ESTs, Weakly similar to AF151900 1 CGI-1 caveofin 2	21	2.2
	434536	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho	21	15.2
	447126	AW150632	Hs.62954	ferritin, heavy polypeptide 1	21 21	2.8
10	442328	AI952430	Hs.265237	ESTs	21	25.0 2.1
	444488	AW192879	Hs.184796	ESTs, Wealthy similar to PET2_HUMAN OLIGO	21	29
	438874	H02780		gb:yj41a11.r1 Soares placenta Nb2HP Homo	21	10.6
	412805	AW954569	Hs.296287	ESTs	21	4.6
15	446334	U52427	Hs.14839	polymerase (RNA) II (DNA directed) polyp	2.1	2.3
13	427201	A8037860	Hs.173933	nuclear factor I/A	21	5.1
	436997 426369	AA741151	Hs.137323	ESTs	21	3.0
	453613	AF134157 F06838	Hs.169487	Kreister (mouse) maf-related leucine zip	21	23
	413276	Z24725	Hs.14763 Hs.75260	ESTs	- 21	2.4
20	422050	AA302741	Hs.25786	milogen inducible 2 ESTs	21	5.5
	424797	AA622394	Hs.153177	ribosomal protein S28	21	4.0
	437365	AW965771	Hs.91065	hypothetical protein DKFZp761B2423	21	21
	412482	AJ499930	Hs.181043	KIAA0788 protein	21 21	3.0
25	418662	AI801098	Hs.151500	ESTs	21	2.7 2.1
25	404030				21	21
	437802	A1475995	Hs.122910	ESTs	21	3.8
	441130	Al160734	Hs.283429	SMC (mouse) homolog, X chromosome	2.1	3.5
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	2.1	7.4
30	409944 425421	BE297925	Hs.57687	four and a half LIM domains 3	21	6.3
20	428399	L11669 NM_006276	Hs.157145	tetracycline transporter-like protein	2.1	7.1
	421313	NM_014923		splicing factor, arginine/serine-rich 7	2.1	2.7
	445229	BE276013	Hs.172364	KIAA0970 protein Homo saplens mRNA for FLJ00086 protein,	21	2.6
	401001			round sopialis intries on FL000000 protein,	2.1	4.7
35	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	21 21	14.7
	438855	AW946276	Hs.6441	tissue inhibitor of metalloproteinase 2	21	7.2 4.9
	433369	Z49254	Hs.3254	mitochondrial ribosomal protein L23	21	25.0
	433228	F28212	Hs.284247	KIAA1491 protein	21	5.1
40	445392	AA057478	Hs.23272	ESTs	20	2.3
40	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo saplens	. 20	2.5
	432572 448474	A1660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN IIII	2.0	2.9
	427045	A1792014 H86504	Hs.13809 Hs.173328	ESTs	2.0	12.1
	444916	AB028958	Hs.12144	protein phosphatase 2, regulatory subuni	2.0	29
45	439177	AW820275	Hs.76611	KIAA1033 protein ESTs	20	4.2
	423533	NM_014339		Interleukin 17 receptor	2.0	3.3
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	2.0 2.0	5.0 2.3
	424429	U63830	Hs.146847	TRAF family member-associated NFKB activ	20	12.7
50	428385	AF112213	Hs.184062	putative Rab5-interacting protein	2.0	4.6
50	458946	AA009716	Hs.42311	ESTs	2.0	16.4
	444816	Z48633	Hs.283742	H.saplens mRNA for retrotransposon	20	4.9
	426829	AI761241	Hs.301719	ESTs	2.0	2.4
	433619 421985	AW965275	Hs.284288	hqp0256 protein	2.0	4.4
55	439895	AK001779 AB037773	Hs.110445	CGI-97 protein	2.0	3.8
	449188	AW072939	Hs.6762 Hs.23200	hypothetical protein FLJ10595	2.0	2.2
	404820	711101 2303	119.20200	myotubularin related protein 1	2.0	2.2
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.0	2.7
	422163	AF027208	Hs.297332	Homo sapiens cDNA: FLJ21471 fis, clone C	2.0 2.0	2.5
60	431172	Al125839	Hs.250666	hatry (Drosophila)-homotog	20	3.7 10.2
	415200	AL040328	Hs.301912	Homo sepiens cDNA: FLJ22920 fis, clone K	20	2.1
	458176	Al961519	Hs.140309	ESTs, Weakly similar to KIAA0681 protein	20	5.0
	407895	R44203	Hs.265540	HSPC042 protein	2.0	4.6
65	449816	AI701457	Hs.38694	ESTs	2.0	2.0
UJ	422976 430220	AU076657	Hs.1600	sec61 homolog	2.0	5.7
	435448	BE378277	Hs.152230	ESTs	20	11.7
	431031	AA682305 AA830335	Hs.133268	ESTs	20	4.2
	425233	Z17861	Hs.105273 Hs.155218	ESTS	2.0	14.1
70	426458	D83032	Hs.169984	E1B-S5kDa-associated protein 5 nucléar protein	2.0	5.6
	421965	AA301100		gb:EST14128 Testis tumor Homo sapiens cD	20	5.9
	427128	AW301984	Hs.173685	Homo saplens cDNA FLJ12619 fis, clone NT	2.0 2.0	2.1
	449722	BE280074	Hs.23960	cyclin B1	20 20	6.3
75	450816	BE271927	Hs.87385	ESTs .	20	21 24
75	453507	AF083217	Hs.33085	WD repeat domain 3	20	13.1
	422801	AF125672	Hs.287994	nuclear receptor co-repressor 2	20	3.5
	418178	AA043951	Hs.83715	Sjogren syndrome antigen B (autoantigen	20	3.9
	417819	AI253112	Hs.133540	ESTs	20	4.0
80	414787 447032	AL049332 AK000310	Hs.77311	BTG family, member 3	2.0	4.0
	431742	AKOOO310 NM 016662	Hs.17138	hypothetical protein FLJ20303	20	7.0
	448431	BE613061	Hs.268281 Hs.300697	CGI-201 protein	2.0	2.5
	456444	AA884517	Hs.31856	ESTs, Weakly similar to CA13_HUMAN COLLA ESTs, Weakly similar to KIAA1453 protein	2.0	6.5
			1000	FR. W. LOOM) OR SEE IN LINA (452) BLOSS U	2.0	25
				400		

	419178	NM_006284	Hs.89657	TATA box binding protein (TBP)-associate		20	
	446437	AW014360	Hs.202119	ESTs. Weakly similar to A46010 X-linked		2.0 2.0	6.0
	449910	A1074585	Hs.58440	ESTs		2.0	2.2 2.1
5	435963	AF271212	Hs.87627	disrupter of silencing 10		2.0	21
,	421283 414482	AJ760018	Hs.205071	ESTs		2.0	26
	450960	S57498 AB013897	Hs.76252 Hs.25722	endothelin receptor type A		2.0	24
	438644	Al126162	Hs.129037	Homo saplens mRNA for HKR1, partial cds ESTs		2.0	2.1
	458343	AI004775	Hs.205091	ESTs, Wealdy similar to WW domain bindin		2.0	2.1
10	412574	BE410731	Hs.74050	folloular lymphoma variant translocatio		20	6.5
	458079	AI796870	Hs.54277	ESTs		2.0	12.4
	450582	Al339732	Hs.13144	HSPC160 protein		2.0 2.0	3.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829		2.0	2.8 3.1
15	426865	D63476	Hs.172813	PAK-interacting exchange factor beta		20	3.3
13	446430	AA346837	Hs.15075	hypothetical protein DKFZp434E2216		20	2.0
	Table 4B:						
	Pkey:	Union	e Foe amber	et identifier number			
	CAT numb		cluster numbe				
20	Accession		ank accession				
	_						
	Pkey	CAT Number	Accession				
	447197 407192	2176805_1		36167 Al366546			
25	429007	2200202_1 327976_1	AA602984				
	429163	1238297_1	AV443145	BF958169 AW904500 AL119015 D80642 AA592975 AA447312 AA884766			
	439579	24302_1		W73990 W79232			
	432060	1235850_1	AA525021	AW971364 AA570759			
20	416913	924456_1	AW934714	AW749864 AW749902 RE162498 RE161006	RF169409 RE161006 A	100440 AWE	19 105 BE199599 BE19199
30	426413	372468_1	*********	14 T 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AI022688	1130449 ATVS	13405 BE182500 BE161007
	433586	32908_1	BCU11194	AW517087 AA601054 T85512			
	448451 442495	7632_32 928718_1	AW000978	R39898 AW015994 Al598202 BF821479 Al5	21706		
	439566	23928_1	AU184/1//	W518883 AF121173 W72711 W77884			
35	407939	600387_1	AW118352	AW196215 W05608			
	453740	612139_1	AL120295	BG291384 T88779			
	433854	899720_1	BG675161	H59558 Al699484 AA610649 Al937812			
	413020	1485885_1	BE048113	R98738 Z42904			
40	458050 440769	61684_1	AK057874	AW901381 AW901380 AV730240 T50211 AA	828756 AA834708		
40	428832	21430_5	66419454	BF924037 R13764 AW793200 RE5R1793 RC	こうりょうしょう スクラス・スクラス・スクラス・スクラス・スクラス・スクラス・スクラス・スクラス		
	414473	1137866_1 35761_3	B1008687 /	VA481363 AA436432 BI008686 AA578229 AA BE302693	481375		
	422343	786037_1	D\332008	AA309282 AA551780 Al628633 AA551995 A			
4-	431319	122030_1	BG435498	BG924768 AV718636 AA873350 T82428 T82	W378461	_	
45	422221	319_18	BG910399	BE826714 BF905312 AA306649 Z40822 N76	423 AU 1834 16 AA66844. 833	2	
	413399	1511159_1	BE091833	BE091874 BE091871	J. J		
	432476	1237465_1	AW973269	AA548913 T94344 AA834800 AA857492			
	438874 433891	52147_1	AF075017	R66779 R22463 H02780			
50	421965	647290_1 1883_13	AW182329	AA613792 T05304 AW858385			
•	421000	1003_13	AW968207	A1/42351 BE6/6249 A1/42341 AW572778 AU	66256 AI538553 BI8379	05 AA301100	AA620903 Al142397 AW082310 Al147387 BF509145
			A11300201	AA468415 AU185163 AW450843 Al568752 A	W137191		
	TABLE 4C	:					
55	Pkey:	Uniqu	e number com	esponding to an Eos probeset			
55	Ref.	Seque	ence source.	The 7 digit numbers in this column are Genban	k Identifier (GI) numbers.	*Dunham, et	al.* refers to the publication entitled "The DNA
	Strand:				402:489-495.		The Diese of the posterior of the Diese
	Nt_position	i lodica	ies DIVA sten tos nucleatide	d from which exons were predicted. positions of predicted exons.			
	,	- 41414	400 1100/00/00/00	positions of predicted exons.			i .
60	Pkey	Ref	Strand	Nt_position			
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570			
	405238	7249119	Minus	51728-51836			
	400992 400860	8096828	Ptus	140390-140822			
65	402524	9757499 9798518	Minus Minus	151830-152104,152649-152744			
	404210	5006246	Plus	20529-21096			
	402604	9909420	Plus	169926-170121 20393-20767			
	402855	9662953	Minus	59763-59909			
70	404029	7671252	Plus	108716-111112			
70	402605	9909420	Minus	47680-47973			
	404049 403549	3688074	Minus	75765-78155			
	404048	8081591 3688074	Minus Minus	137150-137362			
	404171	9930793	Minus Plus	54421-56808 173667-173783,176876-177055			
75	405649	4926908	Minus	50032-50132,50624-50764			
	405268	4156151	Minus	24404-24521			
	405204	7230116	Phus	126569-126754			
	405517	9454624	Plus	114757-114877			
80	405203 405687	7230118	Plus	125295-125463			
	403988	6249668 8568881	Minus Plus	54787-54891,55844-55917 159193 159377 159445 469999			
	402269	3128158	Minus	158193-158277,160116-160290 1168-1324,5492-5611,23445-23851			
	404170	9930793	Ptus	168836-169248			

	40.4000	7071000	_					
	404030 401001	7671252 7229886	Plus Minus	149382-151749 113631-113762				
	404820	4678240	Plus	20475-21085				
5			•					
,	TABLE 5A	: ABOUTT 43 G	NES UPREGI	JLATED IN GLIOBLASTOMA THAT ENCODE PRE	DICTED MEMBRANE DOOTER	NC.		
	Pkey:	Uniqu	re Eos probese	t Identifier number	DICTED MEMBRANE PROTEI	42		
	ExAcon:	Exem	optar Accession	number, Genbank accession number				
10	UnigeneID Unigene Ti		ene number ene gene title					
	R1:		of brain tumor	to body atlas				
	R2:	Ratio	of brain turnor	to normal brain				
	Pkey	ExAcon	UnigenetD	Unigene title				_
15	415817	U88967	Hs.78857	protein tyrosine phosphatase, receptor-t	R1 72.0	R2 11.3		
	447072	D61594	Hs.17279	tyrosylprotein aulfotransferase 1	54.2	7.1		
	451099 415910	R52795 U20350	Hs.25954 Hs.78913	interleukin 13 receptor, elpha 2	22.0	7.6		
	412986	X81120	Hs.75110	chemokine (C-X3-C) receptor 1 cannabinoid receptor 1 (brain)	21.2 18.6	3.0 18.6		
20	417355	D13168	Hs.82002	endothelin receptor type B	16.4	16.4		
	419721	NM_001650	Hs.288650	equaporin 4	16.2	4.4		
	452355 410227	N54926 AB009284	Hs.29202 Hs.61152	G protein-coupled receptor 34 exostoses (multiple)-like 2 ·	13.9	13.9		
0.0	419723	AL120193	Hs.92614	Homo saplens growth differentiation fact	11.9 7.4	2.9 3.5		
25	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4		
	443898 422033	AW804296 AW245805	Hs.9950 Hs.110903	Sec61 gamma claudin 5 (transmembrane protein deleted	4.8	7.2		
	414821	M63835	Hs.77424	Fo fragment of IgG, high affinity Ia, re	4.3 4.2	6.1 34.8		
20	431556	AF016028	Hs.260039	sarcospan (Kras oncogene-associated gene	4.0	3.8	•	
30	435869 440516	AF255910 S42303	Hs.54650	vascular endothelial junction-associated	3.7	4.2		
	428141	D50402	Hs.161 Hs.182611	cadherin 2, type 1, N-cadherin (neuronal solute carrier family 11 (proton-coupled	3.5 3.5	5.1 2.4		
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.4 3.4	2.4		
35	431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	2.4		
55	445070 430890	NM_000677 X54232	Hs.258 Hs.2699	adenosine A3 receptor glypican 1	3.2	7.6		
	423422	AC005175	Hs.128425	NY-REN-24 antigen	3.2 3.2	4.3 4.0		
	413367	NM_006517	Hs.75317	solute carrier family 15 (monocarboxylic	3.1	2.6		
40	447471 427150	AF039843 BE616183	Hs.18676 Hs.173737	sprouty (Drosophila) homolog 2 ras-related C3 botulinum toxin substrate	3.0	4.1		
	422676	D28481	Hs.1570	histamine receptor H1	3.0 3.0	4.1 2.1		
	430293	AJ416988	Hs.238272	inositol 1,4,5-triphosphate receptor, ty	3.0	6.3		
	453496 428281	AA442103 AA194554	Hs.33084 Hs.183434	solute carrier family 2 (facilitated glu	2.8	7.4		
45	417446	AL118671	Hs.82163	ATPase, H+ transporting, lysosomal (vacu monoamine oxidase 8	27 24	3.2 4.4		
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	24	2.2		
	440225 450447	BE295782 AF212223	Hs.159	turnor necrosis factor receptor superfami	24	76.7		
	410310	J02931	Hs.25010 Hs.62192	hypothetical protein P15-2 coagulation factor III (thromboplastin,	23 23	2.3 4.1		
50	452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat	23	2.4		
	447217 447023	BE465754	Hs.17778	neuropilin 2	2.3	3.0		
	422070	AA356764 AF149785	Hs.17109 Hs.111126	Integral membrane protein 2A pituitary tumor-transforming 1 interacti	2.1 2.1	3.0		
<i>c c</i>	456804	Al421645	Hs.139851	caveolin 2	21	4.9 15.2		
55	430057 422163	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	20	23		
	414482	AF027208 S57498	Hs.297332 Hs.76252	Homo sapians cDNA: FLJ21471 fis, clone C endothelin receptor type A	2.0	3.7		
		001420	16.702	alternative control type A	2.0	2.4		
60	TARIES							
00	Pkey:	CABOUI 397 C	SENES DOWN	REGULATED IN GLIOBLASTOMA et identifier number				
	ExAcen	Exe	mplar Accessio	n number, Genhank accession number				
	Unigeneli		ene number					
65	Unigene 1 R1:		jene gene lille o of normal bra	in to body atlas				
	R2:			in to brain tumor .				
	Oken							
	Pkey 439340	Ex Accn AB032436	UnigenelD Hs.6535	Title brain-specific Na-dependent morganic ph	R1	R2		
70	424846	AU077324	Hs.1832	neuropepilde Y	4.47 4.49	77.82 55.32		
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	7.06	45.64		
	416836 401412	D54745 c14p3_2958	Hs.80247	cholecystokinin exon	9.45	44.59		
	451835	T63643	Hs.209715	exun ESTs, Weakiy similar to ALU7_HUMAN ALU S	3.20 3.21	32.56 28.93		
75	412768	AW996044	Hs.26239	ESTs	3.16	28.12		
	415448 411305	T68645 BE241596	Hs.952	solute carrier family 10 (sodium/bile ac	3.27	27.04		
	438054	AA776628	Hs.69547 Hs.62183	myelin basic protein ESTs	13.80 3.59	25.92 25.06		
QΛ	410837	BE145698		gb:ILO-HT0205-231199-145-a07 HT0205 Homo	3.05	25.06		
80	425121 458763	Al797511 AJ271351	Hs.154679	synaptotagmin 1	6.92	23.67		
	429656	X05608	Hs.128180 Hs.211584		3.29 e m	23.32		
	451892	AJ821302	Hs.167834	ESTs	8.03 4.12	22.56 21.82		
				10				

	424922	BE386547	Un 247440	COTA INC. NA. 1 IN CO. C.		
	411666	AF106584	Hs.217112 Hs.71346	ESTs, Wealdy similar to Similarity to Ye neurofilament 3 (150kD medium)	4.41	21.28
	432247	AA531287	Hs.105805	ESIS	5.27 3.25	21.20
5	436812 422234	AW298067 AF119818	U= 442007	9b:UI-H-BWO-zip-9-09-0-UI-s1 NCI_CGAP_Su	3.02	21.14 21.12
_	435708	Al362949	Hs.113287 Hs.75169	discs, large (Drosophila) homolog-essoci ESTs	3.38	20.50
	423135	N67655	Hs.26411	ESTs	8.79	20.45
	440600 405230	Al807691	Hs.126351	ESTs	6.82 3.56	20.28 20.09
10	456915	cNp1_7656 NS5540	Hs.78026	EXTE Weekh similar to al-Tanta at	3.31	19.95
	425130	AA448208	Hs.99163	ESTs, Weakly similar to similar to ankyr ESTs	3.14	19.40
	416812	H91010	Ha.44940	EST8	3.53 3.54	19.20 19.08
	454171 457463	AW854832 AW877031	Hs.272321	gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.78	19.04
15	454589	AW809699	10.212021	Homo saplens cDNA FLJ12571 fis, clone NT gb:MR4-ST0124-241199-028-e12 ST0124 Homo	3.13	18.91
	418104	T05726	Hs.177130	ESTs	4.10 3.17	18.60
	416357 414683	T82050 S78296	Hs.268907	ESTs	3.11	18.41 18.13
00	447694	AJ420083	Hs.76888 Hs.170303	internexin neuronal intermediate filamen ESTs	5.55	18.13
20	427627	R87582	Hs.179915	guanina nucleotide binding protein (G or	3.56 4.63	17.79
	428010 417159	AA806554	Hs.185375	ESTs	3.03	17.65 17.40
	438788	R01761 AA766908	Hs.259047	gb:ye81f10.s1 Soares fetal liver spleen ESTs	3.23	17.38
25	459349	AW749381		gb:QV3-BT0381-170100-060-c02 BT0381 Homo	3.16	17.21
23	450214 438068	BE439763	Hs.227571	regulator of G-protein signalling 4	3.26 3.86	17.10 17.04
	437268	AI927209 AI754847	Hs.283089 Hs.227571	HMT1 (hnRNP methyltransferase, S. cerevi regulator of G-protein signalling 4	3.54	16.48
	435315	AA700240	Hs.165402	ESTs	5.63	16.32
30	424240 412446	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.06 4.69	16,12 15.92
50	449714	AI768015 AB033015	Hs.92127 Hs.23941	ESTs	6.44	15.75
	435832	AA425688	Hs.41641	KIAA1189 protein Bruno (Drosophila) -like 4, RNA binding	4.59	15.43
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	4.63 5.93	14.97 14.81
35	435502 414187	L13266 BE312141	Hs.105	glutamate receptor, ionotropic, N-methyl	3.29	14.61
	417868	AI078534	Hs.122592	gb:601145962F1 NIH_MGC_19 Homo sapiens c ESTs	3.37	14.46
	428536	Al143139	Hs.2288	visinin-like 1	7.57 5.16	14.22 13.98
	402125 440503	c18p3_155 NM_006539	Hs.7235	exon	3.11	13.94
40	419090	T85201	Hs.188468	calcium channel, voltage-dependent, gamm ESTs	3.49	13.92
	437665	AA765417	Hs.292053	ESTs	3.25 3.07	13.79 13.79
	457113 424933	A1734016 AW999974	Hs.270508 Hs.5181	ESTs	3.50	13.69
4	443489	Al073512	Hs.133916	proliferation-associated 2G4, 38kD ESTs	3.59	13.48
45	404289	c6p3_5821		exon	3.24 3.99	13.20
	406534 423280	ph2_4616 AA324037		exon	3.89	13.12 13.10
	455421	AW937661	Hs.288324	gb:EST26901 Cerebellum II Homo saptens c Homo saptens cDNA FLJ13283 fls, clone OV	3.38	13.03
50	433725	AF063569	Hs.283919	Homo sapiens clone HQ0117 PRO0117 mRNA.	3.04 3.71	12.93 12.85
50	416660 407593	R98905 AW044083	Hs.35992 Hs.237008	ESTS	3.92	12.74
	451734	NM_006176	Hs.26944	ESTs neurogranin (protein kinase C substrate,	3.85	12.67
	410366	AI267589	Hs.25214	hypothetical protein	7.41 7.89	12.59 12.50
55	405348 442338	cNp3_13716 Al761976	Hs.156080	exon	3.45	12.42
	424458	M29273	Hs.1780	ESTs myelin associated glycoprotein	3.69	12.35
	431400	AA504607		gb:aa63a02.s1 NCI_CGAP_GCB1 Homo saplens	4.72 3.42	12.31 12.29
	417754 440184	R13027 AB002297	Hs.268703 Hs.7022	ESTs	3.35	12.18
60	431339	AA506294	Hs.257266	dedicator of cyto-kinesis 3 ESTs	6.15	12.11
	452265 419297	BE501516	Hs.114772	ESTs	3.50 3.82	11.97 11.96
	424991	AA446040 AA775471	Hs.98640 Hs.241467	Homo sepiens cDNA: FLJ21069 fis, clone C	3.16	11.86
65	431988	AC002302	Hs.77202	ESTs protein kinase C, beta 1	3.03	11.64
65	450987	AA017202	Hs.32794	ESTs	3.78 3.28	11.62 11.61
	440607 454566	AA894559 AW807605	Hs.192097	ESTs	3.11	11.60
	442000	H38671	Hs.8071	gb:MR4-ST0098-120100-001-b06 ST0098 Homo KIAA0735 gene product; syneptic vesicle	3.26	11.54
70	437948	AA772920		gh:ae73c09.s1 Strategene schizo brein 81	3.44 3.16	11.51
70	401081 438919	c11p3_921 AW979114		exon	3.18	11.46 11.35
	454578	AW809178		gb:EST391224 MAGE resequences, MAGP Homo gb:MR4-ST0118-261099-012-c07 ST0118 Homo	4.16	11.35
	422279	H69644	Hs.114231	C-type lectin-like receptor-2	3.02	11.27
75	453101 455836	AW952776	Hs.94943	ESTs	3.35 3.21	11.13 11.07
	413324	BE145795 V00571	Hs.75294	gb:MR0-HT0208-101299-103-a12 HT0208 Homo corticotropin releasing hormone	3.61	10.83
	412266	N59006	Hs.26133	ESTs	3.72	10.71
_	436887 454968	AW953157 AW849046	Hs.193235	ESTs	3.80 7.24	10.60 10.56
80	418162	AW849046 T11958		gb:tL3-CT0214-150300-085-H06 CT0214 Homo gb:A802R Heart Homo sapiens cDNA clone A	3.05	10.53
	425537	AB007913	Hs.158291	KIAA0444 protein	3.07	10.50
	438230 431169	A1248723 AW071240	Hs.17711	ESTs	3.07 3.09	10.48 10.45
	103	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.02	10.43
				120		

PCT/US02/29560

	447359	NM_012093	Hs.18268	adenylate kinase 5	5.91	10.40
	457187	AA443927	Hs.144360	EST	3.30	10.39
	407539 452855	X91103 R17746	Hs.84469	gb:H.sapiens mRNA for Hr44 protein. ESTs	3.02	10.35
5	440352	A1692322	Hs.65373	ESTs ·	3.02 3.03	10.26 10.20
	456116	228528	Hs.172004	Tin .	3.11	10.17
	458172	BE007237		gb:PMD-BN0139-050500-003-g09 BN0139 Homo	3.32	10.14
•	445881	Al263029	Hs.210689	ESTs	3.04	10.11
10	45405 9 402624	NM_003154 c1p1_2660	Hs.37048	statherin exon	3.27	9.97
	441539	AA937200	Hs.192939	EST _B	3.05 3.27	9.94 9.82
	412172	N76794		gb:yv45g07.r1 Soares fetal liver spleen	3.03	9.78
	427942	AA417856		gb:zv01d05.r1 NCI_CGAP_GCB1 Homo sapiens	4.09	9.73
15	436887	BE041837	Hs.120316	ESTs	3.25	9.73
15	454688 446122	AW814472 Al362790	Hs.181801	gb:MR3-ST0203-010200-109-b06 ST0203 Homo ESTs	3.41	9.73
	420480	AL137381	Hs.98173	hypothetical protein	3.40 3.03	9.71 9.56
	433447	U29195	Hs.3281	neuronal pentradn li	3.72	9.54
20	407178	AA195651	Hs.104106	ESTs	3.89	9.47
20	415614	F12926	Hs.165998	DKFZP564M2423 protein	3.06	9.45
	450518 455675	BE245175 BE065984	Hs.270893	ESTS	3.99	9.39
	456459	AA253074	Hs.146261	gb:RC3-BT0319-120200-014-e06 BT0319 Homo ESTs	3.46 4.08	9.32 9.30
0.5	423420	AJ571364	Hs.128382	Homo saplens mRNA; cDNA DKFZp761I1224 (f	5.18	9.23
25	455844	BE064521		gb:RC4-BT0311-250200-014-d02 BT0311 Homo	3.02	9.20
	419800 430964	AA282392	Hs.191525	ESTs	3.28	9.16
	430504	Y10929 AL117454	Hs.248167 Hs.56027	zinc finger protein 186 (Kruppel type)	3.04	9.00
	412962	AW839578	Hs.18160	Homo saplens mRNA; cDNA DKFZp586J1717 (f Homo saplens cDNA FLJ11550 fis, clone HE	3.02 3.33	9.00 8.99
30	445040	AW444934	Hs.195929	ESTs, Wealthy similar to pre-serum armylol	3.50	8.96
	451496	AW503407		gb:UI-HF-BNO-akw-d-11-0-UI.rt NIH_MGC_50	3.17	8.94
	424617 441914	AA344151	11- 400405	gb:EST50059 Gall bladder I Homo sapiens	3.25	8.91
	405320	AA971496 cNp3_12168	Hs.128465	ESTs exon	3.42	8.88
35	449179	AI633785	Hs.196561	ESTs	3.30 3.43	8.84 8.84
	400335	Y13187	Hs.248066	Homo sapiens dmd gene, intron 11	3.13	8.78
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	4.16	8.74
	407803 455260	AW081681	Hs.269064	ESTs	3.09	8.73
40	433260	AW878317 AA324358	Hs.249227	gb:MR3-OT0007-260300-206-e09 OT0007 Homo Homo sapiens DNA, cosmid clones TN62 and	3.78	8.70
	424481	R19453	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	4.01 8.12	8.67 8.63
	407616	AW054849	Hs.246831	ESTs, Wealdy similar to CIKG_HUMAN VOLTA	3.08	8.53
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.26	8.51
45	439239 410926	AI031540	Hs.235331	ESTs	5.78	8.48
1.5	430004	AW810708 U27768	Hs.227571	gb:MR2-ST0129-051099-007-g07 ST0129 Homo regulator of G-protein signalling 4	3.34	8.47
	409623	AW4491B5	123.227011	gb:UI-H-BI3-akg-e-05-0-UI.s1 NCI_CGAP_Su	4.26 3.32	8.45 8.43
	420156	AW449258	Hs.6187	ESTs	3.40	8.38
50	411555	AF113537	Hs.70669	HMP19 protein	5.85	8.34
50	408509 442368	AA497035 Al698577	Hs.110502 Hs.202481	ESTs CCT-	3.17	8.34
	457870	AA732217	Hs.294054	ESTs ESTs	3.02 3.04	8.33 8.32
	437254	AAB31258		gb:oc73f04.s1 NCI_CGAP_GC81 Homo sapiens	3.35	8.24
55	415508	R39236		gb:yc91d03.s1 Soares infant brain 1NIB H	3.07	8.22
33	409483 435229	U49379	Hs.54506	diacyigiyoerol kinase, epsilon (64kD)	3.31	8.20
	458120	AA676556 W21398	Hs.269515 Hs.54523	ESTs, Moderately similar to ALUB_HUMAN I ESTs, Wealdy similar to cytochrome P-450	3.21	8.19
	444613	H29627	Hs.79092	ESTs	3.22 3.78	8.17 8.16
60	41.7050	N39540	Hs.108029	ESTs	4.06	8.14
60	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	3.68	8.06
	413263 424549	BE075131 Al873205	Hs.183114	gb:PM1-BT0585-110200-003-g03 8T0585 Homo	3.40	8.04
	452689	F33868	Hs.284176	Homo sapiens cDNA FLJ14238 fis, clone NT transferrin	3.27 3.03	8.03
~	405476	cNp3_19940	***************************************	exon	3.28	8.01 8.00
65	403932	c5p1_533		exon	3.58	7.99
	407095	AF011757	Hs.105937	RAGE binding protein	3.32	7.96
	415967 417555	H11124 H65366		gb:ym14h07.s1 Soares infant brain 1NiB H	3.10	7.96
	448985	AA324885	Hs.22777	gb:yr67c10.r1 Soares fetal liver spleen carbonic anhydrase XI	3.05 5.30	7.95 7.70
70	428689	NM_014351	Hs.189810	sulfotransferase-related protein	3.87	7.79 7.74
	424140	Z48051	Hs.141308	myelin oligodendrocyte głycoprotein	4.68	7.74
	441099	AW339393	Hs.126573		3.08	7.74
	448589 408112	AF017090 ph0_24243	Hs.21554	KIAA1107 protein exon	3.10	7.73
75	458439	AV647220	Hs.282889		3.22 3.22	7.70 7.60
	429859	NM_007050	Hs.225952		3.22	7.69 7.68
	412090	AW955826	Hs.12398	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.01	7.67
	413547 447772	8E147440	Un dodana	gb:RC1-HT0229-080100-015-f09 HT0229 Homo	3.01	7.66
80	411132	AI924558 AW819191	Hs.161399	ESTs gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.04	7.63
-	425490	NM_002248	Hs.158173	potassium intermediate/small conductance	3.72 3.15	7.61 7.60
	454568	BE141434		gb:MR0-HT0079-051099-002-d01 HT0079 Homo	3.16	7.59
	439099	AB037800	Hs.6462	KIAA1379 protein	3.40	7.57

	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	5.71	7.57
	428175 413162	A1810774 BE068115	Hs.98376	ESTS	3.04	7.55
	451361	AA053854	Hs.235390	gb:CM1-BT0368-051299-060-g07 BT0368 Homo Homo sapiens mRNA; cDNA DKFZp761B101 (fr	3.43	7.54
5	442527	AF150289	Hs.205436	ESTs	3.11 3.31	7.53 7.53
	450407	NM_000810	Hs.24989	gamma-aminobutyric acid (GABA) A recepto	5.24	7.53
	456966	AJ589569	Hs.190082	ESTs	3.13	7.47
	441799	AW292276	Hs.127872	ESTs	3.38	7.41
10	424185 429783	AA279752 AA811987	Hs.142570	Homo sapiens clone 24629 mRNA sequence	3.16	7.40
10	429268	AA205386	Hs.125779 Hs.198481	ESTs RAR-related orphan receptor 8	3.13	7.38
	400708	c11p1_1292	113.130401	expu	3.48 3.33	7.38 7.35
	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	3.04	7.33
1.5	455377	AW905347		gb:QV2-NN1073-220400-159-108 NN1073 Homo	3.03	7.33
15	435070	AI821270	Hs.116930	ESTs	3.03	7.33
	405427 455149	cNp3_17682		8000	3.03	7.25
	402816	AW861879 c1p3_2531		gb:CM0-CT0341-260100-160-h12 CT0341 Homo exon	3.56	7.24
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	3.13 3.40	7.21 7.15
20	422297	AW961290	Hs.155615	ESTs	3.44	7.10
	412688	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	3.91	7.09
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	3.09	7.09
	412290 415486	BE069037	No. 42204	gb:QV3-BT0379-161299-040-e12 BT0379 Homo	3.04	7.08
25	407728	H12214 AW071502	Hs.13284 Hs.175931	ESTS ESTS	4.22	7.07
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-cht	3.05 5.93	7.06 7.05
	417275	X63578	Hs.81849	parvalbumin	4.08	7.04
	418425	AJ871247	Hs.6262	ESTs	4.10	7.04
20	440558	AA889574	Hs.177511	ESTs	3.28	7.04
30	411427	AW846080	11- 22005	gb:MR3-CT0176-081099-002-b09 CT0176 Homo	3.11	7.03
	422272 410816	AI452421 AW806175	Hs.77965	Clk-associating RS-cyclophilin	3.39	7.03
	418375	NM_003081	Hs.84389	gb:MR1-UM0108-130400-003-a06 UM0108 Homo synaptosomal-associated protein, 25kD	3.30 9.93	7.02 7.01
	421627	Al138551	Hs.97318	ESTs	3.10	7.01
35	447258	BE047911		gb:tz44a05.y1 NCI_CGAP_Brn52 Homo sapien	3.09	6.99
	455547	AW994078		gb:RC3-BN0036-090200-011-h02 BN0036 Homo	3.35	6.98
	432209	AW971278		gb:EST383367 MAGE resequences, MAGL Homo	3.49	6.92
	404541 451539	c8p1_6409 AA059467	Hs.218933	exon ESTs	4.62	6.89
40	429954	AI918130	Hs.21374	ESTS	3.01 3.82	6.88
	411138	AW819500	110.2.1014	gb:RC5-ST0293-180100-012-C07 ST0293 Homo	3.02	6.87 6.87
	447464	AW444957	Hs.201897	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.33	6.85
	454713	AW815111		gb:QV4-ST0212-091199-023-c09 ST0212 Homo	3.16	6.84
45	415734 429667	NM_014747	Hs.78748	KIAA0237 gene product	5.00	6.84
73	403008	AA456275 c21p3_2374	Hs.44841	ESTs exon	3.09	6.80
	446079	T56522	Hs.154030	ESTs	3.04 3.11	6.78 6.75
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4,49	6.75
	437804	AA828257	Hs.124324	ESTs	3.42	6.73
50	436454	AA757615	Hs.291509	ESTs	3.01	6.72
	416334	H53139	Hs.36271	EST8	3.12	6.70
	455985 445085	BE167014 AJ569295	Hs.179285	gb:CM2-HT0502-140200-088-d08 HT0502 Homo ESTs	3.05	6.68
	445611	AW418497	Hs.145583	ESTS	3.19	6.68
55	437762	T78028	Hs.154679	synapiotagmin 1	3.61 7.21	6.68 6.68
	416268	H49111		gb:yo21c07.r1 Soares adult brain N2b5H85	3.02	6.67
	449768	A1668690	Hs.54773	ËSTs	3.25	6.64
	443100 408070	AI033188		gb:ow94e08.s1 Soares_fetat_liver_spleen_	3.07	6.64
60	451602	AW148852 AW008846	Hs.60857	gb::d05d05.x1 NCI_CGAP_Bm35 Homo saplen ESTs	3.12	6.60
••	441447	AA934077	Hs.126980	ESTs	3.05 4.06	6.59 6.59
	445078	AI869975	Hs.4775	Junctophilin 3	4.25	6.59
	434501	AF143878	Hs.194152	Homo saplens clone IMAGE:115304 mRNA seq	3.25	6.58
65	415980	R49020	Hs.24974	ESTs	3.34	6.58
05	403395	c3p1_11541		exon	3.59	6.57
	403051 419232	c2p1_10450 Al382037	Hs.87421	ESTs	3.06	6.56
	425984	AW836277	Hs.165636		3.28	6.56
	403717	c4p1_3133	113.103030	excon	6.50 3.52	6.56 6.53
70	452178	AW043576	Hs.171929		3.38	6.53
	455758	R15709	Hs.284231	Novel human gene mapping to chomosome 22	4.42	6.52
	433858	N69243	Hs.192974		3.58	6.52
	425440 419412	AA357518	U= 00207	gb:EST66256 LNCAP cells I Homo saplens c	3.15	6.49
75	423678	AW161058 AW963357	Hs.90297 Hs.7847	synuclein, beta ESTs	5.60	6.47
. –	416625	R97839	Hs.35758	ESTs	3.47 3.10	6.47 6.46
	451854	T92536	Hs.194096		3.28	6.46
	405732	AA487229	Hs.2064	vimentin	3.71	6.44
80	434619	H43183	Hs.32810	ESTs	3.05	6.44
30	413797 438612	BE167274	Hs.5996	ESTS	3.23	6.44
	412317	AW977980 AW991979	Hs.292129	ESTs gb:RC1-BN0014-210100-012-f05 BN0014 Homo	3.39	6.42
	422159	N76767	Hs.153408		3.46 3.03	6.42 6.41
				· · ·	4.00	0.41

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.48	6.35
	427334	R44789	Hs.119486	ESTs, Weakly similar to transmembrane re	3.93	6.35
	453839	AL138417	11- 400040	gb:OKFZp434B1729_r1 434 (synonym: htes3)	3.06	6.34
5	429096 444609	AB011106 AW571659	Hs.196012 Hs.278081	KIAA0534 protein ESTs	3.12	6.33
	419515	581944	Hs.90791		3.30	6.33
	418900	BE207357	Hs.301709	gamma-aminobutyric acid (GABA) A recepto ESTs	3.11 3.14	6.33 6.30
	437979	AA774318	Hs.121708	ESTs	3.25	6.29
_	410359	R38624	Hs.106313	ESTs	4.74	6.28
10	415990	R76929	Hs.29633	ESTs	3.39	6.28
	419392	W28573		gb:51f10 Human retina cONA rendomly prim	3.00	6.28
	424312	AB013452	Hs.144931	ATPase, aminophospholipid transporter (A	3.06	6.26
	444762	Al733700	Hs.143883	ESTs	3.09	6.25
1.5	447785	AL041765	Hs.161423	ESTs	3.05	6.22
15	418199	AA884555	Hs.86603	ESTs	3.55	6.22
	440582	AA993337	Hs.129082	ESTs	3.73	6.21
	457766	AL119470	Hs.145631	ESTs	3.69	6.21
	426814 412018	AF036943	Hs.172619	KIAA1106 protein	4.71	6.21
20	414699	BE148152 Al815523	11- 70000	gb:RC4-HT0231-041199-012-b04 HT0231 Homo	3.36	6.21
20	420127	AA360399	Hs.76930 Hs.44811	synuclein, alpha (non A4 component of am ESTs	3.68	6.19
	418833	AW974899	Hs.292776	EST8	3.54	6.18
	441265	AA927180	Hs.153261	ESTs	3.08 3.21	6.18 6.17
	413408	R51793	Hs.21745	ESTs	3.56	6.15
25	434512	AW139932	Hs.188941	ESTs	3.56	6.15
	422253	W81526	Hs.118329	ESTs	5.04	6.10
	439950	AW937417	Hs.293561	ESTs	3.24	6.10
	417210	N99228	Hs.49162	ESTs	3.54	6.10
••	414306	BE27219B	Hs.283869	Human DNA sequence from clone RP5-1013A2	3.35	6.10
30	411265	AW834695		gb:RC0-LT0001-261199-031-D05 LT0001 Hamo	3.07	6.10
	412734	AW993498		gb:RC2-BN0033-170300-019-b08 BN0033 Homo	3.36	6.09
	425172	AA447729	Hs.12714	ESTs	5.40	6.06
	451759	W23161	Hs.32886	ESTs	3.21	6.02
35	432154	AJ701523	Hs.112577	EST8	3.50	6.02
22	401313	c13p1_435		exon	3.92	5.96
	448951	Al350575	Hs.156730	ESTs	3.20	5.95
	440917	AA909651	Hs.160025	ESTs	3.06	5.94
	405961	ph0_14521	Hs.192760	exon	3.12	5.91
40	428737 417292	AA984728 N69197	Hs.191361	kinesin family member 5A ESTs	3.05	5.90
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	3.62	5.89
	452524	AW136499	Hs.29798	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	3.52 3.07	5.88 5.88
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	4.08	5.87
	423641	AL137256	Hs.130489	Homo saplens mRNA; cDNA DKFZp761K0912 (f	3.28	5.87
45	420755	AI699437	Hs.165268	EST8	. 3.17	5.86
	448116	AW352276	Hs.170700	ESTs	3.28	5.86
	412694	AW984373		gb:PM3-HN0011-200300-001-f01 HN0011 Homo	3.00	5.83
	437612	AAB27715	Hs.105153	Homo sapiens cDNA FLJ14230 fis, clone NT	3.09	5.82
50	411522	AW850286		gb:IL3-CT0219-161199-031-H11 CT0219 Homo	3.26	5.81
30	456910	BE185921	Hs.98073	ESTs	3.20	5.80
	439915	AJ521791	Hs.252358	ESTs	3.55	5.80
	404403	c8p1_1094		exon	3.23	5.80
	405332 411167	cNp3_13017		90001 	3.51	5.78
55	416139	AW820204 H21109	Hs.172853	gb:QV2-ST0298-190100-029-c11 ST0296 Homo ESTs	3.04	5.78
	434222	AF119886	Hs.283941	Homo saplens PRO2591 mRNA, complete cds	3.63 3.65	5.77
	415247	F02431	Hs.6581	ESTs	3.08	5.77 5.75
	446037	A1076806	Hs.282965		3.42	5.75
	450478	AW451709	Hs.271200		3.80	5.72
60	446588	AV659343	Hs.282954	ESTs	3.29	5.72
	413118	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	3.03	5.72
	416946	NM_012324	Hs.80545	mitogen-activated protein kinase 8 Inter	3.91	5.72
	454751	AW819132		gb:RC3-ST0281-240400-015-c10 ST0281 Homo	3.06	5.72
65	457194	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.54	5.71
03	438601	AAB11713	Hs.163222		3.26	5.71
	439032	AA829487	Hs.274412	similar to yeast Upf3, variant A	3.10	5.67
	408940	M58583	Hs.662	cerebellin 1 precursor	3.32	5.67
	437700 416061	AA766060 R45518	Hs.122848 Hs.26119		3.23	5.66
70	452861	BE177663	rts.20119	ESTs gb:RC1-HT0598-020300-011-h11 HT0598 Homo	3.85	5.65
. •	430330	AA476583	Hs.132981		3.04	5.64
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.51 5.67	5.63 5.62
	400710	c11p1_1297		exon	3.04	5.62 5.61
	457130	NM_005651	Hs.183671		3.31	5.60
75	434513	AF143888	Hs.18213	Homo saplens done IMAGE:121738 mRNA seq	3.93	5.60
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	3.67	5.58
	440854	AW444900	Hs.246715	ESTs	3.30	5.58
	457088	AA412591	Hs.204685	ESTS	3.37	5.57
00	431883	AA731404	Hs.105510		3.67	5.56
80	400758	AA158742	Hs.225084		3.43	5.55
	455374	AW904039		gb:CM3-NN1040-200400-158-d03 NN1040 Homo	3.36	5.52
	440750	AW105131	Hs.245405		3.10	5.50
	451865	H43737	Hs.33188	ESTs, Weekly similar to unknown protein	3.38	5.50

	453100	AW806871	Hs.224788	ESTs		3.30	5.49
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21		3.24	5.49
	454935	AW846075		gb:MR3-CT0176-081099-002-b02 CT0176 Homo		3.26	5.48
5	435447	AI872932	Hs.142442	HP1-BP74		3.89	5.47
5	402953	c20p3_3451		exon		3.28	5.47
	456233	AA203339		gb:zx56a01.r1 Soares_fetal_liver_spleen_		3.02	5.47
	407718	AW070784	Hs.243243	EST		3.30	5.45
	417429	A1950629	Hs-286237	Homo saplens cDNA FLJ11841 fis, clone HE		3.31	5.38
10	446408	AI797169	Hs.208486	ESTs		3.07	5.37
10	441792	AW873635	Hs.143962	ESTs		3.19	5.35
	450681	AW952160	Hs.32916	ESTs		3.70	5.35
	433932	AW954599	Hs.169330	neuronal protein		6.78	5.33
	427002	AA524093	Hs.23158	ESTs		4.00	5.32
15	428741	AA461386		gb:zx70h06.r1 Soares_total_fetus_Nb2HF8_		3.10	5.32
15	446383	T05816	Hs.92511	EST		3.39	5.30
	442988	AI026130	Hs.131683	ESTs		3.07	5.29
	426713	AI655299	Hs.130055	ESTs		3.33	5.29
	421294	AA713488	Hs.180291	ESTs		3.44	5.28
20	406452	ph2_21981		exon		3.20	5.28
20	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1		3.26	5.27
	442114	BE217975	Hs.157021	ESTs		3.32	5.26
	432508	A1808915	Hs.190201	ESTs		3.46	5.26
	425604	U94320	Hs.158330	neuropeptide Y receptor Y5		3.26	5.23
25	417925	R26789	Hs_23995	ESTs		3.08	5.23
23	444448	H66317	Hs.143660	ESTs		3.81	5.22
	413024	AF038268	Hs.75149	SH3-domain GRB2-like 2		3.71	5.22
	437911	AA848010	Hs.124250	ESTB		3.11	5.18
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin		4.95	5.17
30	407131	R98679		gb:yr31c03.s1 Soares fetal fiver spleen		3.30	5.16 .
30	435776	AI537162	Hs.263988	ESTs		3.14	5.13
	455532	AW984828		gb:RC1-HN0015-120400-021-h11 HN0015 Homo		3.14	5.13
	457352	AA489099		gb:aa56h09.s1 NCI_CGAP_GCB1 Homo saplens		3.48	6.12
	428670	AA4316B2	Hs.134832	ESTs		3.17	5.12
35	445962	Al268410	Hs.201386	ESTs		3.14	5.12
33	418153	R13696	Hs.112830	ESTs		3.16	5.10
	440565	AW103823	Hs.131586	ESTs		3.08	5.10
	431446	AW294929	Hs.255369	Homo saplens cDNA FLJ10265 fis, clone HE		3.42	5.09
	456036	BE536554	Hs.75839	zinc finger protein 6 (CMPX1)		3.21	5.09
40	420883	AI735488	Hs.111436	ESTs		3.17	5.08
40	455528	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo		3.35	5.08
	408442	R59608	Hs.21435	ESTs		3.10	5.07
	446093	Al346849	Hs.145896	ESTs		3.30	5.06
	403489	c3p1_2255		exon		3.43	5.05
45	405278	cNp3_1070		exon		3.05	5.03
43	412804	H18857	Hs.22547	ESTs .		3.63	5.03
	458407	W90022	Hs.186809	ESTs, Highly similar to LECT2 precursor		3.52	5.03
	407387	AA130773		gb:zo13d01.r1 Stratagene colon (937204)		3.51	5.02
	439108	AW163034	Hs.6467	synaptogyrin 3		5.63	5.01
50	445335	AI220339	Hs.166775	ESTs		3.21	5.01
50	435404	AI240661	Hs.124995	ESTs		3.99	5.00
	7401500	_					
	TABLE 6B						
	Pkey:			et identifier number			
55	CAT numb		cluster numbe				
55	Accession	Gent	ank accession	numbers			
	~						
	Pkey	CAT Number	Accession				
	410837	282574_1	AW806917 A	W866469 BF898475 BF898476 AW866540 AW866614	BE145698 AW8	86575	
60	436812	659779_1	WARALRI 19 1	W298067 AA810101 AW194180 AA731645 Al690673			
00	454171 454589	1049240_1	AW854832 A	W854798 AW854857 AW854816 AW854834 AW85481	17		
	434308	28039_6	BG674750 E	F374578 AW810080 AW810106 AW810084 BF374755	AW809621 BF3	74734 BF374	4590 BF374594 AW809699 BF374588 AWR10437
	417159	2070200 4					
		2075888_1	R01760 N49				
65	459349 414187	1027822_1	AW749381 I				
05		315279_1		E312141 BF942980			
	423280 431400	881045_1		186636 AA324037			
		1233918_1	AVV969094 A	A504607 AA504705			
	454566	164604_1	AW807605 /	W807690 AW807677 AW807752 AW807673 AW80790	00 AW807955 AV	V807679 AV	/807615 AW807917 AW807849 AW807832 AW807821
70							
, 0							
	427040	220202 4	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	711001 935 VII 001 9 10 VII 001 0 10 VAI 001 VAI 001 VAI VII VAI	56 AW807608 AV	V807683 AV	/807839 AW807601 AW807822 AW807898
	437948	330397_1	~~!! 2320 0	33010 C01131 M331331 BL30(838)			
75	438919	1242818_1	AW9791147	A828060 AA837606 AA829203			
, ,	454578 456936	1670_3	BE150647 A	W971143 AW809224 AW809221 BF753820 AW809220	AW809178 AW	809150 AWE	109195 AW809175
	455836	1518824_1	DE 1430UU B	E 149921 BE 145873 BE 145871 HE 145930 RE 145797 R	E1/6706		
	454988	1085677_1	AW848279 /	\W849039 AW847958 AW847957 AW849046 AW84869	98 AW849034 AV	VB49033	
	418162	2189291_1	111756 120	135 T19729 T11958 T11816 R45874			
80	431169 458172	1235760_1	AW971240 /	AA493723 AA493843			
55	458172	363900_1	BE007237 B	E546311 AA984819 BI256810 W19919 BE007263 BG0	00322 BF32701	1 AA89019B	BE007496
	427942	709034_1	4404120 WA	09/ 935 N992Z L			
	454588	485847_1 1066481_1	DE3754001 A	A417856 AV756446 BG505084 BI460307 BI460993 BG	613293		
	7079000	1,1860001	BF3/5123 A	W814472 AW814474 AW813343 AW816161 AW81338	0 AW813300		

	455675 455644	1490763_1 1489581_1	BE065984 BI BE064521 BI	E066085 BE085942 BE065956 E064441 BE064426 BE064285 BE064286
	451496	85420_1	AA046879 BI	F327988 AW503407 AA018131
5	424617 454962	895912_1 323094_1		A344151 AA34472 NBF (MD TO
,	455260	231032_1	RF161R05 A	W854083 BF962818 AW847791 BI035483 AW847645 BF961514 BF963484 BF952264 BF963521 W876317 BE161759 BF870032 BF869588
	434589	14876_1		47219 T47218
	410926	1064369_1		NW810808 AW810771 AW810924
10	409623 437254	830636_1 1239876_1		3E220971 AW449185
10	415508	1874742_1	R45579 F10	VA831258 AA765857 AA747712 AJ784019 RP2 R39238
	413263	1497122_1		E075131 BE075130 D60395 BF688035
	415967	1899490_1		230 BF383165 H49061 H11124
15	417555 413547	1978200_1 1520005_1		L697143 H65368 E147563 BE147708 BE147440
	411132	1070974_1	AW819177 A	W819242 AW819191 AW819175 AW819252 AW819244 AW819265 AW819269 AW819190 AW819268 AW819183 AW819246 AW819194
		•	AVV019249 A	\W819186 AW819180 AW819188 BE158470 AW819251 BE152602 AW819263
	454568 413162	1061859_1 1492355_1	AW807809 A	WB07824 AW807826 AW807903 AW807766 AW807750 AW807911 BE141434 AW807611 AW807837 AW807899 BF374481
20	455377	154707_1	BF947516 A	E058096 BE058199 BE068115 BE068102 BE068154 BE068103 W905291 BF947512 BF952606 BF952706 BF952525 BF952524 BF952619 BF947500 BF952608 BF952523 BF952532 BF952344
			BF/46516 B	F947614 BF746511 BF952358 AW905400 AW905300 BF947617 AW905349 BF952531 AW905403 BF952528 BE081655 BF746513
	455149	1000453 4	AW905286 E	3F952868 BF947513 BF947610 BF947618 BF947619 AW905347
	412686	1099453_1 1243154_1	AVVOC1079 A	NW861948 AW858447 AW861873 AW858418 AW861871 NW984077 AW984072
25	436383	46767_1		E065178 BE065329
	412290	1163352_1		E069178 AW936034 AW936025
	411427 410816	1083097_1 1060611_1		AW846074 AW846118 AW846130 AW806176 AW806170 AW8061 56
••	447258	1485710_1		IE047911 AA984167
30	455547	1245954_1	AW994078 (BE176183
	432209 411138	1235790_1 1071173_1		AAS28270 AAS53447 AW971281
	454713	1067889_1		AW819503 AW819481 AW819459 BF375618 AW815094 AW815218
35	455965	1555935_1	BE167014 B	3E167058 BE167062
دد	416268 443100	1959926_1 416959_1	H41854 H49	9111 H46317
	408070	632273_1	AW1488521	NW804074 BE089437 BE089439 BE089378 BE089438 BE004795 W02375 Al033188 BF332422 BF332418 BE178660 BG994152
	425440	1228191_1		AA357518 AA360531
40	412317 453839	1164038_1 3209657_1	AW991979 A AL138417 A	AW991981 AW991983 AW936856 AW991977 AW991971 AW936852
. •	419392	215562_2	W28573 W2	
	412018	147109_1	BE148133 E	3E148132 8F736564 BE148152 BE148159 8F893700
	411265 412734	1074383_1 1245451_1		AW834717 AW834714 AW993484 AW993490 BF512974
45	412694	1243393_1	AW984388	AW984392 AW984379 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984373 AW984372 AW984353 AW984362
	411522	1089092_1	BE143505 E	BF374194 BF374190 AW850286
	411167 413118	1071740_1 1490760_1		AW820314 AW820321 BE065939 BE065956
	454751	1070838_1	AW819132	AW819122 AW819018 AW819135 AW819126 AW819024 AW819012 AW819141
50	452861	319757_1	BE177663 /	AW994738 Al923735 BF948431 BF948329
	455374 454935	1161013_1 1083098_1	AW904029	AW904030 AW904039 AW904031 AW904032 AW904046
	456233	2635744_1	AA203339	AW846103 BF333978 AW846077 AW846122 AW846129 AW846095 AW846076 BF333979 BF333978 AW846092 AA906160 AA929005
55	428741	1384399_1	AA461386 /	AA433841 AA433845
در	455532 457352	1243692_1 1233795_1	AW984828	AW984787 AW984806 AW984817 AW984826 AW984822 AW984773 AW984785 AW984803 AW984796
	455528	1243660_1		AA489099 N72933 AA489184 AW984757 AW984797 AW984745
	407387	4907_1		H72550 H72951 AA130773
60	TABLE 60	•		
~ ~	Pkey:	Unic	ine unwper co	rresponding to an Eos probesel
	Ref:	Seq	uence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:	acq	Deliver of Hother	n chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. Ind from which exons were predicted.
65	NL positio	en: India	cates nucleotid	8 positions of predicted exons.
	Dloor	Def	Ctomard	Altti
	Pkey 401412	Ref 7940103	Strand Minus	Nt_position 43347-45776
70	405230	7249032	Minus	97493-97682
70	402125	4033680	Plus	172732-172868
	404289 406534	2769644 7711477	Plus Plus	15049-15286,30267-30457 40463-40586,41191-41336,41856-41986,4300
	405348	2914717	Minus	43310-43462
75	401081	3478647	Plus	105163-105305
. , ,	402624 405320	7885063 3478667	Minus Minus	31308-31439 118511-118926,119175-119331
	405476	2121229	Plus	69890-70883
	403932	7454203	Minus	8142-8753
80	406112 400708	9133145 7249204	Plus Plus	61863-62028 118115-119445
	405427	7243901	Minus	6509-6729
	402816	6723302	Minus	25104-25291
	404541	8318559	Plus	103456-103664

		6070398	Plus		5,95096-95233				
		9438353 8954192	Minus Plus	144947-145 142875-143					
_		7259747	Minus	79166-7975					
5		9212516	Minus	190842-191					
		8190197	Plus	45132-4525					
		7272157 3169141	Minus Minus	72053-7223 70483-7120					
10		7249204	Plus	156753-157					
10		9408724	Minus	122603-122					
		9588380 7331314	Minus	76322-7642					
		6139075	Minus Minus	38897-3921 3863-3965	z 4823-4891,5439-5	529 6043-6170			
1.5				,	,	020,0040-0170			
15	74DI C 74		5 C. (CD) . C						
	DNA sequ	LAIENUE	D GTORIAS	TOMA SEQUENC	E5: This table inc	tudes sequence in	formation for 21 Of	VA and prot	sin sequent
	Gene na			rosine phos	phatase, re	ceptor-type	, Z polypep	tide 1	
20		number	r: Hs.78	867			., - polypop		
20			ssion #:						
			:e: 148-	#: NM_002	851				
	1	11			31	41	51	•	
25	1	<u> </u>		<u>L</u>	1	I	1		
23	CARARAR	ACG CAC	CTCCTTCC	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60	
	CGGCGAG	GGG CCC	CAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	120 180	
	CAGCTCC	TCT GTO	STTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240	
30	CTTGTTG	aag agi	ATTGGCTG	GTCCTATACA	GGAGCACTGA	ATÇARARAR	TTGGGGAAAG	300	
50				CCCAAAACAA				360	
	AACACAT	TCA TT	CATCITAA	GAAACTTAAA TGGGAAAACA	CTCCAGGGTT	GGGATAAAAC	ATCATTGGAA	420	
	GTCAGCG	GAG GAG	TTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	480 540	
25	AAATGCA	ATA TG:	CATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600	
35	GAGATGC	AAA TC	PACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660	
•	GATTTCA	AAG CC	TTAAGAGC	TTTATCCATT TGGAGTCGAA	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720	
	TTAGATC	CAT TO	ATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	780 840	
40	AATGGCT	CAT TO	ACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTABAGAT	900	
40	ACAGITA	GCA TC	TCTGAAAG	CCAGTTGGCT	GTTTTTTTTT	AAGTTCTTAC	AATGCAACAA	960	
	TCTGGTT	ATG TC	ATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG		
	AGTTCAG	AAC CAI	TOTARARA	CTCATACACT TCAGGCTGAC	CCAGAGGAAG	AGATTCATGA	AGCAGTTTGT	1080	
45	TGGGAAA	GAC CT	CGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1140 1200	
45	CAGTTCC	ATG GA	GAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260	
	TOCACTA	TTC TC	AATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320	
	AATCCTG	AAC TT	GATCTTTT	AAAATACAGC CCCTGAATTA	ATTGGAACTGA	ALGALATAAT	CANCGACGAG	1380	
5 0	GAAGAGG	GAA AA	GACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1440 1500	
50	AACCAAA	TCA GG	ADDAAAAA	ACCCCAGATT	TCTACCACAA	CACACTACAA	TOGOLATAGOG	1560	
	ACGAAAT	ACA AT	GAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620	
	ACAGAAA	AAG AT	ATTTCCTT	ATCTTTAAAT	ACTOTORACTO	AACCAGTCAC	TAAATTAGCC	1680	
	GAAGGTA	CTT CA	GCCTCTTT	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCACATATG	1740 1800	
55	AACTTGT	'CGG GG	ACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860	
	AGTTTAT	TGA CC	AGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920	
	GAAAAC	CIG CI	ATCCCATT	CATCTCTGAG ATATGATGTC	CTTATACCAC	AAGGGTATAT	ATTTTCCTCC	1980	
	GAAGATI	CAA CT	TCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2040 2100	
60	GTGTGGT	TTC CT	AGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160	
	AGCTTTC	TCC AG	ACTAATTA	CACTGAGATA	COTOTTGATG	AATCTGAGAA	GACAACCAAG	2220	
	CATTATT	CIG CA	TTTGCCTA	CTTCCCAACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA TACCCCATCC		
~-	TCCAGAC	'AAC AG	GATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	SYNAGYYNAA	2340 2400	
65	GTATACA	ATG GT	GAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TOTTOTAGETO	2460	
	ACCCCTI	TGT TG	CTTGACAA	TCAGATCCTC	AACACTACCC	Cald Cald Calabria	A ACTE ACTE AT	2520	
	TCTTCCT	TGC AT	GCTACGCC	TGTATTTCCC	AGTGTCGATG	TGTCATTTGA	ATCCATCCTG TAGTGAATTG	2580	
	TTTCGCC	ATC TG	CATACAGT	TTCTCAAATC	CTTCCACAAG	TTACTTCAG	TACCGAGAGT	2640 2700	
70	GATAAGG	TIGC CC	TTGCATGC	TTCTCTGCCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGCCC	2760	
	AGCCTTG	CTC AG	TATTCTGA	TOTACTOTO	ልርተልርተርልተር	ごせいこうかい ない	CACCCCCAA	2020	
	TTTGGTA	GTG AA	TCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCACCC		
	GATAATO	BAGG GC	TCCCAACA	CATCTTCACT	GTTTCTTACA	ARCCTTCTTA	TGCCTTGTCT ACCTGTGCAT	2940	
75	GATTCIC	ricg gi	GTAACTTA	TCAGGGTTCC	TTATTTAGGG	GCCCTPAGCCA	ጥልጥክ //// አጥክ	3060	
	CCTAAG	CTT CG	TTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120	
	GGTGATC	iggg aa	TGGTCTGG	AGCCTCTTCT	GATAGTGAAT		TCACACACAT	2100	
	Tererer	TTG OT	CITARCAT AATGDTAD	TANGGOGG	GITTCTGTAG	CTGAATTTAC	ATATACAACA TGGAAATGAG	3240	
80	ACTGAAC	TCC AA	ATTCCTTC	TTTCAATGAG	ATTEMPT	Calar Card y y y G	CACACTCATC	3300	
	CCCAAC	VIGT AI	GATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CLICALCHARTICC.	3420	
	ATTTCTA	AGCA CC	AAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	**************************************	TABRITON	2400	
	TCTCATC	AGA TI	AGTCAAGT CGTGDCDC	TROSCORIA	AACTITTCAG	TTCAACCTAC	ACATACTGTC AGAGCCAGCA	3540	
				- + CGCTTMAA	CLIGIOCITA		AGAGCCAGCA	3600	

	ACCTCTGACC	CTGCTTCTAG	TGAAATGTTA	CTACAACCTT	CTCAGCTCTT	ATTITATGAG TTCTGATGTT	3660
	GACACCTTGC	TTAAAACTGT	TCTTCCAGCT	GTGCCCAGTG	ATCCDATATT	CCTTGALGIT	3720 3780
_	CCCAAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TIGTATCAAA		3840
5	agtgaaaaca	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTTGTTAA	AAAGTGAAAG	TTCCCACCAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	
	TTTGCTACAC	CTGTTTATC	AATTGATGAA	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080 4140
10	CATTCCGATG	AAATTTTAAC	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCTGTAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACTTCTGAG	CTGAGTCATA	GTGCCAAATC		4380
15	GATACTCATC	CCTTATCCA	TCATAACTCT	DATUATUATU	CATCOTATA		4440
	GAAAAGGTAA	TGAATGATTC	AGACACCCAC	GAAAACAGTC	TTATGGATCA		4500 4560
	ATCTCATACT	CACTATCTGA	GAATTCTGAA	GAAGATAATA	GAGTCACAAG	TGTATCCTCA	4620
	GACAGTCAAA	CTGGTATGGA	CAGAAGTCCT	GGTAAATCAC	CATCAGCAAA	TGGGCTATCC	4680
20	CAAAAGCACA	ATGATGGAAA	AGAGGAAAAT	GACATTCAGA	CTGGTAGTGC		4740
20	Chaccracer	CAGATAGCCT	ATGGGCAGTT TAATGAGAAT	CTGACAAGTG	ATGAAGAAAG	TGGATCAGGG	4800
	ACTAATGAAA	AAGATGCTGA	TGGGATCCTG	GCAGCAGGTG	ACTCAGAAAT		4860 4920
	TTCCCACAGT	CCCCAACATC	ATCTGTTACT	AGCGAGAACT	CAGAAGTGTT	CCACGTTTCA	4980
25	GAGGCAGAGG	CCAGTAATAG	TAGCCATGAG	TCTCGTATTG	GTCTAGCTGA	GGGGTTGGAA	5040
25	TCCGAGAAGA	AGGCAGTTAT	ACCCCTTGTG	ATCGTGTCAG	CCCTGACTTT	TATCTGTCTA	5100
	TRACACCACA	CTACATCCC	CATCTACTGG TAGAGTTATA	AGGAAATGCT	TCCAGACTGC	ACACTTTTAC	5160
	TCAGATGATG	TOGGAGCAAT	TCCAATAAAG	CACTETCCAA	AGCATCTTY		5220 5280
20	GCAAGTAGTG	GGTTTACTGA	AGAATTTGAG	ACACTGAAAG	AGTTTTACCA	GGAAGTGCAG	5340
30	AGCTGTACTG	TTGACTTAGG	TATTACAGCA	GACAGCTCCA	ACCACCCAGA	CAACAAGCAC	5400
	AAGAATCGAT	ACATAAATAT	CGTTGCCTAT	GATCATAGCA	GGGTTAAGCT	AGCACAGCTT	5460
	GCTGAAAAGG	ATGGCAAACT	GACTGATTAT	ATCAATGCCA	ATTATGTTGA	TGGCTACAAC AGATTTCTGG	5520
	AGAATGATAT	GGGAACATAA	TGTGGGAGGTT	ATTGTCATGA	TABCABACCT	CGTGGAGAAA	2280
35	GGAAGGAGAA	AATGTGATCA	GTACTGGCCT	GCCGATGGGA	GTGAGGAGTA	CGGGAACTTT	5700
	CTGGTCACTC	AGAAGAGTGT	GCAAGTGCTT	GCCTATTATA	CTGTGAGGAA	TTTTACTCTA	5760
	AGAAACACAA	AAAAAAAA	GGGCTCCCAG	AAAGGAAGAC	CCAGTGGACG	TGTGGTCACA	5820
	ACCTTTCTCA	ACACGCAGTG	GCCTGACATG	GGAGTACCAG	AGTACTCCCT	GCCAGTGCTG TGTCGTCCAC	5880
40	TGCAGTGCTG	GAGTTGGAAG	AACAGGCACA	TATATTGTGC	TAGACAGTAT	GTTGCAGCAG	5940 6000
	ATTCAACACG	AAGGAACTGT	CAACATATTT	GGCTTCTTAA	AACACATCCG	TTCACAAAGA	6060
	AATTATTTGG	TACAAACTGA	GGAGÇAATAT	GTCTTCATTC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	AAGAAACTGA	GGTGCTGGAC	AGTCATATTC	ATGCCTATGT	TAATGCACTC	6180
45	CTCATTCCTG	GACCAGCAGG	CAAAACAAAG	CTAGAGAAAC	AATTCCAGCT	CCTGAGCCAG	6240
-13	CGAACTTCTT	CTATCATCC	TOTTOTAL	TO ACCOTAGE	AATGCAACAG	GGAAAAGAAT CCTGAGTGGA	6300
	GAAGGCACAG	ACTACATCAA	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	6420
	ATCATTACCC	AGCACCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	6480
50	CATAATGCCC	AACTGGTGGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
50	GTTTACTGGC	CAAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACTCTTATG	6600
	GARGCTACAC	ACAMAIGICI BCCATCATTA	TGTACTTGAG	GAAAAACTTA	TAATTCAGGA	CTTTATCTTA	6660
	AATCCAGATA	GCCCCATTAG	TARARCTTTT	GAACTTATAA	GTGTTATGIC		6720 6780
	GCCAATAGGG	ATGCGCCTAT	GATTGTTCAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAACT	6840
55	TTCTGTGCTC	TGACAACCCT	TATGCACCAA	CTAGAAAAAG	AAAATTCCGT	GGATGTTTAC	6900
	CAGGTAGCC	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TIGCTGACAI	TGAGCAGTAT	6960
	ACCICICICI	ACAAAGTGAT	CCTCAGCCTI	GIGAGCACAA	GGCAGGAAGA	GAATCCATCC GAGCTTAGAG	7020
	TCTTTAGTT	ALAGIAAIGG	GGGGTGGGG	GACTCACATC	TGAGCATTG	TTTCCTCTTC	7080 7140
60	CTAAAATTAG	GCAGGAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	7200
	AGTAACTIT	: ATGACATAGG	ATTCTGCCGC	CAAATTTATA	TCATTAACA	TGTGTGCCTT	7260
	TTTGCAAGAG	TTGTAATTTA	CTTATTATGT	TTGAACTAAA	ATGATTGAAT	TTTACAGTAT	
	TTCTAAGAAT	GGAATTGTGG	TATTTTTTC	TOTATIGATI	TTAACAGAA	ATTTCAATTT ATTTTTAGCT	
65	GTATTTGTAC	CAATTATCAC	GTTTGCTAGA	C ALGITIGITI	TIMUIUICA	AGCCTGTAAA	7440
	TAAAACACTO	TTCCATATG	TATTCAACAT	TTTACAACTG	CAGTATTCAC	CTABAGTAGA	7560
	AATAATCTG	TACTTATTGT	* AAATACTGC	CTAGTGTCTC	CATGGACCAZ	TTTATATTA	7620
	ATAATTOTAC	3 ATTTTTATA7	TTTACTACTO	AGTCAAGTT	TCTAGTTCTC	TGTAATTGTT	7680
70	TAGITTAAT	ACGTAGTTC	TTAGCTGGT	TTACTCTAC	AGTTTTCTG	CATTGTATTG	7740
	ATACCTTCA	TPTGAAAGT	GTTTTTATG	- MIGIMAIIII	TTACCABAC	GAAAATAGAA TTGTTCAAAT	7800 7860
	GGTTTTTAT	CAAGGAATT	CAAAAATAA	TATAAATAT	GCCATTAAA	AAAAAAAAA	7920
	AAAAAAAA	AAAAAAAAA	A A				
75							
15	Protein se	equence 1					
	Unigene m	umber: Hs.	tyrosine pno	ospnacase, i	receptor-ty	pe, Z polype	ptide 1
	Protein A	ccession #:	NP 002842				
o'n	Signal se	quence: 1-2	20 _				
80	Pfam doma:	in: carb an	nhydrase (3)	3-300]			
	Transmemb:	rane domain	1639-16	51			
	l	LOCALIZATION 11	ı: plasma t 21	nembrane 31	43	C1	
	î	ī	1	1	41	51 	
	•	•	•	•	•	•	
						139	

	MRILKRFLAC	IQLLCVCRLD	WANGYYROOR	KLVEEIGWSY	TGALNOKNWG	KKYPTCNSPK	60
	A35 THITDEDA	IOVNVNLKKI.	KPTY:WINKTEI.		-		120
							180
5	TOTVDWIVFK	LDFKAIIDGV DTVSISESQL	AVECEVITED	WINDER IT FINE	LPNSTDKYYI	YNGSLTSPPC	240
							300 360
	upt ningion	TYPE THE PROPERTY OF	NMSYVLATUA	TOTACTVOV	COAT TITLE		420
	DIGIOSTIVE	REFRINGER	ALVNPORDSA	TWOTPICTOR	TOTAL		480
10	GSKTVLREDH	GKGDVPNTSL MNLSGTAESL	NSTSQPVTKL	ATEXDISLTS	OTVTELPPHT	VEGTRASLND	540
	PUIDOCITES	SENPETITYD	VLIPESARNA	SENSTRUCE	DOT UNDOWNER	ATT MATTER CO.	600
							660 720
	TOATEDWEIL	BERGOULVST	VXVVVCOTTO		have commen		780
15	************	DSALHATPVF SDKVPLHASL	PSVDVSPKSI	LESSYTMADIT.	DRECLERCED	T TITLET INTO	840
	VITALEDGARD	PSSDAMMHAR	SEGPEPSYAL.	STARGEOUTP	THOUGOSTMI	TITLE OF SECTION AND ADDRESS.	900
	OUTSCHOUTH	IPKSSLITPT	ARLIOPTUAL.	REPRIVED A	Chappy + non	-	960 1020
	A A DAWRETTT	ISVIGDONKA	LSKSETTYCN	RTELATORDA	DWWDCCCOMI	147454	1080
20	mwardet51	DISSIMMED	USLAHITIKU	FRURT COURS	MATE CANADADA	110010000	1140
	AVPSDPILVE	ASSDPASSEM TPKVDKISST	MI.BI.TUONON	ETBASFSTEV	LLQPSPQASD	VDTLLKTVLP	1200
	TINGONICAL	PVLLKSESSH	OVVPSLYSND	RI.POTANT.PT	MARKEDDVCDII	11777	1260
	DA MATOTIVE	INSULTETST	KHHVTGKVFA	GIPTUACHTD	VOTHUGUETA	MOTERIA PROPERTY	1320 1380
25	LUKTO2A I P.I.	RLLLPPSKATS	ELSHSAKSDA	GT.VICCCEDCD	STUDENTON PROPERTY	-	1440
	PGKSPSANGI.	QEKVMNDSDT SQKHNDGKEE	HENSLMDONN	PISYSLSENS	EEDNRVTSVS	SDSQTGMDRS	1500
	MOTOTOLDEW	DINEKHADGI	LAAGURRETTD	GPDACDTOCU	TODACORDINA	AMILES	1560
	POVIGER	ESEKKAVIDI.	VIVEALTETC	TARRAGET TV	LIDY/CROSSING		1620 1680
30	TOTALLTER	ISDDARMINI	KHEPKHVADI.	RIGGODTED	DET VERVARE	^~~	1740
50							1800
	LAYYTVRNFT	LRNTKIKKGS	OKCESSORAN	TOVEVETOWER	PADGSEEYGN	PLVTQKSVQV LTFVRKAAYA	1860
	MATTARET	MUSAGVGRIG	TYIVLDSMIO	OTOUCGTANIT	PORT WITHOU	D1011111	1920 1980
35	TALIEDINAD	WITTSVELEAT	DSHIRAYUNA	I.I.I DADAAVT	DI DUADATTA	AMITAA	2040
55							2100
	T TIME HINGS IN	NUMMOTAAMT	PLASINMARDR	POAMBNIKUED	TMCCCCCC	MAEEHKCLSN AANROGPMIV	2160
	un pudeo I vo	TECALITIMH	OLEKENSVDV	YOVAKMINIM	PECTRALKER	AANROGPMIV	2220
40	LVSTRQEENP	Steldengaa	LPDGNIABSL	ESLV	OTTADIDO	IGEDIKATES	2280
40	DNA SEQUENC						
	Gene name:	tvroeving					
	Gene name: Unigene num		otein sulfot 10903	ransferase	1		
15	Unigene num Probeset Ad	mber: Hs.11 cession #:	L0903 D61594		1		
45	Unigene num Probeset Ad Nucleic Aci	mber: Hs.11 Cession #: Id Accession	10903 D61594 1 #: NM 003		1		
45	Unigene num Probeset Ad Nucleic Aci	mber: Hs.11 cession #: ld Accession Lence: 82-1	10903 D61594 1 #: NM_003 1194	3596			
45	Unigene num Probeset Ac Nucleic Aci Coding sequent	mber: Hs.11 cession #: ld Accession lence: 82-1 11	10903 D61594 T#: XM_003 1194 21	3596 31	41	51	
	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC	mber: Hs.11 cession #: ld Accession lence: 82-1 11 CATGGCCTGA	L0903 D61594 1 #: NM_003 L194 21 	3596 31 	41 	1	60
45 50	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA	mber: Hs.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA	D61594 #: NM_003 194 21 ACATITICG GATEGITGSA	31 AAAATCATTT	41 TGAGCAAAAT	ATCTGTTTAA	60 120
	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATTA CTGGTGATTA CGGATAGAGG	mber: Hs.11 cession #: d Accession tence: 82-3 11 CATGGCCTGA ACCACATCAA AACGTAGCCA	L0903 D61594 1 #: NM_003 L194 21 ACATTTTCCG GATGGTTGCAAAA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC	120 180
	Unigene num Probeset Ac Nucleic Ac Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CTGGTAGAGG GGCCTGGACC	nber: Hs.11 cession #: dd Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA ATCAAGCCAA	L0903 D61594 1 #: NM_003 L194 21 } ACATTTTCCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGC	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA CAAGGACCAC	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT	120 180 240
50	Unigene num Probeset Ad Nucleic Adi Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCTGGACC ATTGGGGTG	mber: Hs.11 Cession #: Id Accession tence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA TGCCTCGGAG TGCCTGGAG TGCCTGGAGGCAA	L0903 D61594 1#: NM_003 1194 21 J ACATITICGS GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CCAAAACCTTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT	120 180 240 300
	Unigene num Probeset Ac Nucleic Aci Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCGCT	mber: Hs.11 cession #: dd Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA TGCCTCGAG GTTGAGGAGG	L0903 D61594 H: NM_003 L194 21 ACATITICCS GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CCAGCAACACCTTT TGGAACCACGAACACCTTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC CTGGAGAGCA GCCTATCACA GCCTATCACA GCCTATCACA	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA ATGAGGACCAC AAGATATGCC CCATGCTGGA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT	120 180 240
50	Unigene nur Probeset Ac Nucleic Ac Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTGGTG GACATTCGCT TGGTCACCGT TGGTCACCGT CTGGATTCTG	mber: He.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GCTAGCCA TCAAAGCCAA TGCCTCGAG GTGGGGGGAGAGGA CAAGTAAAGA CCATGCAGAGCAA CCATGAAAGCCAA CCATGAAAGCAA	L0903 D61594 # #: NM_003 L194 21 ACATITICCG GATGGTTGGA GCCAGTCAAA CCAAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC GAAGATCCGC GAAGATCCGC	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA GCCTATCACA ATTCCCGAA CTGATGAGGG	41 TGAGCAAAAT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CAGGTGTTAC CTCGGGCCT CTGGTGTTAC	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCAGATG TGATGAAGTG	120 180 240 300 360 420 480
50	Unigene nur Probeset Aci Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CTGGTGATTA CTGGTGATGG GGCCTGGACC ATTGGRGGTG GACATTCGCT TGGTCACGGT CTGGATTCTG CCTTATTTAT	mber: Hs.11 cession #: dd Accession lence: 82-1 11	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CAAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTAC	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA CTGGATGAGG GAAATTATCG	41 TGAGCARAAT AGBACTTACT ATGCCATGGA CAAGGATGGC CCATGCTGGA TCCTGGCCCT TTAAGCATGG	ATCIGITTAA ATTIGGCATGT ATGICATCAC TGIGAGAACT TTTAATATTT CGCACATCTI GAAGCAGATG TGATGAAGTG GGAGCCAGCC	120 180 240 300 360 420 480 540
5 0	Unigene nur Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCGC TTGGTCACGT CTGGTTCACGT CTGGTTCACGT CTGGTTCACGT TTGCCCATG	mber: He.11 cession #: dAccession lence: 82-3 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGCCTCGGAG GTGGAGAGGGA CAAGTAAAGCA CCATGCAAGC CTAGCAAGC CTAGCAAGC CTAGCAAGC CTAGCAAGC CCATGCAAGC CCATGCAAC	LO903 D61594 1 #: NM_003 L194 21 ACATTTTCCG GATGGTTGGA TGTGTTTAC GCCAGTCAAA CCAAACCTTT TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTTGCCA	31 AAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA CTCATGAGGG ATTCCCGAA ATTCCCGAA CTGGATGAGC GAAATCATT	41 TGAGCARAAT AGRACTTACT ATGCCATGGA CAAGGACCAC AGATATGCC CCATGCTGGA TCCTGGCCCT CTGGTGTTAC TTAAGCATGC TAACTTACCT	ATCIGITTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA	120 180 240 300 360 420 480 540
50	Unigene nur Probeset Ac Nucleic Aci Coding sequ 1	mber: He.11 cession #: dd Accession lence: 82-1 l CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA TGCCTCGGAG GTGGAGAGGA CCAAGTAAAGA CCAAGTAAAGA CCAAGTAAAGA ACCATGCAAGC GTAATAAAGA AAGTAAAGA AAGTAAAGA AAGTAAAGA AAGTAAAGA	L0903 D61594 1 #: NM_003 L194 21 ACATITICCE GATEGITIGEA TOGGATCHAA CCHAAACCITI TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTTGCC CCTGATGGTC CTGTTTGCC	31 AAAATCATTT AAGCTGAAGC CTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA CTGGATGAGG GAAATTATCG CTGAAATCTT CGAGGATGGCC	41 TGAGCARAAT AGRACTTACT ATGCCATGGA CAAGGACCAC AAGATATECC CCATGCTGGA TCCTGGCCCT CTGGTGTTAC TTAAGCTACCT GGGCATCAGT	ATCIGITTAA ATGCCATCAC TGIGAGAACT TTTAAIATITI GCACCATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACAITCAATG	120 180 240 300 360 420 480 540
5 0	Unigene num Probeset Ac Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCGCT TGGTCACCGGT CTGGATTCTG CCTTATTTCTCGAAT ATTTCTCGAAT ATTTCTCGAATC	mber: He 1: cession #: dd Accession ience: 82-: 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAGGCCA TGGGCTGA TGGAGAGGA CCATGCAAGC CTAGCAAGG CCAAGTAAAGA CCAAGTAAAGA CCAAGTATCTA AGGTACTACTAT CAAGTTACTAT CTGCTATGC	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTTGGA TGTGTTTTAC GCCAGTCAAA CAAAACCTTT TGGAACCACA AACCAGGGTC AACCAGGGTC CAAGATCCGC CTTCTTACTA TCCTTTTGCC CCTGATGGTC AGCTGGATTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA CTGGATGTGGG GAAATTATCG CTGAAATCTTT CGAGATGGCC GATCTGAACC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CCATGCTGGA TCCTGGCCTTAC CTGGTGTTAC TTAAGCATGG TAACTTACCT GGGCATCAGT GGGCATCAGT GCTATAGGGA	ATCIGITTAA ATCIGCATGI ATGCCATCAC TGIGAGAACT TTIAATATTI CGCACATCCT GAAGCACATG TGATGAAGTI GGAGCCAGCC TTCTAGGTIA ACATICAATG CTGTTTGACA	120 180 240 300 360 420 480 540 660 720 780
5 0	Unigene nur Probeset Ac Nucleic Ac Nucleic Ac Coding sequ 1 GTAGACTGTC TAACAAGATTA COGATAGAGG GGCCTGGACC ATTGGGGTG GACATTCGCT TGGTCACCGT TGGTCACCGT TTGCCCAATTCT TTCCCCAATTCT TTCCCCAATTCT TTCCCAATTTGAA AAGTGGAATC TGCATGTTGG TTAACTTTTC	mber: He.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA TCAAAGCCAA GTGGAGAGGA GTGGAGAGGA GTGGAGAGGA GTAATAAAGA CCAAATTTCT AAGTTAACTAT GTGCTATAGA TTCACTATGC	LO903 D61594 # #: NM_003 1194 21 ACATITICCE GATGGTIGGA TGTGTTTTACA CAAAACCTIT TGGAACCACA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTGCCC CCTGATGGTC AGCTGGATTTTGCC CCTGATGGTC AGCTGGATTTT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGCA GCTGATGAGG GAAATTATOG GAAATTATOG CTGAAATCTT CGAGATGGCC GATCTGAACA AACCAGTGTA TTACATCCTG	41 TGAGCARAAT AGRACTTACT ATGCCATGGA CAAGGACCAC CCATGCTGGA TCCTGGCCT TTAGGTGAC TTAAGTACCT GGCATCAGT GCTATTAGGGA TGGAGGTTGG AACGTGGAT	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT GCACATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAAAG GAGAACACTC	120 180 240 300 360 420 480 540 600 720 780 840
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5 0	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG CTGGTCACGGT CTGGTCACGGT TTCCCCAATG ATTTCTCGAA AAGTGGAATC TTCCCAATG ATTTCTCGAA AAGTGGGATC TTCACTGTTGG TTAAAGTTCC AAAGCTGGGG GTCAATGTAG GTCAATGTAG	mber: He.11 cession #: dA Accession lence: 82-3 11 CATGGCCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGACTCAGGAG GTGGAGAGGA CAAGTAAAGA CCAAGTAAAGA CCAAGTTACTAG GTGATATAAAGA TCAAGTTACTAT AGTTACTAT AGTTACTAT TCCAGATTCC GAGTGTCTATCA GAGTGTCTATCA GAGTGTCTAT	LO903 D61594 1 #: NM_003 1194 21 ACATTITICES GATGGTTGGA TGTGTTTTAC GCCAGTCAAA ACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTACTA TCCTTTTGCA CCTGATGGTT AGCAGGTTT AGCATGGTT AGCATGGTT AGCATGGTT ACACTTGTC ATGGAACCAC ATGGAACCAC AACATGGTT ATGGAACCAC AACATGGTT ATGGAACCAC AAAAGGTTT	31 AAAATCATTT AAAGTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA ATTCCCCGAA CTGGAATTTTC CAGAATCATT CAGATGGCC GATCTGAACA AACCAGTGTA AACCAGTGTA TCAGTCCTG TCAGTATTGC GAGAGATCAT CTCAGTATTGC GAGAGATCAT CAGGAGATTAC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCCTGGCCCT CTGGTGTTAC TTAAGCATCAG GGCATCAGT GGCCATCAGT GGCCATCAGT AACGGTGGA ACGGTGGA ACCATGAGA ACCATGAAGA CAGAACCAAGT	ATCIGITTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCAGATG TGATGAAGTG GGGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAAG GAGAACACTC GATGATTCAGG AATCAAGCCA	120 180 240 300 360 420 480 540 600 720 780 840
50 55 60	Unigene nur Probeset Ac Nucleic Ac Nucleic Ac Coding sequ 1 GTAGACTGTC TAACAAGATT CGGATAGAGG GGCCTGGACC ATTGGGGTG GACATTCGCT TGGTCACCGT TGGTCACCGT TTGCCCAATG CTGGATTCTG CCTTATTTAT TTCCCCAATG AAGTGGAATC TGCATGTTGG TTAATGTTCC AAAGTGGAATC AAAGTGGAATGTAG GTCAATGTAGG TTAAAGTTGC AAAGCTGAGG ATTGCAATGTAGG ATTGCAATGTAGG ATTGCAATGTAGG ATTGCAATGTAGA	mber: He.11 cession #: id Accession lence: 82-1 11 CATGGCCTGA ACCACATCAA GCTAGCCA ACCACATCAA TGCATGGCCA ACGAGCAGCA ACGAGCAGCA CAAGCCAGA GTGGAGAGGA GTGGAGAGGA GTGAGAGGA GTAATAAAGA CCAAGTAAAGCA GTAATAAAGA TCCAGATTTCT GTGCTATAGA TCCAGTATTCC GAGGTGTCTCT GAGCTCTTATC GAGCTCTTATC CTGCTCTTAT	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTGGA TGTGTTTTAC GCCAGTCAAA AACCAGGGTC GAAGATCCGC CTTCTTACTA TCCTTTTTTTTTT	31 ANANTCATTT ANGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGA CTGGATGAGG GAAATTATCG CGAGATGAC CTGAAATCTT CGAGATGGCC GATCTGAAC TACAGTGTA TTACATCCTG CGAGATGTG CGAGAGATCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGTCT CGAGAGATCT	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CCATGCTGGA TCCTGGCCTT TTAACTTACT TTAACTTACCT TTAACTTACCT GGGCATCAGT GCTATAGGGA TGGAGGTTGG AACGGTGGGA ACCATGAAGA CCATGAAGA CCAGACCAAGT CGCCAGATGT CGCCAGATGT	ATCTGTTTAA ATTGGCATGT ATGCCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT GCACATCCT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA ATTATAAAAAG GAGAACACTC GATGATTGGG AATCAAGCCA TTTACAAGAC	120 180 240 300 360 420 480 540 660 720 780 840 960
50 55 60	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTGC TGGTCGCGT TTGGTCACGGT TTGGTCACGGT TTGCCCAATG ATTTCTCGAA AAGTGGAATC TTCCACAGT TTCACCAGT TTCACCAGT ATTCTCGAA AAGTGGAATC GGATTGG TTAAAGTTCC AAAGCTGGGG GTCAATGTGG AAGCTGGGG GTCAATGTAG ATTCCACGGAA ATTCCACGTACTACCTAC	mber: He.11 cession #: dA Accession lence: 82-1 1 CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TCAAGCCAA TCACAGGAGGA CAAGTAAAGA CCAAGTAAAGA CCAAGTTACTAT GTGCTATGA TCACGATTCC GAGTGTCTTT TGCTCTAT AACCTGATC TTGCTCTAT AACCTGATC TTGCTCTTAT AACCTGATC TTGCTCTTAT AACCTGATC TTGCTCTTT TTGCTCTTTT TTGCTCCTTT TTGCTCTTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTTCTT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTCTTCT TTGCTTCTT TTGCTTCTT TTGCTTCTT TTGCTTCTT TTGCTCTTCT TTGCTCTTCT TTGCTTCTT TTGCTTCTT TTGCTCTTCT TTGCTTCTT TTGCTCTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTCT TTGCTCTTTT TTGCTCTTTT TTGCTCTTT TTGCTCTTTT TTGCTCTTTT TTGCTCTTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTTTT TTGCTCTTT TTGCTCTTT TTGCTCTTT TTGCTTTT TTGCTCTTT TTGCTTTT TTGTTTT TTGTTTTT TTGTTTTT TTGTTTT TTGTTTTT TTGTTTTT TTGTTTTTT	LO903 D61594 1 #: NM_003 1194 21 ACATTTTCCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA ACCAGGGTC GAAGATCCGC CTTGTTACTA TCCTTTACTA TCCTTTACTA TCCTTTTGCA CCTGATGGTT GACCATGTAT ACACCTTGTC ATAGAACCAC ATAGAACCAC ATAGAACCAC ACACTTGTC ATAGAACCAC GTCAAAAGTT GCTTGCCAAAG GTCTGCCAAAG CCAAAATTATT TAAAAATTATT TAAAAATTATT	31 AAAATCATTT AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA CTCATGAGGG ATTCCCCGAA ATTCCCCGAA CTGGAATTTC CAGATTGAC GATCTGAACA AACCAGTGTA TCAGTATTGC GAGAGATTCC GAGAGATTCC GAGAGATTCC CTTGGAATTCC GAGAGATTCC CTTGGATTTG CAGAGATTCC CACAGACCC CACAGACC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACCC CACAGACC CACAGACC CACAGACCC CACAGACC CACACACC CACACAC CACACACC CACACACC CACACACC CACACACC CACACACC CACACAC CACACAC CACACACC CACACACC CAC	41 TGAGCARAAT AGAACTTACT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCCTGGCCCT CTGGTGTTAC GGCATCAGT GGCATCAGT GGCATCAGT ACCATGAGA ACCATGAGA ACCATGAGA ACCATGAGA ACCATGAGA ACCATGAGA ACCATTATGC GAAGGGTCTA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTTAATATTT GCACATCCT GAAGCAGATG TGATGAAGTG TGATGAAGTG TGATGAAGTG TGATGAAGTG TGATGAATG GGAGCCAGCC TTTCTAGGTTA ACATTCAATG CTGTTTTGACA GATGAATTCGG AATCAAGCCA TTTACAAGAC TTTACAAGAC CAACCCACCT TAAGGGAGAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140
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50 55 60	Unigene nur Probeset &c Nucleic Aci Coding sequi 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGOTG GACATTCGC TTGGTCACGGT CTGGATTCTG CCTTATTTAT TTCCCCAATG ATTTCTGAA AAGTGGAATC TGCATGTTGG GTCAATGTTGG GTCAATGTAG ATGCAGTGA ATGCAGTGA ATGCAGTGA ATGCAGTGA ATGCAGTGA CAGGAGCCTC CAGGAGCCTC AGGATCGC AGGATCGC AGGATCGC	mber: He 11 cession He 11 d Accession lence: 82-1 1 CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGAGAGCAA TGAGAGCAA TGAGAGCAA TGAGAGCAA TGAGAGCAA TGAGAGCAA TGAGAGCAA TGCTCGAG TGAGAGGA TGCTCAGAGC GTAGATAAGA CCAAATTTCT AAGTTACTAT GTGCTATAGA TCCAGATTCC GAGTGTCTTCT TGCTCCTAT AACCTGATCC CTGACTTCT TTCCATACAT TT	LO903 D61594 1 #: NM_003 1194 21 1 ACATTITCCG GATGGTTGGA TGTGTTTTAC GCCAGTCAAA AACCAGGGTC CATAGTACCAC AACCAGGGTC CATAGTACCAC AACCAGGGTC CATGTTACTA TCCTTTACTA TCCTTTACTA TCCTTTACTA TCCTTTACTA TCCTTTACTA ACACTTGTC AGCAGGTTC ATGGAACCAC GTCAAAAGTG TAAAAGTG TAAAAGTTGCTAAAGTT TAAAGAAAAA GAGGAAAGAA AAGCATGGTT TAAAGAAAAA AAGGGAAAGAA AAGCATGGTT TAAAGAAAAAA AAGCTTGCTACAAAGAAAAAAAAAA	31 AAAATCATTT AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA CTCATGAGGG ATTCCCCGAA CTGGAATCATC CAGGATGACCA GAACTGGACCA AACCAGTGTA TTACATCCTG TCAGGATATCA GGGAAGATCA GGGAAGATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CTTGGATATCA CACAGGACTCA CACAGC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCCTGGCCCT TTAAGCATGG GCTATCAGT GCGCATGTTAC GGGCATCAGT GCGCAGGATGT ACCATGAGA ACCATGAGA CCGCAGATGT ACCCATATGC GAAGGGTTGG GAAGGGTTGG TCGCAGATGT ACCCATATGC GAAGGGTTGA ACCATGAGATGT ACCCATATGC GAAGGGTTGA TCAGCAGAGT TCAGCAGAGT TCAGCAGAGT TCAGCAGAGAG TCAGCAGAGAGT TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAG TCAGCAGAGAGAG TCAGCAGAGAG TCAGCAGAG TCAGCAG TCAGCAGAG TCAGCAG TCA	ATCTGTTTAA ATTTGCATGTA ATTGCATGTA ATGCCATGAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCT GATGATTCG AATCAAGCC AATCAAGCC CAACCCACCT TAAGGGAAGAA GTAGCAGAAC GGAAATTCCT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140
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50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTCACGT TGGTCACGT TTGGTCACGT TTGCCCAATG ATTTCTCGAA AAGTGGAATT TTCCCAATG TTAAGGTTGG GTCAATGTTG TTAAGGTTGG TTAAAGTTCC AAAGTTAGG TTAAAGTTCC AAAGTTAGG ATTCCAACTAC CAGGAGCCTC AGGATTGGCT AAGGAGCCTC TTATGACTTT AGTTTAGTTT	mber: He.11 cession #: dd Accession lence: 82-1 l CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TCACAGCCAA TCACAGCCAA TCACAGCCAA TCACTAGCCAA TCACTAGCAA CCAAGTAAAGCA CCAAGTAAAGCA CCAAGTTACTAT GTGCTATGAA TCCACTATCA TCCACTATCA TCCACTATCA TCCACTATCA TCCCCTCCT TTCCATACAT GTCCCCTCCC CCTCCTGAGC GAAGGAACATTCC TTCCATACAT TCCCTCCC CCTCCTGAGC GAAGGAACAT TGTTTTCACAT TGTTTTCACAT TGTTTTCACAT TGTTTCACAT TGTTTTCACAT TGTTTCACAT TGTTTTCACAT TGTTTCACAT TGTTCACAT TGTTTCACAT TGTTTCACAT TGTTTCACAT TGTTCACAT TGTTTCACAT TGTTCACAT TGTTTCACAT TGTTTCACAT TGTTTCACAT TGTTCACAT TGTTTCACAT TGTTCACAT TGTTCA	LO903 D61594 1 #: NM_003 L194 21 1 ACATITICCE GATGGTTGGA TOTGTTTTACC GCCAGTCAAA CAAAACCTIT TGGAACCACA AACCAGGTC GAAGATCCGC CTTCTTACTA ACCAGGGTC AGCTGGATTT GACCATGGTT AGCACTGGATT ACAACTTGTC AGCTGGATTAT ACAACTTGTC AGTGGACCAC ATGAAACCAC GTCAAAAGTG CAAAATTATT TAAAGAAAAAT AGGTTGCTG ACTGGAGGA AAAGAGTCT GTTTCCTGCTAG AAAAGGTTT TGTTTCCTG GAGAGGTTT TGTCTGTACA AATAATATTA	31 ANANTCATTT ANANTCATTT ANGCTGAAGC CTGGGCCAGC CTGGGCCAGC CTGGAGAGCA CTCATGAGGG ATTCCCCGAA CTGAAATCAT CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TGAAACACTT GAAAACACTT TGAAACCATT TGAAGGTTCT TGAGGGTTCT TGAAGGTTCT TAAAACTCC AAAAATGGGA TGTTCTAAAG TGTTCTAAAG	41 TGAGCARAAT AGGACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCTGGCCCT TTAAGCATGA GGCATCAGT GGCATCAGT GGCATCAGT ACCATGAGGA ACCATGAGA TCAGCAGAGT TCAGCAGAG TCTAGCAGAA TCTTGTTCTC TCCTGTAAGC TTCTGTAAGA TTTTGTAAGA	ATCTGTTTAA ATTGGCATGT ATGCCATGT ATGCCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT GCACATCGT GAAGCAGATG TGATGAAGTG GGAGCCAGCC TTCTAGGTTA ACATTCAATG CTGTTTGACA ATTATAAAAAG GAGAACACTC GATGATTGGG AATCAAGCCA TTTACAAGAC CAACCCACCT TTAAGGAGAA GTAGCAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT GCCCTGCAGT TTTTCTACA AGACTTGGGC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500
50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCGCT TGGTCAGGT CTGGATTCGCT TTGTCACGGT CTGGATTCTG CCTTATTTAT ATTCTCGAA AAGTGGAATC TTGCATGTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GAGGGATCTG AGGAGGCTC AGGGAGCCTC AGGAGCCTC AGGAGCCTT AGGTTGCATTGGCT GCATTTGCCA TTATGACGTT AGGTCTCCTTT GTTTAAGTTG TTCTGAGAA TTCTGAGAA TTTTCTGAGAA TTTTCTGAGAA	mber: He 11 cession He 11 d Accession lence: 82-1 11 CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCAA TGCATGAGGGA TGAGAGGGA CCATGCAAGCAA TGCATGAGGGA CCATGCAAGC AAGTTACTATG TGCATAAGA CCAAGTTCT AAGTTACTAT GTGCTATAGA TCCAGATTCC GAGTGCTCT TGCTCTATC TGCTCTATC TGCTCTATC TTCCATACT TTCCATCAT TCCATCAT TCCATCAT TTCCATCAT TTTCCATCAT TTTCCATCAT TTTCCATCAT TTTCCATCAT TTTCCATCAT TTTCCATCAT TTTCCATCAT TGTTTTCAAG TGAAATAGGT TATTGGGAAAT TATTGGGAAAT TATTGGGAAAT TATTGGGAAAT TAAAAGGTTT	LO903 D61594 1 #: NM_003 L194 21 1 ACATITICCE GATGGTTGGA TOTGTTTTACC GCCAGTCAAA CAAAACCTIT TGGAACCACA AACCAGGTC GAAGATCCGC CTTCTTACTA ACCAGGGTC AGCTGGATTT GACCATGGTT AGCACTGGATT ACAACTTGTC AGCTGGATTAT ACAACTTGTC AGTGGACCAC ATGAAACCAC GTCAAAAGTG CAAAATTATT TAAAGAAAAAT AGGTTGCTG ACTGGAGGA AAAGAGTCT GTTTCCTGCTAG AAAAGGTTT TGTTTCCTG GAGAGGTTT TGTCTGTACA AATAATATTA	31 ANANTCATTT ANANTCATTT ANGCTGAAGC CTGGGCCAGC CTGGGCCAGC CTGGAGAGCA CTCATGAGGG ATTCCCCGAA CTGAAATCAT CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC CAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TCAGAATCATC TGAAACACTT GAAAACACTT TGAAACCATT TGAAGGTTCT TGAGGGTTCT TGAAGGTTCT TAAAACTCC AAAAATGGGA TGTTCTAAAG TGTTCTAAAG	41 TGAGCARAAT AGGACTTACT ATGCCATGGA CAAGGACCAC AAGATATGCC CCATGCTGGA TCTGGCCCT TTAAGCATGA GGCATCAGT GGCATCAGT GGCATCAGT ACCATGAGGA ACCATGAGA TCAGCAGAGT TCAGCAGAG TCTAGCAGAA TCTTGTTCTC TCCTGTAAGC TTCTGTAAGA TTTTGTAAGA	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATCCT GAAGCACATC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCC GATGATTGGC AATCAAGCC CAACCCACCT TAAGGGAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT TTTTCTTACA AGACTTGGGC CACGTGTGCC CACGTGTGCC CACGTGTGCC CACGTGTGCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500
50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ I I GRAGACTGTC TAACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTGC TCGGATTCGCT TCGTCACCGT TCGCATTGT TTCCCCAATG ATTCTCGAA AAGTGGATTC TGCATGTTGG TTAAAGTTCC AAAGCTGGGG GTCAATGTGG TTAAAGTTCC AAAGCTGGGG GTCAATGTGG ATTCTCGAA AAGTGGATTC CAGGAGCTC AAAGCTGGGG GTCAATGTAG ATTCCACTAC CAGGAGCCTC AGGAGTTGGCT GCATTTGCCA GAGGGATCTG AAGGAGCCTC TTATGCCA TTATGACGTT AGTCTCCTTT TGTTTAAGTTT TGTTTAAAAA Protein sec	mber: He.11 cession #: dd Accession lence: 82-1 l CATGGCTGA ACCACATCAA GTTCTGTGAC AACGTAGCCA ACGAGCAA CAAGCCAA CAAGCCAA CAAGCCAA CAAGCCAA CAAGCCAA CAAGCCAA CAAGCCAA CAAGTAAAGA CCAAGTTACTA CAGATTACTA TCACTATGA TCCACTATCA TCCACTATCA TCCCCTGCT TTCCATACAT TCCCTTCCT TTCCATACAT TCCCTGCCC CCTCCTGAGC GAAGGAACATT TTCCATACAT TGTCTCTCCC TTCCTTCCC TTCCTTCCC TTCCTTCC	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTGGA TGTGTTTTAC GCCAGTCAAA AACCAGGTC GAAGATCCGC CTTCTTACTA TCGTTGCTC CCTGATGGTT AGCTGGATTT AGCACTGATTT AGCACTGATTT AGAACTGTC ATGGACCACA GTCAAAGTGTC ATGGACCACA GTCAAAAGTGT CAAAATTATT TAAAGAAAAA AAGAGTCT GATGTGCAAG CTTAGAGGGA AATAGTTGTC GAGAGGGTT TGTTGGTG GAGAGGGTT TGTTGTACA AATAATATTA TACCATTATA CAATGTGA AATAATATTA TACCATTATA CCATGTGAA AATAATATTA TACCATTATA CCATGTGAA AATAATATTA TACCATTATA CCATGTGAA	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA GCCTATCACA CTCATGAGGG GAAATTATCG GAAATCTT CGAGATGACC GATCTGAACA TTACATCTG AACAGTGTA TTACATCTG GGGAAGATCT CAGAGATGTA TGACATCTGACT GAGAGTTTA GAGAGTTTA GAGAGTTTC CCACAGACTG TGATCTGATT GAGAGGTTGC TGATCCGAT TTAAAACTCC AAAAATGGGA AATATCCTAATG AATATCCTAATG AATATCCTAATC AAAAATGGGA CTTTTAATACACC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CAAGGACCAC CCATGCTGGA TTCATGCCCCT TTGGTGTTAC TTAACTTACT TAACTTACT GGCCAT TAACTTACT ACCATGAGGA TCAGCAGATT TCAGCAGACT TTCATGCAC TCTGTTAGGCA TCTGTTAGGA TTTTGTAGGA TTTTTTAGAA TTATTTAATT CTAATGACTT	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATCCT GAAGCACATC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCC GATGATTGGC AATCAAGCC CAACCCACCT TAAGGGAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT TTTTCTTACA AGACTTGGGC CACGTGTGCC CACGTGTGCC CACGTGTGCC CACGTGTGCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500
50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC TAACAAGATA CTGGTGATTA COGATAGAGG GGCCTGGACC ATTGGRGGTG GACATTCTG GACATTCTG GACATTCTG TTGTCACAGT TTCCCCAATG ATTTCTCGAA AAGTGGAAT TCCAATGTAGTTG GTAATGTAG GTCAATGTAG ATTCAGGAA TTCAACTAC CAGGAGCCTC AGGATTGGCT AAGGAGCTC AGGATTTGCT AAGGAGCTC AGGATTTGCT TATTAGAGTT TTCTAATTGCT TTATTAGAGTT TTCTAATTGCT TTTTCTAATTG TTTTCTAATTG TTTCTGAGAA TTCTTCAAAA TTTTTCAAAAA TTTTTCAAAAA Protein sec Gene name:	mber: He 11 cession He 12 dd Accession lence: 82-3 ll Accession Accactana GTTCTGTGAC AACGTAGCCA ACGTAGCCA ACGTAGCCA TGAGAGGAGGA TGAGAGCAA TGCTCGGAG GTGAGAGGA CCATGCAAG CCATGCAAG CCATGCAAG TCCATATAA TTCATATAT TTCATATAT TTGCTCCTAT TTGCTCCTAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTTCCTCCC CCTCCTGAGC CCTCCTGAGC CCTCCTGAGC TTTTCATAG TGAAATAGGT TATTGATGT TATTGATGT TTTGAGGAATT TATTGATGT TTTGAGGAATT TATTGATGT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAAGCT TTTAAAAGCT TTTAAAAGCT TTTAAAGCT TTTTTCT TTTTTT TTTTTTT TTTTT TTTTTT TTTTT TTTT	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTGGA TGTGTTTAC GCCAGTCAAA AACCAGGGTC GAAGATCCGC CTTCTTACTA AACCAGGGTC AGCTGGATTA ACAGTGGATT ACAGTGGATT ACAGTGATT ACAGTGATT ACAGTGATT ACAGTGATT TAAGAACAC CAAAATTATT TAAGAAAAA GAGGAAAGAT ACAGTGGGT AAGTGGGAT TTTAAGAAAAA GAGGAAAGAT ACAGTGGATAT TAAGAAAAAT TTAAGAAAAA TAAGAGTTT TAAGAAAAAT AAGATTGTGA AATAATATTA TACATTATA CAAATTTATA CAATGTGA AATAATATTA CAATGTGA ACTGGTGA AATAATATTA CAATGTGA ACTGGTGA ACTGGTGACA AATAATATTA CAATGTGA ACTGGTGA ACTGGTGACA AATAATATTA CAATGTGA ACTGGTGA ACTGGTGACA AATAATATTA CAATGTGA ACTGGTGA ACTGGTGACA AATAATATTA CAATGTGA ACTGGTGA ACTGGTGA ACTGGTGA ACTGGTGA ACTGGTGACA ACTGGTGA ACTGGTA ACTGGTGA ACTGGTA ACTGGTGA ACTGGTGA AC	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA GCCTATCACA CTCATGAGGG GAAATTATCG GAAATCTT CGAGATGACC GATCTGAACA TTACATCTG AACAGTGTA TTACATCTG GGGAAGATCT CAGAGATGTA TGACATCTGACT GAGAGTTTA GAGAGTTTA GAGAGTTTC CCACAGACTG TGATCTGATT GAGAGGTTGC TGATCCGAT TTAAAACTCC AAAAATGGGA AATATCCTAATG AATATCCTAATG AATATCCTAATC AAAAATGGGA CTTTTAATACACC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CAAGGACCAC CCATGCTGGA TTCATGCCCCT TTGGTGTTAC TTAACTTACT TAACTTACT GGCCAT TAACTTACT ACCATGAGGA TCAGCAGATT TCAGCAGACT TTCATGCAC TCTGTTAGGCA TCTGTTAGGA TTTTGTAGGA TTTTTTAGAA TTATTTAATT CTAATGACTT	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATCCT GAAGCACATC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCC GATGATTGGC AATCAAGCC CAACCCACCT TAAGGGAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT TTTTCTTACA AGACTTGGGC CACGTGTGCC CACGTGTGCC CACGTGTGCC CACGTGTGCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500
50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ 1 GTAGACTGTC GTAGACTGTC TAACAAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGRGGTG CCTTATTTAT TTCCCCAATG ATTTCTGAA AAGTGGAATC GTAAGTTGG TTCACAATGTTG TTCACAATGTTGG GTCAATGTTGG TTCACAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG GTCAATGTTGG TTCACACTAC CAGGGATCTG AGGATTGGCT AGGATTGCCT AGGATTGCCT TATGACGTT AGTCTCCTTT TGTTTAAGTT TTTTTCAAAA TTTTTCAAAA TTTTTCAAAA Protein sec Gene name: Unigene num	mber: He.11 cession He.11 ld Accession lence: 82-1 ll categoriga Accacatcaa GTCTGGGCCTGA ACCACATCAA GTTCTGTGGC AACGTAGCCAA TGCCTCGGAG GTGGAGAGGA CCATGCAAGCCAA CCATGCAAGC GTAATAAGA CCATGCAAGC GTAATAAGA CCAAGTTCT AAGTTACTAT ATCCATATGA TCCAGATTCC GAGTGTCTCT TGCTCCTATC TGCTCCTATC TTCCATACAT TCCATACAT TCCATACAT TCCATACAT TGTTCCTCCC CCTCCTGAGC GAGGGAACAT TGTTTCCATACAT TGTTTCCATACAT TGTTCCTCCC CCTCCTGAGC GTTTCCTCCC CCTCCTGAGC GTTTCCTCCC CCTCCTGAGC TGAAGAACAT TGTTTCAAG TGAAATAGGTT TATTGGGAAAT TAAAAAGCTTT TMEGC 2 LYCOSYlprc ber: He.11	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTGGA TGIGTTTTAC GCCAGTCAAA ACCAGGGTC CATCATATCCTA ACCAGGATC TCCTTTACTA TCCTTTACTA TCCTTTACTA TCCTTTACTA ACACTGTTA ACACTGTTA ACACTGTTA ACACTGTC AGGAACCAC GTCAAAAGTA AAAATTATT TAAAGAAAAA AAGAGCTCT GTGTGCAAG GAGAAGAGTTGTC AGGAAAATTATT TAAAGAAAAA AAGAGTCGT GAGAGGGAAAAA AAGAGTCGT GTGTTCCTGGAAAAATTATT TAAAGAAAAATAATTA TACATTATA CAATGTGA ACATGTGAAAATTATA TACCATTATA CAATGTGAAAATTATA CAATGTGAAAATTATA CAATGTGAAAATTATA CAATGTGAAAATTATA CAATGTGAAAATTATA CAATGTGAA CLEGIN BULFOT	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA GCCTATCACA CTCATGAGGG GAAATTATCG GAAATCTT CGAGATGACC GATCTGAACA TTACATCTG AACAGTGTA TTACATCTG GGGAAGATCT CAGAGATGTA TGACATCTGACT GAGAGTTTA GAGAGTTTA GAGAGTTTC CCACAGACTG TGATCTGATT GAGAGGTTGC TGATCCGAT TTAAAACTCC AAAAATGGGA AATATCCTAATG AATATCCTAATG AATATCCTAATC AAAAATGGGA CTTTTAATACACC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CAAGGACCAC CCATGCTGGA TTCATGCCCCT TTGGTGTTAC TTAACTTACT TAACTTACT GGCCAT TAACTTACT ACCATGAGGA TCAGCAGATT TCAGCAGACT TTCATGCAC TCTGTTAGGCA TCTGTTAGGA TTTTGTAGGA TTTTTTAGAA TTATTTAATT CTAATGACTT	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATCCT GAAGCACATC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCC GATGATTGGC AATCAAGCC CAACCCACCT TAAGGGAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT TTTTCTTACA AGACTTGGGC CACGTGTGCC CACGTGTGCC CACGTGTGCC CACGTGTGCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500
50 55 60 65 70	Unigene nur Probeset & Nucleic Aci Coding sequ 1 TARACAGATA CTGGTGATTA CGGATAGAGG GGCCTGGACC ATTGGTGT TGGTCACGGT TCGGATTCGCT TTGGTCACGGT TTCCCCAATG ATTCTCGAA AAGTGGATTC TTCCCAATG ATTCTCGAA AAGTGGAGTC TGCATGTTG TTAAAGTTCC AAAGCTGGGG GTCAATGTGG TTAAAGTTCC AAAGCTGGGG TTAAAGTTCC AAAGCTGGGG AACTACGGAA ATTCCACTAC AAGGAGCCTC AGGATTGGCT AGGATTGGCT AGGATTGGCT TTCTGAGAA TTTTCAAAA Protein sec Gene name: Unigene nu Protein Acc	mber: He 11 cession He 12 dd Accession lence: 82-3 ll Accession Accactana GTTCTGTGAC AACGTAGCCA ACGTAGCCA ACGTAGCCA TGAGAGGAGGA TGAGAGCAA TGCTCGGAG GTGAGAGGA CCATGCAAG CCATGCAAG CCATGCAAG TCCATATAA TTCATATAT TTCATATAT TTGCTCCTAT TTGCTCCTAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTCCTCATACAT TTTCCTCCC CCTCCTGAGC CCTCCTGAGC CCTCCTGAGC TTTTCATAG TGAAATAGGT TATTGATGT TATTGATGT TTTGAGGAATT TATTGATGT TTTGAGGAATT TATTGATGT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTTAAAGCT TTTAAAGCT TTTAAAGCT TTTAAAAGCT TTTAAAAGCT TTTAAAAGCT TTTAAAGCT TTTTTCT TTTTTT TTTTTTT TTTTT TTTTTT TTTTT TTTT	LO903 D61594 1 #: NM_003 1194 21 1 ACATITICCE GATGGTGGA TGTGTTTTACA GCAGTCAAA AACCAGGTC GAAGATCCGC CTTCTTACTA TCCTTGTTTTGCC CCTGATCGTC AGCTGGATTTTGCC CCTGATCGTC AGCTGGATTTT ACAACTTGTC ATGGACCACA GTCAAAAGTGT CAAAATTATT TAAAGAAAAA AAGAGTCT GTTGCCAAG CAAAATTATT TAAAGAAAAA AAGAGTCT GTGTTCCTG GAGAGGGTT TGTTTGCTG GAGAGGGTT TGTTTGCTG CAAAATTATT TAATATATATA AAGAGAGGTT TGTTTCCTG CAAATTATA CAATGTGA AATAATATATA CAATGTGA AATAATATATA CAATGTGA DEEIN BUIFOT 00903 NP 003587	31 AAAATCATTT AAGCTGAAGC CTGGGCCAGC TTGGAGAGCA GCCTATCACA GCCTATCACA CTCATGAGGG GAAATTATCG GAAATCTT CGAGATGACC GATCTGAACA TTACATCTG AACAGTGTA TTACATCTG GGGAAGATCT CAGAGATGTA TGACATCTGACT GAGAGTTTA GAGAGTTTA GAGAGTTTC CCACAGACTG TGATCTGATT GAGAGGTTGC TGATCCGAT TTAAAACTCC AAAAATGGGA AATATCCTAATG AATATCCTAATG AATATCCTAATC AAAAATGGGA CTTTTAATACACC	41 TGAGCARAAT AGAACTTACT ATGCCATGGA CAAGGACCAC CAAGGACCAC CCATGCTGGA TTCATGCCCCT TTGGTGTTAC TTAACTTACT TAACTTACT GGCCAT TAACTTACT ACCATGAGGA TCAGCAGATT TCAGCAGACT TTCATGCAC TCTGTTAGGCA TCTGTTAGGA TTTTGTAGGA TTTTTTAGAA TTATTTAATT CTAATGACTT	ATCTGTTTAA ATTGGCATGT ATGCCATCAC TGTGAGAACT TTTAATATTT CGCACATCCT GAAGCACATCCT GAAGCACATC TTCTAGGTTA ACATTCAATG CTGTTTGACA TTATAAAAG CAGACACCC GATGATTGGC AATCAAGCC CAACCCACCT TAAGGGAGAAC GGAAATTCCT CGCCGCCTGT TGGGCCTCGT TTTTCTTACA AGACTTGGGC CACGTGTGCC CACGTGTGCC CACGTGTGCC CACGTGTGCC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1250 1320 1340 1500 1500 1500

	Transmembrane domains: none found	
	Cellular Localization: plasma membrane 1 11 21 31 41 51	
5		
,		50 20
	KIRLDEAGVT DEVLDSAMQA FILEIIVKHG EPAPYLCNKD PPALKSLTYL SRLPPNAKFL 16	30
		10
10	KWVGKIPPDV LQDMAVIAPM LAKLGYDPYA NPPNYGKPDP KIIENTRRVY KGEFQLPDFL 36	50
	KEKPQTEQVE	
	DNA sequence 3	
15	Gene name: interleukin 13 receptor, alpha 2 Unigene number: Hs.25954	
	Probeset Accession #: R52795	
	Nucleic Acid Accession #: NM_000640 Coding sequence: 94-1236	
•	1 11 21 31 41 51	
20		
		60 20
	TGCTTATATA CCTTTCTGAT AAGCACAACA TTTGGCTGTA CTTCATCTTC AGACACCGAG 1	80
25		40 00
	GAACTAAAAT ACCGAAACAT TGGTAGTGAA ACATGGAAGA CCATCATTAC TAAGAATCTA 3	60
	***************************************	20 80
20	ATATCACCAC AAGGAATTCC AGAAACTAAA GTTCAGGATA TGGATTGCGT ATATTACAAT 5	40
30		00 60
		20
	TTCTATATTT GTGTTAATGG ATCATCAGAG AACAAGCCTA TCAGATCCAG TTATTTCACT 7	80
35	AGTTCATGTG AAATTAAGCT GAAATGGAGC ATACCITTGG GACCTATTCC AGCAAGGTGT 9	40 00
	TTTGATTATG AAATTGAGAT CAGAGAAGAT GATACTACCT TGGTGACTGC TACAGTTGAA 9	60
		80 20
40		40
70		60
	GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA TATGAGTCTC AATAAACTGA 13	20
	ATTTTTCTTG CGAAAAAAA AAAAAAAAA AAAAAAAA AAAAAAAA 13	80
45	Dusheda assures a	
	Protein sequence 3 Gene name: interleukin 13 receptor, alpha 2	
	Unigene number: Hs.25954	
50	Probeset Accession #: R52795 Protein Accession # NP_000631	
	Signal sequence: 1-23	
	FN3 domain: 155-322 Transmembrane domains: 340-362	
55	Cellular Localization: plasma membrane	
33	1 11 21 31 41 51	
	MAFVCLAIGC LYTPLISTTP GCTSSSDTEI KVNPPQDFEI VDPGYLGYLY LQWQPPLSLD	60
		120 180
60	AŁQCVDYIKA DGQNIGCRFP YLEASDYKDP YICVNGSSEN KPIRSSYFTF QLQNIVKPLP 2	240
		300 360
	LLLRKPHTYP KMIPEPFCDT	300
65	DNA sequence 4	
	Gene name: chemokine (C-X3-C) receptor 1	
	Unigene number: Hs.78913 Probeset Accession 8: U20350	
70	Nuclaic Acid Accession #: NM_001337	
70	Coding sequence: 46-1113 1 11 21 31 41 51	
	GGGGCAGATC CAGATTCCCT TTGCAGTCCA CGCCAGGCCT TCACCATGGA TCAGTTCCCT	60
75	ATCGTGGTCT TTGGGACTGT GITCCTGTCC ATATTCTACT CCGTCATCTT TGCCATTGGC	120 180
	CTGGTGGGAA ATTTGTTGGT AGTGTTTGCC CTCACCAACA GCAAGAGCC CAAGAGTGTC	240
		300 360
80	ACCECCTTCT TCTTCATCGG CTTTTTTGGA AGCATATTCT TCATCACCGT CATCAGCATT	420
50	GGCGTCACCA TCAGCCTAGG CGTCTGGGCA GCAGCCATTT TGGTGGCAGC ACCCCAGTTC	480 540
	ATGTTCACAA AGCAGAAAGA AAATGAATGC CTTGGTGACT ACCCCGAGGT CCTTCAGGAA	600
		660 720

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AAAGCCAAAG CCATTAAACT GATCCITCTG GIGGTCATCG TGITTITCCT CTTCTGGACA CCCTACAACG TTATGATTIT CCTGGAGAG CTTAAGCCT ATGACTTCTT TCCCAGTTGT GACATGAGGA AGGATCTGAG GCTGGCCCTC AGTGTGACTG AGACGGTTGC ATTTAGCCAT TGTTGCCTGA ATCCTCTCAT CTATGCATT GCTGGGGGAG AGTTCAGGAG ATACCTTTAC CACCTGTATG GGAAAATGCT GCTGCTCTG TGTGGGCGCT CAGTCCACGT TGATTTCTCC TCATCTGGAT CACAAAGGAG CAGGAATGAA AGTGTTCTGA CCCAAAGCCT TGTGTCTCAC AGGAACTGG AGTTCCTGAA CCTGATGCTG ACTAGTGAG AAGATTTTTT TTGTTATTTC TTACAGGAC AAAATGATG ACCCAAAGCA CCCAAAACCA CCCAAAGCAT TGTGTCTACAGAGT TTGTGCTCAA AATTTGAAGA ATGAACAAAT TGAACTCTTT GAATGACAAA GAGTGCA CACAAACAA CCCTGATGGAG ATGATCAAACAA TTGTGCTCAA AATTTGAAGA ATGAACAAAT TGAACTCTTT GAATGACAAA GAGTGACAAACAG CCTGATGAGGG TGTTTGAGGAA TTCCTTACT GCAAAATGAG GTGGGGAACCA GGCCTGAGC CAAACACA AGCAAAAAAGG GTGTCTGAGA GTTAAATGAG GTGGTGGAAT ATTGTTCATA TTGTGGCACA AGCAAAAAGG GTGTTGAGACAACG CACAAAACAG CACAAAACAG CACAAACAG CCCAAAGCCT TGAGAGTGAAAAAGG GTGTGTGAAA ATTGTTCATA TTGTGGCACA AGCAAAAAGG GTGTTGAGACCAA AGGGGAACCA GGGCCTGAGC CAAGCTA
                                                                                                                                                                               840
                                                                                                                                                                              900
                                                                                                                                                                               960
   5
                                                                                                                                                                            1020
                                                                                                                                                                            1080
                                                                                                                                                                            1140
                                                                                                                                                                            1260
10
                                                                                                                                                                           1380
15
                Protein sequence 4
Gene name: chemokine (C-X3-C) receptor 1
                 Unigene number: Hs.78913
                 Protein Accession #: NP_001328
                Signal sequence: 1-44
Pfam domain: 7tm_1 [48-293]
20
                Cellular Localization: plasma membrane

1 11 21 31
                25
                                                                                                                                                                               180
                                                                                                                                                                               300
30
                 DNA sequence 5
                 Gene name: cannabinoid receptor 1 (brain)
                Gene haume: Cannability technology (Midgene number: Hs.75110 Probeset Accession #: 412986 Nucleic Acid Accession #: NM_001840
35
                 Coding sequence: 92-1510
             11
                                                                    21
 40
                                                                                                                                                                               180
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 45
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 70
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                                                                                                                                                                            1920
                                                                                                                                                                            2040
                 AAATAAACCT TAATATTTCT TCCCAAAAAA AAAAA
75
                 Protein sequence 5
                 Gene name: cannabinoid receptor 1 (brain)
Unigene number: Hs.75110
Protein Accession #: NP_001831
80
                Signal sequence: none found

Fignal sequence: none found

Pfam domain: 7tm_1 [133-397]

Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400

Cellular Localization: plasma membrane

1 11 21 31 41 51
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	KMTAGDNPQL	VPADQVNITE	Fynkelsspk	ENEENIQUE	NPMDIECPMV	LNPSOOLAIA	120
5	VLSLTLGTFT	VLENLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIP	VYSFIDPHVP	180
3	HRKDSRNVFL	PKLGGVTASF	TASVGSLFLT	AIDRYISIHR IDETYLMFWI	PLAYKRIVTR	PKAVVAFCLM	240
	AHSHAVRMIO	RGTOKSIIIH	TSEDGKVOVT	RPDOARMOTE	GVTSVLLLFI	VYAYMYILNK VLIICWGPLL	300 360
	AIMVYDVPGK	MIKLIKTUPA	FCSMLCLLNS	TVNPIIYALR	SKOLRHAFRS	MPPSCEGTAO	420
10	PLDNSMGDSD	CLHKHANNAA	SVHRAAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	
10	TWO						
	UNA sequence	endothelir	recentor t	·vne B			
		mber: Hs.82		.,pc b			
15		cession #:					
13		d Accession		115			
	cooing sequ	lence: 238- 11	1566 21	31	41	51	
	ī	ī	ĩ	ĩ	ī	1	
20	GAGACATTCC	GGTGGGGGAC	TCTGGCCAGC	CCGAGCAACG	TGGATCCTGA	GAGCACTCCC	60
20	AGGTAGGCAT	TTGCCCCGGT	GGGACGCCTT	GCCAGAGCAG	TGTGTGGCAG	GCCCCCGTGG	120
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	CAGCCGCCTC	CAAGTCTGTG	CGGACGCGCC	CTGGTTGCGC	TGGTTCTTGC	CTGCGGCCTG	240 300
25	TCGCGGATCT	GGGGAGAGGA	GAGAGGCTTC	CCGCCTGACA	GGGCCACTCC	GCTTTTGCAA	360
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35	ATTGTTTTGA	TITGGGTGGT	CTCTGTGGTT	CTGGCTGTCC	CTGAAGCCAT	AGGTTTTGAT	960
22	ATAATTACGA	TGGACTACAA	AGGAAGTTAT	CTGCGAATCT	GCTTGCTTCA	TCCCGTTCAG	1020
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	TAAAATATTA	AGTGTAATTA	TTTTAACACT	CACAGCTACA	TATGACATTT	AGCACACTAT TATGAGCTGT	1680 1740
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	CAAAGAGAAA	TAGAATGITT	GAAAGGCTAT	CCCAAAAGAC	TTTTTTGAAT	CTGTCATTCA	2400
60	TOACTATOOT	GAAGACAATA	CTATCTACAA	TITITTCAGG	ATTATTAAAA	TCTTCTTTTT	2460
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	GCCAGTGACC	TCATAATAAA	GACTOTGAAC	TGCCTGGTGC	AGTGTCCACA	TGACAAAGGG	2640
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	TIGITITICIO	; TCAATATTGA	ATGTGATGGT	' ACAGTAAACC	AAAACCCAA	AATGTGGCCA	3300
75	GAAAGAAAGA ACAAA	GCAATAATAA	TTAATTCACA	CACCATATGG	ATTCTATTT	TAAATCACCC	3360
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	TCCTGATACC	: CITICCITCI	CCATGTCAGT	ATCATGTTCT	CTAATTATC	TTCCAAATTT	3600
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	TTCTTTACAT	CARARATOR 1	AAGATAGAA	AAGGTGCTAT	COTTCAACT	CAATTATAAT	3720
	TTCCTAGTA	TAAGGACTT	' ADTATACCA!	CAGACAAAA1	TATEVOTE AND	A THE PARTY OF THE	3780 3840
	CAGCTCAAA	LAATTTATAA	AGATTTTAAC	CTATTTTCTC	CCTTATTATE	TRATIONION	3 900
	GIGGATGTA	GTTCAAACAC	CTTTTAGTAT	TGATAGCTT	CATATGGCC	A AAGGAATACA	3960

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GITTATAGCA AAACATGGGT ATGCTGTAGC TAACTTTATA AAAGTGTAAT ATAACAATGT AAAAAAATTAT ATATCTGGGA GGATTTTTG GITGCCTAAA GTGGGTATAG TTACTGATTT TATATATATT AAGCAAAAAC AATAAAAATT TAAGTTTTTT TAACAACTAC CTTATTTTCC 4180 ACTGTACAGA CACTAATTCA TTAAATACTA ATTGATTGTT TAAAAAGAAAT ATAAATGTGA 4200 AAAATGCCAC ATTTCTGGGC TCTGGG
                                        Protein sequence 6
Gene name: endothelin receptor type B
Unigene number: Bs.82002
    10
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                                      15
                                    MOPPPSLCGR ALVALVLACG LSRINGEERG FPPDRATPILL OTABIMTPPT KTLWPKGSNA SLARSLAPAE VPKGDRTAGS PPRTISPPPC QGPLEIKETP KYINTVVSCL VFVLGIIGNS TLLRIIYKNK CHROGNILI ASLALGDLLH IVIDIPINVY KLLAEDWPFG ABMCKLVPPI CKASVGITVL SLCALSIDRY RAVASWSRIK GIGVPKYTAV BIVLLWVUSV VLAVPEAIGP DIITHDYKGS YLRICLLHPV QKTAPHQFYK TAKDWHLPSP YFCLPLAITA PFYTLMTCEM LRKKSGMQIA LMDHLKORRE VAKTVPCLVL VFALCWLPLH LSRILKLTLY MONDENRCEL LSFLLVLDII GIMMASLNSC INPIALYLVS KRFKNCFKSC LCCWCQSFEE KQSLBEKQSC
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                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                   300
   25
                                       LKPKANDHGY DNFRSSNKYS SS
                                       DNA sequence 7
                                     DAM sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Probeset Accession #: N54926
Nucleic Acid Accession #: AF039686
Coding sequence: 79-1224
   30
                                 1 1 21 31 41 51

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ACAGACTTCC CAGGACACC ACAATGCTACT TCCACTCCCA TGGATGGAAA ATTGCTATCT
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TCTCCAATGTT CTAAAAGTAC TCTGAGGTAAA CATACTAAAA CATACTAAAAA CATACTAAAA CATACTAAAAA CATACTAAAA CATACTAAAA CATACTAAAA CATACTAAAA CATACTAAAA CATACTAAAA C
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                                                                                                                                                                                                                                                                                                                                                                           1140
 55
                                                                                                                                                                                                                                                                                                                                                                           1260
                              Protein sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Protein Accassion #: AADSO531
Signal sequence: none found
Pfam domain: 7tm_1 (71-327)
Transmembrane domains: 90-112, 126-148, 171-193, 217-239, 263-285
Cellular Localization: plasma membrane
1 11 21 31 41 51
 60
65
                                 MRSHTITMTT TSVSSMPYSS HRMRFITNHS DQPPQNPSAT PNVTTCPMDE KLLSTVLTTS
YSVIFIVGLV GRIIALYVFL GIRKKNSIQ IYLLNVAIAD LLLIPCLPPR IMYHIQNKW
TLGVILCKVV GTLFYMMYI SIILLGFISL DRYIKINSI QQRKAITTQ SIYVCCIVWM
VALGGFLTMI LITLKGGGHN STMCFHYRDK HNAKGBAIRN PILVVMFWLI PLLIILSYIK
IGKNILRISK RRSKPNSGK YATTARNSFI VLIIFTICFV PYHARRFIYI SSQLNVSCY
WKEIVHKTNE IMLVLSSFNS CLDFVMYFLM SSNIRKIMCQ LLFRRFQGEP SRSESTSEPK
PCYSLEDTSV AVKIQSSSKS T
70
                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                 240
75
                                   DNA SEQUENCE 8
                                   Gene name: exostoses (multiple)-like 2
Unigene number: Hs.61152
Nucleic Acid Accession #: NM_001439
80
                                    Coding sequence: 288-1280
                                                                                       11
                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                51
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	AAGACAAGAT GCTCATGTTG CGTAGGGAAA TAAAATCC		480
	CCTTTACTCT CATAATGCAG ACGTACAACA GAACAGAT		540
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10	AGGCACCAGA TGAATTATGG AATTCTCTAG GGCCCCAC		660
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1.5	CTTCATCAGG TATCTACAGT TATGGAAGTT TTGAAATG	CA AGCACCAGGG TCTGGAAATG	900
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	ACTITIGCCA TCC		-0-0
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	Protein sequence 8		
50	Gene name: exostoses (multiple)-like 2		
	Unigene number: Hs.61152		
	Protein Accession #: NP_001430		
	Signal sequence: 1-38		
	Transmembrane domains: none found		
55	Cellular Localization: plasma membrane		
	1 11 21 31	41 51	
		í í	
	MRCCHICKLP GRVMGIRVLR LSLVVILVLL LVAGALT	ALL PSVKEDKMLM LERRIKSOGK	60
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65	DNA SEQUENCE 9		
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	Unigene number: Hs.92614		
	Probeset Accession #: AL120193		
	Nucleic Acid Accession #: NM_021267		
70	Coding sequence: 73-1125		
	1 11 21 31	41 51	
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10	TCCACCCCCT	CCAACICIGC	TCCTCTAGGG	CUGCCGCCAC	CTCCCCTGGG	ACCCCGCCCC	1260
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	CGCCTGGGAG	GAAGATGCCA	CCGCCGCAGC	AAGGTCCCTG	CCCCCACCAC	COCCOCCOCCO	1440
	TCCTGGCCCCT	GCTGCTGCCC	TCGCTGCCCC	TGACCCGCGC	CCCCCTTCCC	CCACCCCCAC	1500
15	CCGCCGCCCT	GUTULAGGET	CTAGGACTCC	COLTABATOR	CONCORROR	~~~~~~~~	1560
15	GGCCGGTTCC	CCCGGTCATG	TGGCGCCTGT	TTCGACGCCG	GGACCCCCAG	GREACCROOM	1620
	CTGGCTCGCG	GCGGACTTCC	CCAGGGGTCA	ריים ע עייניינייניי	באונים עלים באונים	030010cmoo	
	GGGTCGCCGG	AAACATGGTG	CCCCACATOC	CCCTCCCCC	TOCOCCACGIG	CGGGCCTCGG	1680
	AGCCTGTCTC	GGCCGCGGGG	CATTROCTO	ACTICALCACIO	COTCOMO	CTGTCGGCTG	1740
	TEGAACCCCC	TGAGCGCCCC	yeccesses.	VOI GOVEYOT	CGICITCUAC	GCGGCGGCTG	1800
20	CCCACCCCC	CCACCCCCCC	MOCCOGGCCC	GCCTGGAGCT	GCGTTTCGCG	GCGGCGGCGG	1860
~~	CCCC CCCCC	GGAGGGGGG	TGGGAGCTGA	GCGTGGCGCA	AGCGGGCCAG	GGCGCGGGCG	1920
	CGGACCCCGG	GCCGGTGCTG	CTCCGCCAGT	TGGTGCCCGC	CCTGGGGCCG	CCAGTGCGCG	1980
	CGGAGCTGCT	GGGCGCCCCT	TGGGCTCGCA	ACCCCTCATG	GCCGCGCAGC	CTCCGCCTGG	2040
	CGCTGGCGCT	ACGCCCCCGG	GCCCCTGCCG	CCTRCGCGCG	CCTGGCYY3AG	CONTROP CONTROL	2100
25	TGCTGGTGAC	CCTCGACCCG	CGCCTGTGCC	ACCCCCTGGC	CCGGCCGCGG	CCCCNCCCCC	2160
25	AACCCCGTGTT	GGGCGGCGGC	CCCGGGGGGGG	CHINALIANCASCASIC	OCCOPORTION.	TROOMER COM	2220
	TCCGCGAGGT	GGGCTGGCAC	CGCTGGGTCA	TCGCGCCGCG	CCCCTTCCTC	CCCAACTACT	2280
	GUUNGGIUN	GIGCGCGCIG	CCCGTCGCGC	TGTCGGGGGTC	CCCCCCCCCC		2340
	ACCACGCTGT	GCTGCGCGCG	CTCATGCACG	CCCCCCCCC	GGGAGCCGCC	GACCTGCCCT	
	GCTGCGTGCC	CGCGCGCCTG	TOGCCCATCT	CCCTCCTCTT	CTTTCACAC	AGCGACAACG	2400
30	TGGTGCTGCG	GCAGTATGAG	GACATGGTGG	0001001011	CITICACAAC	AGCGACAACG	2460
			4141100100	IGGNCGNGIG	COGCIGCOC	TAACCCGGGG	
	Protein sec				•		
	Cana	dence a					
	Gene name:	Homo sapie	ns growth	iifferentia:	tion factor	1 (GDF1)	
35	Unigene num						
22	Protein Acc						
	Signal sequ	ence: none	found				
	Transmembra	une domains:	106-128,	148-169, 18	4-206, 244	-266, 285-30	7
	Cellular Lo	calization:	plasma me	mbrane		,	•
40	1	11	21	31	41	51	
40	1	1	1	ī	1	ì	
	MAAAGPAAGP	TGPEPMPSYA	OLVORGUGSA	TAAABCCTDC	CWCLADDCT A	PUBUI SESSI	
	MAAAGPAAGP	TGPEPMPSYA TALBSAATAR	QLVQRGWGSA	LAAARGCTDC	GWGLARRGLA	EHAHLAPPEL	60
	WENT REPUTATION	TALRSAATAR	LFRPLAKECC	LOPRDAAKMP	ESAWKPI.RVI.	GCWGVCAVI.I.	120
	FGTDYPFFHD	TALRSAATAR PPSVFYDWTP	LFRPLAKECC GMAVPEDIAA	LQPRDAAKMP	ESAWKPLPYL	GSWSYSAYLL	120 180
45	FGTDYPFFHD LHHVVTLILI	TALRSAATAR PPSVFYDWTP VSSYAPRYEN	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD	LQPRDAAKMP AYLLQGSFYG ISDVOLRPTK	ESAWKPLFYL HSIYATLYMD LNIVEKSEGG	GSWSYSAYLL TWRKDSVVML	120
45	FGTDYPFFHD LHHVVTLILI DLGCLSFGFS	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLLL	GSWSYSAYLL	120 180
45	FGTDYPFFHD LHHVVTLILI DLGCLSFGFS	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLLL	GSWSYSAYLL TWRKDSVVML	120 180 240
45	FGTDYPFFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL	TALESAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELKDL	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLLL	GSWSYSAYLL TWRKDSVVML	120 180 240
45	FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC	TALRSAATAR PPSVFYDWTP VSSYAPRYEN WFWFRLYWFP TGQVHELKDL CE 10	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL	120 180 240 300
	FGTDYPFFHD LHHVVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name:	TALRSAATAR PPSVFYDWTP VSSYAFRYEN WFWFRLYWPP TGQVHELKDL CE 10 epidermal	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth face	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL	120 180 240 300
45	FGTDYPFFHD LHHAVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur	TALRSAATAR PPSVFYDWTP VSSYAFRYHN WFWFRLYWPP TGQVHELKDL CE 10 epidermal nber: Hs.7	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS Growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIFF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML	120 180 240 300
	FGTDYPFFHD LHHAVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur	TALRSAATAR PPSVFYDWTP VSSYAFRYHN WFWFRLYWPP TGQVHELKDL CE 10 epidermal nber: Hs.7	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS Growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIFF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL	120 180 240 300
	FGTDYPFFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac:	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' 1d Accession lence: 187.	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 432 #: NM_00: 3819	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIFF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL	120 180 240 300
	FGTDYPFFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac:	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' 1d Accession lence: 187.	LPRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 432 #: NM_00: 3819	LOPPDAAKMP AYLLQGSFYG AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto:	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic	120 180 240 300
50	ELLARGALGH FGTDYPFHD LHKVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ	TALRSAATAR PPSVFYDWTP VSSYAPRYHN WFWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7' 1d Accession lence: 187.	LFRPLAKRCC GMAVPRDIAM VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432	LQPRDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIFF LKPSKAEKPL	ESAWKPLPYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWFL	120 180 240 300
	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGPS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal mber: Hs.7' td Accession lence: 187. 11	LFRPLAKRCC GMAVPRDIAA VGILVLPIHD LKVLYATSHC REYDTAEAQS growth fact 7432 1 #: NM_00: -3819 21	LOPPDAAKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT recepto: 5228 31	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLL RNGLVKDKRF (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic	120 180 240 300
50	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence 1	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL E 10 epidermal hber: Hs.7 Id Accession tence: 187 11	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS Growth fact 7432 1 %: NM_00: 3819 21 CGAGGTAGCC	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT receptor 5228 31)	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er;	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic	120 180 240 300 leukemia
50	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENK Gene name: Unigene nur Nucleic Ac: Coding sequent 1 GCCGCGCTGC AGGCCACCTC	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal nber: Hs.7' ld Accession Lence: 187' 11 GCCGGAGTCC GTCGGGGTCC	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCCC	LOPRDARKMP AYLLQGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT receptor 5228 31 CCGGCGCCCCGC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL RNGLVKDKRF (avian ex)	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic	120 180 240 300
50	PETTYPFFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequence 1 GCCGCGCTGC ACGCCACTC GCACGGCCCC GCACGGCCCC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession lence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact /432 3#: NM_00: 3819 21 CGAGGTAGCC GCCGGAGTCC CCAGGTTGA	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL TOT receptor 5228 31 CCGGCGCCCGC CCGCCTCGC	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTIMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC	120 180 240 300 leukemia
50	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGGGCTGC AGGCCACTC GCAGGGCCCC GCAGGGCATGC	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL CE 10 epidermal nber: Hs.7 td Accession tence: 187 t1 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG	LFRPLARRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 #: NM_00: 3819 21 CGAGGCTAGCC GCCCGAGTCC CCAGTACTGA GACTACTGGA	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCCC CCGCCTCGCC TCGGGAGAGC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er; 41 CGCCGCCCAG GCCAACGCCA GGCAACGCCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA	120 180 240 300 leukemia
50 55	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequence GCCGCGCTGC AGGCCACCTC GCAGGGCCCC GCAGGGCGCCC GCAGGGGGCGCCC GCAGGGGGGGG	TALRSAATAR PRSVFYDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELKDL CE 10 epidermal nber: Hs.7' Id Accession Lence: 187' Il GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCCTCCGG GTCCGGGCTCC GTCGGGCTCT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 1432 1 #: NM_00: 3819 21 CGAGCTAGCC GCCGAGTCC CCAGTATTGA GACGGCCGGG GAGGCCGGG	LOPRDARKMP AYLLOGSFYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT receptor 5228 31 CCGGCGCCGC TCGGGAGAGC TCGGGAGAGC GCAGGCTTCGCC	ESAWKPLFYL HSIYATLYMD LNIYFKSRGG YFFFNALLL RNGLVKDKRF (avian ex) 41 CGCCGCCCAG GGCAACGCCA GGCAACGCCA CGGAGCGAGC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC	120 180 240 300 leukemia 60 120 180
50	PETTAPPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac Coding sequence 1 GCCGCGCTGC AGGCCACCTC GCACGGCCCC GCAGGGATGC TGCCCGGCGA AGGCAATGC TGCCCGGCGA AGGCATTGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACCTCCGG GTCGGGCTCT GACCTTCGG	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth fact 7432 #: NM_00: 3819 21 GAGGTAGCC GCCGGAGTCC CCAGTATTGA GACGCCGGG GGAGGAAAAG AGATGATTTT	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL COT receptor 5228 31 CCCGCGCGCCGC CCCGCCTCGCC TCCGGGAGGC GCAGCGCTCCCAAAGTTTGCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA CGGAGCGAGC TGGCGCTGCT AAGGCAACGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC TCTTCGGGGAC TCTTCGGGGAC TCAACAAGCTC TAACAAGCTC	120 180 240 300 leukemia 60 120 180 240 300
50 55	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGGGCTGC AGGCACCTC GCACGGATGC TGCCCGGCAA AGGCAGTGGTAGCAGGTATGC TGCCCGGCGAAGGATGC TGCCCGGCGAAGGGAGGGAG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 id Accession lence: 187 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCTGG GTCGGGCTCT GCACTTTTGA TTGGGAATTT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 COAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGGCGGG GCAGGAAAAG AGATCATTTTCC	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCC CCGCCTCGCC TCGGGAGAGC CCAGCCTCCC AAAGTTTGCC AAAGTTTGCC TCAGCCTCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GGCAACGCCA TGGCGCTGCT AAGGCACGAG AOAGGATGTT ACGAATATCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTCTCGGGTA	120 180 240 300 leukemia 60 120 180 240 300 360
50 55	PETDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene nu Wheleic Ac: Coding sequence GCCGCCTGC GCACGGCTGC GCACGGCCCC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC GCACGGCATGC TGCCCGGGGA ACGCAGTTGG GACGTAGTCG GACGTAGGTCC TTAAAGACCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession Lence: 187 il GCCGGAGTCC GTCGGCGTCC GTCGGCGTCC GGACTCCGG GTCGGCTCCGG GTCGGGCTCT GCACTTTTGA TTGGGAATTT TCCAGGAGTTT TCCAGGAGGT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 growth faci /432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGGTATGC GCCCGAGTATGC GCAGGAAAAG AGATCATTTT GGAAATTACC GGCTGGTATTA	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGC CCGGCGCCGC CCGCCTCGC AAAGTTTGCC AAAGTTTGCC TTTTGCAGT	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YPFFNALLLL RNGLVKDKRF (avian er; (avian er; (GCCGCCCAG GCCAACGCCA GCCAACGCCAG AGGCAGCAG TGGCGTGGT AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGGCACGAG AAGATTATGA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCAC TCTTCGGGG GGCTGCGCT TAACAAGCTC TCAATAACTGT TCTTTCCTTC AGTGCCCA	120 180 240 300 1eukemia 60 120 180 240 300 360 420
50 55	PETDYPFHD LHHVVTLILI DLGCLSFGS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac Coding sequence (GACGGCCCC GCAGCGACTC GCACGGCCCC GCAGCGATGC GCAGGGCCC GCAGCGATGC GCAGGGCCC GCAGGGATGC TTAAAGACCA ATTCCTTTGG	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQGTCC TGACTCCGT GACCTCCGG GTCGGGGTCC TGCACTTTGA TTGGGAATTT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TCCAGGAGGT TAAAACTGCA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 18: NM_00: 3819 21 GAGGTAGCC GCCGGAGTCC CCAGTATTGA GAGGAAAAG GAGGAAAAG GAGAAATTATC GGAAATTACC GGCTGGTTATA	LOPRDAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCC TCGGCGCCCCC TCGGGAGC GCAGCTCC AAAGTTTGCC CTCAGCTCC TATGTGCAGA GTCATTGG	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GGAGCGAGC TGGAGCTAGT AAGGCAACACA AGAGGATTATGA CCCTCAACAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGGGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGGGAA	120 180 240 300 leukemia 60 120 180 240 300 360 420 480
50 55 60	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGCGCTGC AGGCCACTC GCACGGCCCG GCAGGGATGC TGCAGGGCCT TTAGAGACCA ATTCCTTTGG TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 td Accession ence: 187. 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGG GTCGGCGTCC GACCTTTGA TTGGGAATTT TCCAGGAGGT AAAACCTGCA TATCTAACTA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9rowth fact 7432 1 %: NM_00: 3819 21 COAGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCCGGG GGAGGAAAAG AGATCATTATC GGCTGGTTAT GGATATTACC GGCTGGTTAT GATCATCAGAAT TGATGCAAAT	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGOGCCGC CCGCCTCGCC TCGGGAGAGC CCAGCCTCC AAAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACTGACA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er: 41 GCCCGCCCAG GCCAACGCCA CGGAGCGAGC TGGCGCTCAGCA AGAGGATGTT AGAGCACGAG ACTACGAAAA ACTACGAAAA TGAAGAAAA TGAAGAACAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA TTCCTATGCC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540
50 55	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGCGCTGC AGGCCACTC GCACGGCCCG GCAGGGATGC TGCAGGGCCT TTAGAGACCA ATTCCTTTGG TTAGCAGTCT TTAGCAGTCT TTAGCAGTCT	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWPP TGQVHELRDL EE 10 epidermal nber: Hs.7 td Accession ence: 187. 11 GCCGGAGTCC GTCGGCGTCC CTGACTCCGG GTCGGCGTCC GACCTTTGA TTGGGAATTT TCCAGGAGGT AAAACCTGCA TATCTAACTA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9rowth fact 7432 1 %: NM_00: 3819 21 COAGCTAGCC GCCCGAGTCC CCAGTATTGA GACCGCCGGG GGAGGAAAAG AGATCATTATC GGCTGGTTAT GGATATTACC GGCTGGTTAT GATCATCAGAAT TGATGCAAAT	LOPRDARKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGOGCCGC CCGCCTCGCC TCGGGAGAGC CCAGCCTCC AAAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACTGACA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er: 41 GCCCGCCCAG GCCAACGCCA CGGAGCGAGC TGGCGCTCAGCA AGAGGATGTT AGAGCACGAG ACTACGAAAA ACTACGAAAA TGAAGAAAA TGAAGAACAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL ythroblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA TTCCTATGCC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600
50 55 60	PETDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene nu Wheleic Ac: Coding sequence GCACGCCTGC GCACGCCTGC GCACGGCCCC GCACGGATGC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC GCACGGTGGCCC TGCCCGCGGA AGGCTGGTCC TTAAAGACCA ATTCCTTTGG TAATTACAGG	TALRSAATAR PSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession Lence: 187 11 GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GACCTCCGG GTCGGGCTCT GACCTTTMA TTGGGAATTT TCCAGGAGT AAAACCTGCA AAATCTGCA AAATCCTGCA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 1 #: NM_00: -3819 21 CGAGGTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GGAGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTAT GGCTGGTTAT GATCATCAGA TGATGCAAAT TGGCGCGTTG TGGCGCGTTG	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGC CCGGCGCCGC CCGCCTCGC CCGCCTCGC GCAGCGCTCC ARAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACCGGAC CCGCTCAGC	ESAWKPLFYTL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er; (accedeccag GCCAACGCCA GCCAACGCCA ACGAGCAGCA AGGGCAGGAGC TGGCGCTGCT AAGGCACGAG ACGAATTATGA ACTACGAAAA TGAAGGAGGAT TGAAGGAGAGAGAGAGAGAGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCAC GGCTGCGCT TAACAAGGTC CAATAACTGT TCTTTCCTTC AGTGGAGGGA ATTCCTATGCC GCCCATGAGCA CCCCATGAGCA CCCCCTCCAACA CCCCCCCC	120 180 240 300 leukemia 60 120 180 240 360 420 480 540 600 660
50 55 60	PETDYPFHD LHHVVTLILI DLGCLSFGS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac Coding sequence (GACGGCTGC AGGCCACCTC GCACGGCCC GCAGCGATGC GCAGGGTGC GCAGGGTGC TTAAAGACCA ATTCCTTTGG TTAGCAGTCT AATTTACAGG GTGGAGAGCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQGTCC TGACTCCGT GACCTCCGG TGCCTCCGG TGCCTCCGG TCCGGGCTCT TCCAGGAGGT TTCCAGGAGGT TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA TCCAGTGCA TCCAGTGCG	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 CGAGGTAGCC GCCGAGTCC CCAGTATTGA GACGGCCGGG GGAGAAAAG AGATCATTTT GGAAATTACC GGCTGGTTAT TGCACATCATCAGA TGATCACAGA TGATCACAGA TGATCACAGAT TGGCGCCGTG GGACATGTCAGA TGATCACAGAT TGGCGCCGTG TGATCATCAGA TGATCACAGAT TGGCGCCGTG TGATCACAGAT TGGCGCCGTG TGATCATCAGAT TGGCGCCGTG TGGACAGTC TGGCGCCGTG TGATCATCAGAT TGGCGCCCTGT TGGCGCCGTG TGGACAGTC TGGCGCCGTG TGGACAGTC TGGCGCCGTG TGGACAGTC TGGCCCCTGT TGGCACAGTC TGGCCCCTGT TGGCACAGTC TGGCCCCTGT TGGCACAGTC TGGCCCCTGT TGGCACAGTC TGGCCCCTGT TGGCACAGTC TGCACAGTC TGCACAG	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31 CCGGCGCCCC TCGGCGCCCC TCGGGAGC GCAGCCTCC TCAGCCTC CTCAGCTTCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACCGGAC CCGTTCAGCA AAAATATGC AAAACCGGAC AAAATATGC AAAACCGGAC AAACCGGAC AACCGGACGAC AACCGGACGAC AACCGGACGAC AACCGGACGAC AACCAGTGAC AACCAGTCAC AACCAGTGAC AACCAGTGAC AACCAGTGAC AACCAGTGAC AACCAGTGAC AACCAGTGAC AACCAGTCAC AACCAC AACCACAC AACCAC AACCAC AACCAC AACCAC AACCAC AACCAC AACCAC AACCAC AACCAC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GGAACGCCA TGGAGCTAGT AAGGCAACGCT AAGGCAACAC ACTACAACA TGAAGCAGC ACTACAACA TGAAGCAGCT ACAACCCTGC ACACCCTCCAACAC TGAAGCAGCT TGAAGCAGCT ACAACCCTGC TGCTCACACAC TGAAGCAGCCT	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC TAACAAGCTC TAACAAGCTC TATCTTCTTC AGTGGAGCAA TCCTATGCT GCCCATGAGA CCTGTGCAAC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600
50 55 60	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGCGCTGC ACGCCCC GCACGGATGC TGCCCGGCAA ACGCACTC GCACGGATGC TGCCCGGCAA ACGCAGTGCT TAAAGACCA ATTCCTTTGG TTAGCAGTCT AATTACAGG GTGGGAGGGC GTGGGAGGGC AGTTCCAGAA ACTCCAGAA	TALRSAATAR PSYPTOWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7 Id Accession lence: 187 II GCCGGAGTCC GTCGGCGTCC GTCGGCGTCC GACTCCGG GTCGGGCTCT GCACTTTGA ATTGGGAATT TCCAGGAGTT TCCAGGAGTT TACTACTA AAATCCTGCA TCCAGTGGC ACCACTGGG ACCACCTGGG	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9 rowth fact 7432 1 %: NM_00: 3819 21 COAGCTAGCC GCCCGAGTCC CCAGTATTGA AGATCATCAGA AGATCATCAGA AGATCATCAGA TGACCAGATTTAC GCTGGTATT GATCATCAGA TGACGCAGT TGGCACATTT	LOPRDAAKMP AYLLOGSPYG ISDVQLEPTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 CCGGCGCCCCC CCGCCTCGCC TCGGGAGAGC CCGCCTCGCC TCAGCCTCC AAAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT CAGCTCC AAACCGGAC AACCGGAC AACCGGAC AACCAGTGACT AAACCGGAC AACCAGTGACT AAACCGGAC AACCAGTGACT AACCAGTGACT AACCAGTGACT AACCAGTGACT AACCAGTGACT AACCAGTGACT	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YPFFNALLLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GCAACGCCA CGAGCGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CCAACCACCGC TCTTCGGGGA GGCTGGGCT TCTTTCCTTC CAATAACTGT TCTTTCCTTC GCCATGAGGC TCTTCCTTCAGCGC GCCCATGAGGA CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CATGTCGATGC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	PETIDIPIPHO LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequin GCCGCGCTGC AGGCCACTGC AGGCCACTGC GCACGGATGC TGCACGGGTGGTC TGCACGGGTGTC TTAAAGACCA ATTCCTTTGG TTAAGAGTCT TAAGCAGTCT TAAGCAGTCT TAAGCAGTCT TAAGCAGTCT TAATTACAGG GTGGAGAGCA GACTTCCAGA TGCTGGGGTG GACTTCCAGA TGCTGGGGTG	TALRSAATAR PSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession lence: 187- 11 GCCGGAGTCC GTCGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC TGACTCCGT GACCTTCGG GTCGGGGTCC TGACTTTGA TTGGGAATTT TCCAGGAGT TTCCAGGAGT TATCTAACTA AAATCCTGCA TCCAGTGGG ACCAGGGGG ACCAGGGGGG	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 3 #: NM_00: 3819 21 CGAGGTAGCC GCCCGAGTCC CCCAGTATGA GACGGCCGGG GGAAATTACC GGCTGGTTAT GATCATCAGA TGATGCAAAT TGGCGCCGTG GGACATAGCC GCTGGTTAT GGCACATAGCAAT CGCCGCTG GGACATAGCAAT CGCCCGTG GGACATAGCC AGACTGCCAA AGACTGCCAA AGACTGCCCAA AGACTGCCCAG AGACTGCCCAA AGACTGCCCAG AGACTGCCCAA AGACTGCCCAG AGACTGCCCAA AGACTGCCAA AGACTGCCCAA AGACTGCCAA AGACTG	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCCGGGAGAGC GCAGCGCTCC TATGTGCAGA GTCCTCATTGC TATGTGCAGA GGAATATGT AAAACCGGAC CGGTTCAGCA AAGCATGACT AAGTTTGACC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 CGCCGCCCAG GCCAACGCCA AGGCAACGCCA AAGGCACCAG ACAACACAC ACTACAACAC ACTACAACAC TCAACACC TTCTCAGCAA CAAGCTGTCC AAGGCTGTCC AAGCTGTCC AAGCTGTCC AAAGCTGTCC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACCACCGC CAACCACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC TCATTACATGCT TCTTTCCTTC AGTGGAGGGAA TCCTATGCC GCCATGAGA CCTGTGCAAC CAATGGGAGC CAATGGGAGC CAATGGGAGC CCTGTGCATG	120 180 240 300 1eukemia 60 120 180 240 360 420 480 540 600 660 720 780 840
50556065	PETIDIPPETID LHHVVTLILI DLGCLSFGSS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequence (Coding sequence) (Coding se	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQUHELRDL TGQUHERDL TGQUH	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 GAGGCTAGCC GCCGAGTACC CCAGTATTGA GAGGCCGGG GGAGGAAAAG AGATCATCATCAGA TGATCATCAGA TGATCATCAGA TGATGCAGATTGATCATCAGA TGATGCAGATTGCAAGTCCAG	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF recepto: 5228 31 COGGCGCCCC TCGGGAGGC CCCTCGCC TCGGGAGGC CCTCAGCCTC CTCAGCCTCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAACCGGAC AGGTTCAGCA AGGTTCAGCA AGGTTCAGCA AGGTTCAGCA AAGTTGTGATC AAACTGACCA AAGTGACTCC AAAGTGTGATC AAACTGACCA AAGTGACTCC AAAACTGACCA AAGTGACTCCT AYLOGSPYGATCA AAAACTGACCA AAGTGACTCCT AAAACTGACCA AAGTGACTCCT AAAACTGACCA AAGTGACTCCT AAAACTGACCA AAGTGACTCCT	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA TGGGGCTGCT AAGGCACGAG AAGGCATGTT GGAATTATGA CCCTCAACAC TGAACACCTGC TCTCAGCAA ATGAAGGAGCT TCTCAGCAA ACAGCTGTC AAATCATCTG AAATCATCTG ACAACCTGCC AAATCATCTG AAATCATCTG ACAACCTGCC AAATCATCTG ACAACCTGCC AAATCATCTG ACAACCTGCC AAATCATCTG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GGCTGGGCAC TCATCGGGCAC TCTTCGTCC AGTGGAGCGA TCCTATGCTC AGTGGAGCGA CCTGTGCAAC CATGTGCAAC CATGTCAAC CATGTGCAAC CATGTCAAC CATGTGCAAC CATGTGCAAC CATGTCAAC CATGTGCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CATGTCAAC CA	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene nur Nucleic Ac: Coding sequ 1 GCCGCGCTGC ACGCCCC GCAGGGACCT GCACGGCCCC GCAGGGATGC TGCCCGGGAA ACGCAGTTGC TTAAAGACCA ATTCCTTTGG TTAGCAGTCT AATTACAGG GTGGAGAGCT TGAGAGGCC TGAGAGGCC TGCAGGGGCT TGAGAGGCC TGCAGGGGT TGCTCGGGGT TGCTCCGGGC TGCTCGGGGT TGCTCCGGGC	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7 td Accession ence: 187. 11 GCCGGAGTCC GTCGGGGTCC CTGACTCCGG GTCGGGGTCC GCACTTTTGA ATTGGGAATTT TCCAGGAGGT TATCTAACTA AAATCCTGCA TCCAGTGGG ACCACCTGGG ACCACCTGGG CAGGAGGGA ACCACCTGGG CAGGAGAGGA ACCACCTGGG CAGGAGAGGA CCCCCGGGGA GCCCCCGGGGA GCCCCCGGGGA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS 9 rowth fact 7432 1 %: NM_00: 3819 21 COAGGTAGCC GCCGAGTCC CCAGTATTGA AGATCATCAG AGATCATCAG AGATCATCAG GAACTAGCAAT TGGCGCCGTG GCAGCTAGTAT TGGCGCCGTG GCAGTATGCAAT TGGCGCCGTG GCAGTAGCAAT TGGCGCCGTG GCAGTAGCAAT TGGCGCCGTG GCAGTAGCAAC GAACTGCCAG GAACTGCCAG GAACTGCCAG GAACTGCCAG GAACTGCCAG GAACTGCCAG	LOPRDAAKMP AYLLOGSPYG ISDVQLEFTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGOGCCGC CCGCCTCGCC TCGGGAGAGC CCGCCTCGCC TCAGCTCC AAAGTTTGCC TATGTGCAGA GTCCTCATTG GGAAATATGT AAAACCGGAC AGCAGTGACT AAGTTGACCA AGCAGTGACT AAAGTTGACCA AGCAGTGACT AAAACTGACCA AGTGACTGCC CTCGGCTCCC CTCGGCTCCC CTCGGCTCCC CTCGGCTCTCC CTCGGCTCTCC CTCGGCTCTCC CTCGGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CTGCTCTCC CTGGTCTGCC CT	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YFFFNALLL RNGLVKDKRF (avian er: 41 CGCCGCCCAG GCCAACGCCA GGAGGAGGAGC TGGCGCTCAGCAACAC ACTACGAAA TGAAGGAGTTTCTCAGCAA TGAAGCTGTC AAATCATCTG GCCACACCTG ACTACTCTC ACAACCTGC ACTACTCTC ACAACCTGC ACATCATCTG GCCACACCTGC ACAACCTGC ACACACCTGC ACAACCTGC ACAACC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CCACCGC TCTTCGGGGA GGCTGCGCT TCTTCCTTC CAATAACTGT TCTTTCCTTC GCCATGAGC CCCATGAGC CCTGTGCAAC CATGCGATC GCCATGAGA CCTGTGCAAC GCCATGAGA TCCTATGCC GCCATGAGA TCCTATGCC GCCATGAGA TTCCTATGCC GCCATGAGA TTCCTATGCC GCCATGAGA TTCCTATGCC GCCATGAGA TTGCTGCAAC CATGTGGAAC CATGTGGAAC CATGTGGAAC CATGTGGAAC AATGGGAGG TTGCCCAGCAG GTGTGCTGCA AAACAACAACAACAACAACAACAACAACAACAACAAC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 660 720 780 840 900
50556065	PETIDIPIFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequin GCCGCGCTGC AGGCCACTGC AGGCCACTGC GCACGGATGC TGCACGGGTGTC TGCACGGGTGTCC GAGGGTGGTCC TTAAAGACCA ATTCCTTTGG TTAAGAGTCT TAAGTATCAGG GTGGAGAGCA GACTTCCAGA GGCTTGCCAGG GGCTGCACAG GACTTCCAGA AGCTCCAGA ACGTCCAGAG ACGTCACAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACGCAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACGTCCAGAG ACG	TALRSAATAR PSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 id Accession lence: 187- 11 GCCGGAGTCC GTCGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC TGACTCCGT GACCTTCGG GTCGGGTCC TGACTTTGA TTGGGAATTT TCCAGGAGT TTCCAGGAGT TTCCAGGAGT ATATCTAACT AAAATCCGCA ACCACTGGG GCCCCGGGG GCCCCCGGGG GCCCCCGGGG ACCACTGCC	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci 7432 1 #: NM_00: 3819 21 CGAGGTAGCC GCCCGAGTCC CCCAGTATGA GACGCCGGG GGAAATTACC GGCTGGTTAT GATCATCAGA TGATGCAAAT TGGCGCCGTG GGACATAGTC CAGCTGCCAA GAACTGCCAG CAAGTCCCCC GAGCGACTGC CAAGTCCCCC GAGCGACTGC CAAGTCCCCC GAGCGACTGC CCCACTGCTATG	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGAGC GCAGCGCTCC TAGGGAGAGC GCAGCGCTCC TATGTGCAGA GTCCTCATTG AAAACCGAC CGGTTCAGCA AAGTGTGATC AAGTGTGATC AAACTGACC AAGTGACTGC CTCGGCTGCC CTGGTCTGCC CTGTCTGCC CTCGTCTGCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 CGCCGCCCAG GCCAACGCCA AGGCAACGCCA AAGGCACCAG ACAACCAC ACTACAACAC ACTACAACAC ACTACAACAC ACTACAACAC ACTACAACAC ACTACAACAC ACTACAACAC ACATCATCAGCAA CAAGCTGTCC AAATCATCG GCCACAACCA GCCACAACCA GCCACAACCA GCCACAACCA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC TCATTACATGC GCCATTAGA TCCTATGCAC CATGTGCAAC CATGTGCAC CAGACGAAGC CCCACTACAC CAGACGAAGC CCCACTACAC CACACCAC CCCACTACAC CCCACACCAC CCCACTACAC CCCACACTACAC CCCACATACAC CCACATACAC CCCACATACAC CCCACAT	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50556065	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGSS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequing GCCGCGCTGC AGGCCACTC GCAGGGCCCC GCAGGGATGC TGCCCGGGGG AGGCTGCAGGGCCC TTAAAGACCC TTAGCAGTCT AATTTACAGG TTAGCAGTCT AATTTACAGG TTAGCAGTCT AATTTACAGA TGCTGGGGC GTGGAGGAGCA GACTTCCAGA TGCTGGGGC GGCTGCACAG ACGTTGCAAGG GGCTGCACAG ACGTTGCAAGG GGCTGCACAG GCTGCACAGG GTGAACCCCG GTGTGCACCG	TALRSAATAR PSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TE 10 epidermal nber: Hs.7: Ld Accession ence: 187: 11 GCCGGAGTCC GTCGGGGTCC CTGACTCCGT GACTCTCGG GTCGGCTTCT GCACTTTTAA TTGGGAATTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT AAAACCTGCA AAATCCTGCA AAATCCTGCA ACACCTGCG CAGGAGAGGA ACACCTGCG GCCCCGGGA ACACCTGCG ACACCTGCG ACACCTGCG ACACCTGCAACAATA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 GAGGCTAGCC GCOGAGTCC CCAGTATTGA GAGGCCGGG GGAGGAAAAG AGATCATCAGA TGATCATCAGA TGATGCAGCT GGCGCGTTAT GGAAATTACC GGCTGGTAT CGCGCCGTG GGACTAGCC GGACTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA CAGCTCCCC CAGCGCACTCTTGT CAGCTTCTTGT CAGCTTCTTTGT CAGCTTCTTTGT CAGCTTCTTTTT CAGCTTCTTTT CAGCTTCTTTT CAGCTTCTTTTT CAGCTTTTTT CAGCTTTTT CAGCTTTTT CAGCTTTTT CAGCTTTTT CAGCTTTTT CAGCTTTTT CAGCTTTTT CAGCTTT CAGCTTT CAGCTTT CAGCTTT CAGCTTT CAGCTT CAGCT CAGCTT CA	LOPRDAAKMP AYLLOGSPYG ISDVQLEPTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGCGCCCC CCCCCCCC TCGGGAGGCC CCCCCCCC AAAGTTTGCC CTCAGCCTCC TATGTGCAGA GGCAATATGT AAAACCGGAC AGCTTCAGCA AGCAGTGACT AAATGTGACC AAGTGACTGCC CTCTGCCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er) 41 CGCCGCCCAG GCCAACGCCA GCCAACGCCA AGAGCAGGAG AGAGGAGAG AGAGGAGAT AGAGGAAA TGAAGGAGGT TCTCAGCAA CATCAGAAA TCAACCTGC AAATCATCTG GCCACACCA GCCACACCA GCCACACCA CCACCACGTA AGAGCTGTCC CACCACGTA AGCCACGCA AGAGCTGTCC CACCACGTA AGCCACGCA AGCCACGCA AGCCACGCA AGCCACGCA AGCCACGCA AGCCACGCA AGCCACGCA AGCCACGCA AGCACCACGTA AGCACCACGTA AGCACCACGTA AGCACCACGTA AGCACACGCACACGTA AGCACCACGTA AGCACACGCACGTA AGCACACGCACACGTA AGCACACGCACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACGCACACGTA AGCACACACGTA AGCACACACGCACACACACACACACACACACACACACA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCAT TCTTCCTTC AGTGGAGCGA TTCCTATGCTC AGTGGAAC CCATGCGAC GCCCATGGA CCTGTGCAAC CATGTCGAAC CATGTCGATG CAATGGGAGC TGCCCAGCAG GTGTGCTGCA AGACGAGCC CCAGATGGAT TCCCATGCA	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50556065	PETIDIPIPHO LHHVVTLILI DLGCLSFGFS YTVAFARVL DNA SEQUENC Gene name: Unigene nui Wheleic Ac: Coding sequence GCCGCCTGC GCAGGCACTGC GCAGGGCCCC GCAGGGATGC GCAGGGATGC TGCCCGGGGA AGGCAGTTGG GAGGTGGTCC TTAAAGACA ATTCCTTAGG GTGGAGGAG TGCTCGGGC TGCCGGGTG TGCTCGGGC AGCTTGCGGGTG TGCTCGGGC TGCCGGGCAAGGAGGA TGCTCGGGG TGCTCGGGG TGCTCGGGG ACGTGCACAG ACGTGCAAGG TTATGTGTGA	TALRSAATAR PSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL CE 10 epidermal nber: Hs.77 id Accession Lence: 187 il GCCGGAGTCC GTCGGGGTCC CTGACTCCGG GACCTCCGG GACCTCCGG GTCGGGGTCC CTGACTTTGA TTGGGAATTT TCCAGGAGTT TCCAGGAGT AAAACCTGCA TATCTAACTA AAATCCTGCA ACACTGGG ACACCTGGG ACACCTGGG ACACCTGGG ACACCTGGG ACACCTGGG ACACCTGCC AGGGGAAATA ACACTGCC AGGGCAATACCGG	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGGCGGG GGAGAAAAG GGAGGAAAAG GGATCATTTT GGAAATTACC GGCTGGTAT GATCATCAGA TGATGCAGAT GATCATCAGA TGATGCAGA CAGTGCCAG CAGTGCCCC GAGCGACTGC CAGCTGCCAG CAGTCCCCC CAGCGACTTGGT CAGCTTTGGT CAGCTTTGGT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CAGCTTTGGTT CTCATGCGTC	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGC CAAGTTTGCC AAAGTTTGCC AAAGTTTGCC AAAGTTTGCATA GGAAATATGT AAAACCGGAC AGCAGTCGCC CGGTCGCCC CGGTCAGCA AGCAGTGACT CTGGCAAACCGGCC CGCTCACTGCC CTCTACAACC GCCACCTGGC CGGTCTGCC CCTCTACAACC GCCACCTGGC CGGCCCTCTCC CGGCCCCTCTCCC CGCCCCCCCC	ESAWKPLFYL HSIYATLYMD LNIYPKSRGG YPFFNALLLL RNGLVKDKRF (avian er; (avian er; (GCCGCCCAG GCCAACGCCAG ACGAGCAGC TGGCGCTGAG ACGAGCAGC ACGAGCAGCAG ACTACGAACA ACTACGAAAA TGAAGGAGGT TCTCAGCAA CAAGCTGTCC AAGTATCTG GCCACAACCA GCAAATTCG GCCACAGGTA TGAAGAATTCG GCCACCAGGTA TGAAGAAGT TGAAGAATTCG GCCACCAGGTA TGAAGAAGT TAAGAAGT TGAAGAAGT TGAAGAAGT TGAAGAAGT TGAAGAAGT TGAAGAAGAAGT TGAA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL \$1 ACCGGACGAC CAACCACCAC TCTTCGGGGA GGCTGCGCTC TAACAAGCTT TCTTTCCTTC AGTGGAGCGA TCCTATGCCA CCATGAGCA CCATGGAGCGA CCATGGAGCGA CCATGGAGCGA CCATGGAGC GGCTGCTGCAC CCAGGAGGAG GTGTGCTGCA CCAGGAGGAG TCCCCAGGAG GTGTGCTGCC CCAGGAGGAT TCCCCGTAAT TCCCCTAAT TCCCCTAAT TCCCCTAAT TCCCCCTAAT TCCCCCTAAT TCCCCCTAAT TCCCCCTAAT TCCCCC	120 180 240 300 leukemia 60 120 180 240 300 420 480 540 600 660 720 780 840 900 960 1020
5055606570	PETIDIPIFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac Coding sequence (GCCGCGCTGC AGGCCACCTC GCACGGCCC GCACGGCCC GCACGGCCC TGCCCGGCGG TGCCCGGCGG TTAAAGACCA ATTCCTTTGG TTAGCAGTCT TAATTACAGG GTGGAGAGCA GACTTCCAGA TGCTCCAGG GTGCACAGG GTGCACAGG GTGCACAGG TGCTCCAGGC TATTTGTGTACAGC TTATTGTGTACAGA GTGAACCCCG TATTTGTAGTA GTGAACCCCG TATTTGTGTAG GTGAACCCCG TATTTGTGTAG GTGAACCCCG TATTTGTGTAG GTGAACCCCG TATTTGTGTAG GTGAACCCCG TATTTGTGTAG GAGGAAGACA GAGGAAAGACG	TALRSAATAR PSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GTCAGCTCCGT GACCTTCCGG GTCAGGCTCT GACTTTGA TTGGGAATTT TCCAGGAGTTTTA TTCAGGAGT TTCAGGAGT ATACTAACTA AAATCCTGCA ACCACTGGG GCCCCGGGA GCTCCCCTGG GCCCCCGGG GCCCCCGGG GCCCCCGGG GCCCCCGGG GCCCCCGGG GCCCCCGGGA ACACTGCC AGGGCAAATA CAGATCACGC AGGGCAAATA	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC REYDTAEAQS growth faci /432 growth faci /432 ji in nm_00: 3819 CGAGGTAGCC GCCCGAGTCCC CCAGTATTGA GACGGCCGGG GGAGAAAAG GAACTGCCAG GGACATATTACC GGCTGGTTAT GGACATTTC GGACATTTC GGACATTGCAAT TGCCGCCGTT GGACATGCCAG GAACTGCCAG GAACTGCCAG CAAGTCCCCC GAGCGACTGC CCAGTTCGGT CCAGCTTTGGT CCAGCTTTGGT CCCCCTCTTGGT CTCGTGGTAGAAA	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCCGC CCGCCTCGCC CCGCGCGCGCGCGCGCCGCCTCGCC TATGTGCAGA GCAGTCAATTG AAAACCGGAC AGGAGTCAATTG AAAACCGGAC AGGAGTCACT AAGTTTGACC AAACTGACC CCGCTTCACAACC CCTCTACAACC CCCTCTACAACC CCCACCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCAGCCTGCG CCACCTGCG CCACCTGCAC CCACCTGCG CCACCTGCAC CCACCTCCACCTGCG CCACCTGCAC CCACCTGCAC CCACCTCCACCTCC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCTCCACC CCACCTCCACCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCCCGCCCAG GCCAAGGCCA CGGAGCGAGC CGAGCGAG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACACCGC CAACACCGC CAACACCGC CAACACGGC CAACACGGC CAACACGGC CAACACGGC CAACACGGC CAACACGGC CCAACACGC CCAACACGC CCAACACGC CCAACACGC CCAACACGC GCCATGGAC CAATGGAC CCAGTGGAC CCAGTGGAC AGACGAAGCC CCAGTTGAT TCCCCGTAAT CTATGAGATG CTCCCGGTAAT CTATGAGATG CTATGAGAG CTATGAGATG CTATGAGAG CTATGAGATG CTATGAGAG CTATGAGATG CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGAT CTATGAGAG CTATGAGA CTATGAGAG CTATGAGA CTATGAGAG CTATGAGA CTATGAGA CTATGAGAG CTATGAGA CTATGAGAG CTATGAGA CTATGAGAG CTATGAGA CTATGAGA CTATGAGAG CTATG	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 900 1020
50556065	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequence (GCCGCGCTGC AGGCCACTC GCAGGGCCC GCAGGGATGC TGCCGGGGGAGGATGC TGCCGGGGGAGGATGC TTAGCAGTTGG TTAGCAGTC AATTTCAGGA GTGGAGGAGCA GCTTCCAGA TGCTGGGGC GGGGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG GGGAAGCCCG TATGTGCGGC GGAATAGGGA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TE 10 epidermal nber: Hs.7: Ld Accessio: 11 GCCGGAGTCC CTGACTCCGT GACTCTCTG GACTCTCTG GACTTTTAA TTGGGATTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT AAAACCTGCA AAATCCTGCA ACACTTGGA TCCAGTGGG CAGGAGAGGA ACACTGGG GCCCCGGGA ACACTGGG GCCCCGGGA ACACTGACCT AGGGTACCT CAGGATCACCG GCCTCCGCAA TTGGTGAATA CAGATCACGG GCTCCGCAA TTGGTGAATT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 GAGGCTAGCC GCOGAGTCC CCAGTATTGA GAGGCCGGG GGAGGAAAAG AGATCATCAGA TGATCATCAGA TGATGCAGCCGTTAT GGAAATTACC GGCTGGTTAT CGAAATTGCAGA TGATCACAGA CGACTGCCAG GAACTGCCAG GAACTGCCAG CAGCTGCCAA CAGCTGCCAA CAGCTGCCAC CAGCTGCCAC CAGCTGCTGC CCCACTCATG CAGCTTGGT CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGAGAAGACT CAGCTTAGAGAAG CAGAGACTCACT CTCGTGCGTC CTCGTGCGTC CTCGTGAGAAGACT CAGCTTAAGAAG	LOPRDAAKMP AYLLOGSPYG ISDVQLEPTK SLRTVPDIPF LKPSKAEKPL OF receptor 5228 31 COGGCGCCCC CCGCCCCCC CCGCCCCCC CCGCGCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er) (GCCGGCCAG GCCAACGCCA GCCAACGCCA GCCAACGCCA AGAGGAGG TGGGGTGCT AAGGCACGAG ACAACCAGC ACTACGAAA TGAAGGAGGT TCTCAGCAA CATCAGCAC CAAACCTGC GCCACACCA ATGAAAA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GGCTGCGGCT TAACAAGCTC TCATTCGTC AGTGGAGCGA CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CATGTGCAAC GTGTGCTGCA GTGTGCTGCA TCCCCGTAGAA TCCCCGTAAT AGTGGAAGCC CCAGATGGAT TCCCCGTAAT AGTGTGAAT CTATGAGATG AGTGTGTAAC CTATGAGATG CTATGAGATG AGTGTGTAAC CTATGAGATG AGTGTAAC CTATGAGATG AGTGTGTAAC CTATGAGATG AGTGTGTAAC CTATGAGATG AGTGTAAC	120 180 240 300 1eukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1080 1140
5055606570	PETIDIPIPHO LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene nu Wheleic Ac: Coding sequence GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC TTAAAGAGTA ATTCCTTTGG GTGGAGAGCA ATGCTGCGGGT GGCTGCCAGG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG GTGCACAG GTGCACAG ACGTGCACAG ACGTGCACAG GGCTGCACAG ACGTGCACAG GGCTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG GGAACACG GGAATAGGTA TTCAAAAACT TTCAAAAACT	TALRSAATAR PSSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.77 Id Accession lence: 187 II GCCGGAGTCC CTGACTCCGG GCCCCTCGGG GTCGCCTCCGG GTCACTTTMA TTGGAATTT TCCAGGAGTCC AAAACCTGCA AAAACCTGCA ACCACTGGG GCCCCCGGG ACCACTGGG GCCCCCGGG ACACTGGC ACCACTTGGG GCCCCCGGGA ACACTGCCC AGGGCAAATA ACAGATCACGG GCCCCGGAA TTGGTGAATT GCACTTCCCC AGGGCAAATA ACAGATCACGG GCCTCCGCAA TTGGTGAATT GCACCTCCCCAT GCGCTCCCCAT GCGCTCCCCAT TGGTGAATT GCACCTCCCT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GCAGTATGA GACGCCGGG GCAGTATATACATTTT GGAAATTACC GGCTGGTAT GATCATCAGA TGATGCAAAT TGAGGCCGTG GGACATAGTC CAGCTGCCAA GAACTCCCC GAGCGCCTCATG CCCACTCATG CCCCACTCATG CCCCACTCATG CCCGTGCGTC CCCACTCATG CCCGTGCGTC CTGTGCGTC CTGTGCGTC CTGTGCGTC CTGTGAGAAG TAAAGACTCA CAGTTGGTA	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGGC TCCGGAGGCTCC TANGTTGCC TANGTGCAGA AGTCTCATTG GGAAATATGT AAAACCGAC CGGTTGACC AAGTGACTA AGTGACTAC CGGTCAGCA CGGTCAGCC CGGTCAGCC CGGTCAGCC CTCAGCA CGCTCGCG CGAGCCTGCG CGAGCCTGCG CGAGCCTGTG TGCCAAAGGGC CTCTCCATAA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er; (avian er; (accedence of control of cont	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGACGAC CCTGTGCAAC CTATGGGAGC TCCCCGTATGGAAC TCTATGAGATT TCCCCGTAAT TCCCCGTAAT TCCCCGTAAT TCTATGAGATG TATTAAACAC TATTAAACAC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 990 91020 1020 1020 1020 1140 1200 1260
5055606570	PETIDIPIPHO LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene nu Wheleic Ac: Coding sequence GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC GCACGGTGGC TTAAAGAGTA ATTCCTTTGG GTGGAGAGCA ATGCTGCGGGT GGCTGCCAGG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG GTGCACAG GTGCACAG ACGTGCACAG ACGTGCACAG GGCTGCACAG ACGTGCACAG GGCTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG ACGTGCACAG GGAACACG GGAATAGGTA TTCAAAAACT TTCAAAAACT	TALRSAATAR PSSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.77 Id Accession lence: 187 II GCCGGAGTCC CTGACTCCGG GCCCCTCGGG GTCGCCTCCGG GTCACTTTMA TTGGAATTT TCCAGGAGTCC AAAACCTGCA AAAACCTGCA ACCACTGGG GCCCCCGGG ACCACTGGG GCCCCCGGG ACACTGGC ACCACTTGGG GCCCCCGGGA ACACTGCCC AGGGCAAATA ACAGATCACGG GCCCCGGAA TTGGTGAATT GCACTTCCCC AGGGCAAATA ACAGATCACGG GCCTCCGCAA TTGGTGAATT GCACCTCCCCAT GCGCTCCCCAT GCGCTCCCCAT TGGTGAATT GCACCTCCCT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS growth faci /432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCAGTATTGA GACGCCGGG GCAGTATGA GACGCCGGG GCAGTATATACATTTT GGAAATTACC GGCTGGTAT GATCATCAGA TGATGCAAAT TGAGGCCGTG GGACATAGTC CAGCTGCCAA GAACTCCCC GAGCGCCTCATG CCCACTCATG CCCCACTCATG CCCCACTCATG CCCGTGCGTC CCCACTCATG CCCGTGCGTC CTGTGCGTC CTGTGCGTC CTGTGCGTC CTGTGAGAAG TAAAGACTCA CAGTTGGTA	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL FOR recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC TCGGGAGGC TCCGGAGGCTCC TANGTTGCC TANGTGCAGA AGTCTCATTG GGAAATATGT AAAACCGAC CGGTTGACC AAGTGACTA AGTGACTAC CGGTCAGCA CGGTCAGCC CGGTCAGCC CGGTCAGCC CTCAGCA CGCTCGCG CGAGCCTGCG CGAGCCTGCG CGAGCCTGTG TGCCAAAGGGC CTCTCCATAA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian er; (avian er; (accedence of control of cont	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGACGAC CCTGTGCAAC CTATGGGAGC TCCCCGTATGGAAC TCTATGAGATT TCCCCGTAAT TCCCCGTAAT TCCCCGTAAT TCTATGAGATG TATTAAACAC TATTAAACAC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1020 1140 1200 1260 1320
5055606570	ELLARGALGM FGTDYPFHD LHMVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequence (GACGGCTGC AGGCCACTC GCACGGCCC GCAGCGATGC TGCCCGGCGA AGGCAGTTGG GACGTGTTGG GACGTGTTGG GACTTCAGAA ATTCCTTTGG TTAACACC TAATTACAGG GGTGCACAG GACTTCCAGA GGCTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGGTGCACAG GGGTGCACAG GGGTGCACAG GGGTGCACAG GGGAACCCC TATTTGGTGA ACGTGCAGG GGGAACCCC TATTTGGTGA GAGGAAGACG GGAATAGGTA TTCAAAAAT TTCAAAAAT TTCAAAAAT TTCAAAAAT TTCAAAAT TTCAAAT TTCAAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAAT TTCAAT T	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession ence: 187' II GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GTCAGGAGTCC GTCAGGAGTCC TATCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TAAACTGCA TATCTAACTA AAATCCTGCA TCCAGTGGC ACCACTGGG GCCCCCGGGA ACACTGCG ACGAGTAGTA GCACTTCCA TGGGAATTA CAGATCACGC AGGGCAATTA CAGATCACGCA TGGTGAATT GCACTCCTC ACCTCCCA TGGTGAATT CCACTCCTC CACTCCTC CACTCC CACTCCTC CACTCC CACTC CACT CACTC CAC	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC REYDTAEAQS growth faci //432 growth faci //432 jt: NM_00: 3819 cqagctagcc GCCCGAGTACT GCAGTATTGA GACGCCGGG GGAGAAAAG GAACTGCCAG GGACTAGCAATTTC GGAATTTC GGCAGTGTCC GCCCAGTGTCC GCCCAGTGTCC GCCCAGTGTCC CAGCTGGTTA CAGCTGCCAG CAAGTCCCCC GAGCGACTGC CCCACTCATG CCACTCATG CCCCCTGGTT CTCCTGGTT CTCAGTTCC CAGTTGCGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTC CAGTTGCGGTT CAGCTTCGGTT CAGCTTCGGTT CAGTTGCGGTC CAGTTGCGGTT CAGCTTCGGTT CAGCTTCCGGTT CAGCTTCGGTT CAGCTTCGGTT CAGCTTCGGTT CAGCTTCCGGTT CAGCTTCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCTCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCGGTT CAGCTTCCCC CAGTTCCCGGTT CAGCTTCCCC CAGTTCCCC CAGTTCCC CAGTTCCCC CAGTTCCCC CAGTTCCCC CAGTTCCCC CAGTTCCC CAGTTCC CAGCTC CAGCTC CAGCTC CAGCTC CAGCTC CAGCT C	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO receptor CCGGCGCCCCC CCGCCCCCCCCCCCCCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GGCCGCCCAG GCCAACGCCA CGGAGCGAG CTGAGCGAACAC CGAACTACAC CCTCAACAC ACTACAACAC CTTCTCAGAA TGAAGAGTGTC AAATCATCTG GCCACACCA GCAAATCATCTG GCCACACCA GCAAATCATCTG GCCACACCA GCAAATCATCTG GCCACACCA GCAAATCATCTG GCCACACCA GCAAATCATCTG GCCACACCA GCAAATTCCAGCA AATCATCTG CTGACACCA CTGCCCCACA TGCAGGACCA CTGCCCCCAA TGCCCGCACA TGCCCGCACA TGCCCGCACA TGCCCGCACA TGCCCGCACA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA ACCGGACGAC CAACACACGC CAACACACGC TCTTCGGGGAC CAATAACTGT TCTTTCCTTC AGTGGAGCAC GCCCATGGAAC CATGTGCAAC CATGTGCAAC CATGTGCAC CATGTGCAC GTGTGCAAC CATGTGCAC CCAGGTGGAT CCAGTGGAT CCAGTGGAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCCGTAT TCCCGTAT TCCCCGTAT TCCCC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320
5055606570	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGSS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequity GCCGCGCTGC AGGCCACTC GCAGGGCCC GCAGGGATGC GCAGGGATGC TGCCGGGGGAGGATGC TTAAAGACC TTAAAGACC TTAGCATTGG TTAGCAGTC AATTTCCAGA TGCTGGGGT GTGGTGGAGGA ACGTGCAAGG GTGAGAGAC GCTGCAAGG GTGACCCC TATGTGGTGA GAGGAAGACC GGAATAGGTA TTCAAAAACT GACTCCTTCA GAGGAAATCA	TALRSAATAR PSSYPDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQVHELRDL TGQCGTGC TGCCTCCGG TCGGCGTCC TGCCTTCCGG TCGGCGTCC TGCACTTTTAA TTGGGGATTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTT TCCAGGAGTTTAA TAAAACCTGCA TATCTAACTA AAATCCTGCA TCCAGCTGG CAGGCACTGGG CAGGAGAGGA TCCAGCTGGG GCCCCGGGA ACACCTGCG ACACCTGGG GCCCCCGGGA ACACCTGCG TCCCCGGGA ACACCTGCGCAA TGGTGAATT CACATACTCC TCCAGGATTTT TCCAGGAGTTTT TCCAGTAGTTTT TCCACTCCAT TCCAGTAGTTTT TCCAGTAGTTTT TCCAGTAGTTTT TCCAGTAGTTTT TCCACTCCAT TCCAGGTTTT TCCAGGTTTT TCCAGTTTT TCCACTCCAT TCCAGGTTTT TCCAGTTTT TCCAGTTT TCCAGTTTT TCCAGTTT TCCAGTTTT TCCAGTTT TCCAGTTT TCCAGTT TCCAGTTT TCCAGTTT TCCAGTTT TCCAGTTT TCCAGTT TCC	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATSHC REYDTAEAQS GYOWTH fact 7432 1 %: NM_00: 3819 21 GAGGTAGCC GCOGAGTCC CCAGTATTGA GACGGCCGGG GGAGGAAAAG AGATCATCAGA TGATGATAAT GGCACTGTTAT GGAAATTGCCGCGTGT GGACATAGCC GAGCTGCCAA TGATGCCAC GAGCTGCCAA CAGCTGCCAA CAGCTGCCAC CAGCTGCCTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CAGCTGGCGTA TAAGAAAT CCTCGTGCGTC CAGCTGCGTC CTCGTGCGTC CTCGTGCGTC CAGCTGCGTAAGAAG CAGCTGCCGAC CAGTGCCGAT CCTCGTGCGTC CAGCTGCGTC CAGCTGCGTAAGAAG CAGTGCCGAT CCTCGTGCGTC CAGCTGCGTC CAGCTGCGTC CAGCTGCCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CTCGTGCGTC CCTCGTGCGTC CCTCGTGCTTCCAT	LOPRDAAKMP AYLLOGSPYG ISDVQLEPTK SLRTVPDIPF LKPSKAEKPL OF receptor CCGGCGCCCCC CCGCCTCGCC CCGCCTCGCC CTCGGGAGGCCC CTCAGCCTCC CTCAGCCTCC CTCAGCCTCC CTCAGCTCC AAAGTTTGCCA AGGAATATGT AAACCGGAC AGGTCAGCA AGGTCAGCA AGGTCAGCA CCGCTCCCCCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) (GCCGGCCAG GCCAACGCCA GCCAACGCCA GCCAACGCCA GCCAACGCCA GCCAACGAG AGAGGAGGT AGGGCACGAG AGAGGAGGT AGAGGAGT TGCAACAC ACTACGAAA TCAACCTGCC AAATCATCTG GCCACACCA TTCAGCAA TGAAGAAGT GCCACACGTA TGAAGAAGT TGAAGAAGT TGAAGAAGT TGCACGCAC ATGCACACGCA ATGCTACGAA ATGCTACGAA ATGCTACGAA ATGCTACGAA TGCCGGTGGC TGGGTATTCT ABABAGTG	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL STHRIHALAA CCAACCGC CCAACCGC CCACTGGGAC CCAGTGGAAC CCATGTGCAAC CATGTGCAAC GTGTGCTGCA TCACTGGAAC CCAGATGGAT TCCCGTAGT AGACGAAGCC CCAGATGGAT TCCCCGTAGT AGACGAAGCC AGATGGAT CTATGAGATG AGTUTGTAAC TATTAAACAC TATTAAGAGT GAAAACCGTA ATTTAGGGGT GAAAACCGTA CCACCCCACC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320
50 55 60 65 70 75	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YTVAFARKVL DNA SEQUENC Gene name: Unigene nu Nucleic Ac: Coding sequil GCCGCGCTGC GCACGGCTGC GCACGGCCCC GCAGGGATGC TGCCCGGCAA ACGCAGTTGG GAGGTGGTCC TTAAAGACA ATTCCTTTGG GTGGAGGGC GGCTGCACAG ACTTCCAGG GTGCACAG GACTTCCAGG GTGCACAG ACGTGCACAG ACGTCCTTCA AAGGAAAACT GACTCCTTCA AAGGAAATACAA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELRDL E 10 epidermal nber: Hs.77 Id Accession lence: 187- 11 GCCGGAGTCC GTCGGGGTCC GTCGGGGTCC GTCGGGGTCC GACCTCCGG GTCGGGGTCT GCACTTTTGA TTGGGAATTT TCCAGGGGTC AAACCTGCA ACACCTGCG ACCACCTGGG GCCCCCGGGA ACACCTGCCA ACGCTGCCG ACGCACTGCC AGGGCAAATA CAGATCACCG GCCCCCGGAA TTGGTGAATT GCACCTCCCAT CACATACTCC CAGGGTTTTA	LFRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci /432 GGAGGTAGCC GGAGGGAAATGC GGAGGGAATAGT GGACTGCTATG GGACTGCAG GAAGTCCCC GAGGGACTGC CAGCTGCTATG CAGCTTCATG CAGCTTCATG CAGCTTCATG CAGCTTTAGAAAG CATAGTGCAG TCTCTGGAT TCTCTGGAT CCTCTGGAT GCTGATTCAG GCTGATTCAG CATACTGGC CATACTGC CATACT	LOPRDAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC CCGGCTCCC GCAGCGCTCC AAAGTTTGCC AAAGTTTGCCA AGCAGTGACT AAGTGACA AGCAGTGACT AAGTGACA CCGCTCGCC CCAGCAGCCCCC CCAGCAACC CCTCTCCCACAC CCACAGGAAC CCCACAGGAAC CCCACAGGAAC CCCACAGGAAC CCTTGCCAACC CCACAGGAAC CCTCACAACC CCACAGGAAC CCCACAGGAAC CCTCACAACC CCACAGGAAC CCTTGCCAACC CCACAGGAAC CCTTGCCAACC CCACAGGAAC CCTCACAACC CCACAGGAAC CCTTGCCAACC CCACAGGAAC CCTCACAACC CCACAGGAAC CCTTGCCAACC CCACAGGAAC CCTCCAACAC CCACAGGAAC CCTCCAACAC CCACAACC CCACACC CCACAACC CCACACC CCACACC CCACACC CCACACC CCACACC CCACACC CCACA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGCA CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC CCTGTGCAAC TCCTTGCATG CAATAGGAGC TGCCCAGCAG GTGTGCTGCA AGACGAAGCAC CCCAGTGGAT TCCCGTAAT TCCCGTAAT TCCCGTAAT TCCCGTAAT TCTATGAGATG AGTTGTAAC TATTAAACAC ATTTAGGGTT GGAAACCTTCA GGAACCTCCAT	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1140 1200 1320 1380 1440 1500
5055606570	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequing GCCGCGCTGC AGGCCACCTC GCACGGCCCC GCAGCGATGC GCAGGGCCC GCAGCGATGC TGCCCGGCGA AGGCAGTTGG GAGGTGGTCC TAATATACACG GTGTAGAGACC GACTTCCAGA TGCTGGGGT TGCTCCGGGC GGCTGCACAG GCTTCACAG ACGTGCAAGG TGCTACAGG ACGTGCAAGG GTGAACCCCG TATTTGTGAA ACGCAGTT TTCAAAAACT TTCAAAAACT TCAAAAACT TGCTCACAG GCATTTGAGA AGGGAAATCA AGGAAATCA ACGCATTTGAGA ACGCTTTGAGA ACGCTTTTAGA ACGCATTTAGAAACT AAGGAAATCA GCCTTTTGAGA ACGCATTTAGGA ACGCTTTTAGAA ACGCATTTTAGGA ACCTTTTAGGA ACGCATTTTAGGA ACCCTTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTAGGA ACGCATTTTAGGA ACGCATTTTAGGA ACGCATTTAGGA ACGCATTTAGGA ACCCTTTTAGGA ACGCATTTAGGA ACGCATTAGGA ACGCATTTAGGA ACGCATTAGGA ACGCATTTAGAA ACGCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTTAGAA ACCCATTAGAA ACCCATTTAGAA ACCCATTAGAA ACCCATTAGA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession [COCCESSION CTGGCGTCC GTCGGCGTCC GACCTTCGG GTCTCGGGCTCT GCACTTTGA TTGGGAATTT TCCAGGAGGT TATCTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA ACACTGGG GCCCCGGGA ACACTGCG ACCACTGGG GCCTCCGGGA ACACTGCC AGGGTAATA CAGATCACGC GCGTCGCAA TTGGTGAATT GCACTTCCT CAGGGTTTT ACCTAGAATT ACCTAGAACT GCCTGAACT	LFRPLAKRCC GMAVPRDIAA VGILVLPLHD LKVLYATEHC REYDTAEAQS growth faci //432 i #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCCAGTATTGA GACGCCGGG GGAGAAAG GGACTAGCC GGCTGGTTAT GGAAATTACC GGCTGGTAT GGCACCTGGT GACCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCC CAGCTGCTAG CAGCTGCCAC CAGCTGCCAC CAGCTGCCAC CAGCTGCCAC CAGCTTGGT CTCCTGGTC CTCTAGGTC CTCTTAGGTAAGAG TAAAGACTCA CAGTTGCGAT CCTCTTGGT CTCTTGGTT CCTCTGGTT CCTCTGGT CCTCTTGGT CACCTTCT	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO receptor CCGGCGCCCCC CCGCCCCCCC CCGCCCCCCC CCGCGCCCCCC	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian erg 41 GCGCCGCCCAG GCCAACGCCA CGGAGCGAG GCCAACGCCA AGAGCGAG AGAGCATGAT AGAACATGTC AAATCATCTG GCCACACTGC AAATCATCTG GCCACACGC AAATCATCTG GCCACACGC AAATCATCTG GCCACACGC AAATCATCTG GCCACACGT ACACCCTGC AAATCATCTG GCCACACGT ACACCCTGC AAATCATCTG GCCACACGT ACACCTGC CCACCACGT ACACCCTGC AAATCATCTG GCCACACGT ACACCCTGC CCACCACGT ACACCC CCACCACGT ACACCC CCTCACGT ACACCC CCTCACGT ACACCC CCACGT CCCACGT CCCACGT CCCACGT AGACCACGT CCCCACGT ACACCC CCCACGT AAACCGGT CCCCACGT AAAACACGGC AACATGGT AAAACAGGAC AACATGGT AAAACAGGAC ACCCTCACACC ACCCCACACCA ACCCTCACACCA ACCCTCACACACA	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL /throblastic 51 ACCGGACGAC CAACCACCGC TCTTCGGGGAC GACTCTTCGGGGAC TCTTCGGGGAC TCTTTCGTTC AGTGGACGCA TCCTATGCC GCCCATGGAG CCAGTGGAAC CCAGTGGAAC CCAGTGGAAC CCAGTGGAAC CCAGTGGAT CTATGAGAGC TCCCCAGTGGAT CTATGAGAGC AGACGAAGCC CCAGTGGAT CTATGAGATC AGTTGTAAC ATTTAGGGGT GAAAACCTTA AGTTGTAACAC ATTTAGGGGT GGAACCCTTA GGTCTCCTT	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1320 1320 1340 1500
50 55 60 65 70 75	ELLARGALGH FGTDYPFHD LHHVVTLILI DLGCLSFGFS YTVAFARVL DNA SEQUENC Gene name: Unigene nui Wheleic Ac: Coding sequ 1 GCCGCGCTGC ACGCCACTG GCACGACGT GCACGGCCC GCACGATGG TGCCCGGCATGG TGCCCGGCATGG TGCCGGGGA ACGCATTGG GAGGTAGTCT TAAATTACAGG GTGGAGAGCA TTCCTTACAGG TTGGTGGAGGA ACGCTCCAGA ACGCACTC GACTCCAGA TGCTCCAGA TGCTCAGA TGCTCAGAG TGCTCAGAG CGTTTGAGAG GGAATAGGT TATTTAGTGT GACTCCT AATTTAAAAACT GACTCCTTAA ACGCAATACA GCCTTTGAGA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCCTCA GCAGTCGTCA GCAGTCCTCA GCAGTCGTCA GCAGTCCTCA GCAGTCGTCA GCAGTCCTCA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCCTCA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCGTCA GCAGTCCTCA GC	TALRSAATAR PSSYPDWTP VSSYAPRYHN WFWFRLYWFP TGQVHELKDL CE 10 epidermal nber: Hs.77 id Accession lence: 187 il GCCGGAGTCC GTCGGGGTCC CTGACTCCGG GACCCTCCGG GACCCTCCGG GTCGGGGTTCC GCACTTTTQA TTGGGAATTT TCCAGGAGTC AAAACCTGCA AAATCCTGCA ACCACTGGG ACCACTGGG ACACTGGG ACACTGCGG ACACTGCGG ACACTGCGG ACACTGCC AGGGCAATAT TGATGAATT GCACCTCCAT CACATACTCC CAGGGTTTTT ACCTAGAAAT TCCAGGAATT TCCAGGAATT TCACTGCATTTT ACCTAGAAAT TCCTGCAATT TACCTGAAAT TACCTGAAAT TACCTGAAAT TACCTGAAAT TAATTCAGG	LFRPLAKRCC GMAVPRDIAA VGILVLPHD LRVLYATSHC REYDTAEAQS growth faci 7432 1 #: NM_00: -3819 21 CGAGCTAGCC GCCCGAGTCC CCCGAGTCC GCCGGAGTCC CCAGTATTGA GAGCTACCGG GGAGAATAGCC GGCTGGTAT GATCATCAGA TGATGCAAT TGATGCAAT TGATGCAAT TGATGCAAT CAGCTGCCA GAGCATCCCCC CAGCTGCTA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTGCCAA CAGCTTCGGT CTCCTGGTC TCCTTGGT TCCTTGGT TCCTTGGT TCCTTGGT CAGCTTCTGGAT TCCTTGGAT TCCTTGGAT TCCTTGGAT CCTGCTCGAT CCTCTGGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTCTGGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTGCTCGAT CCTGCGCC AACATCCTTG	LOPRDAAKMP AYLLOGSFYG 1SDVQLEFTK SLRTVPDIPF ENFSKAEKPL FOR recepto: 5228 31 CCGGCGCCCCC CCGCCCCCCC CTCGGGAGGCTCCC AAAGTTTGCC AAAGTTTGCC AAAACCGGAC GCAATCACTC CTCATGG GGAAATATGT AAAACCGGCT AAGTGATCAC CCGTTCACAACC CCGTCACACC CTCTACAACC CCCACTGGC CTCACACC CCCACTGGC CTCACAACC CCACAGGAAC CTCCACTAC CCCACTGGC CTCACAACC CCACAGGAAC CTCCACTAC CCCACAGGAAC CTCTGGCCT CCACAGGAAC GCTTGGCCT AGGACCAAGC GCTTGGCCT TGCGCACTCC CCACAGGAAC CTCTACAACC TCTTGCCC CTCACATCC CCACAGGAAC CTCTACAACC CCTTGGCCT TGCGCACTCC CTCACATCC CCACAGGAAC CTCTACTCC CTCACTCC CTCTCCTTTGCC CTCTCTCTTTGCC CTCTCTCT	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLI RNGLVKÖKRF (avian er; (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACCACCGC TCTTCGGGGA GGCTGCGCTC TAACAAGCTC CAATAACTGT TCTTTCCTTC CAATAACTGT TCTTTCCTTC AGTGGAGCGA CCATGGAGC GCCATGAGA CCTGCCAGGAG GTGGCGCC CCAGGAG GTGGCGCC CAATAGCAC CATGCGAC CATGCGAC CATGCGAC CATGCGAC CATGCGAC TCCCCGTAAT TCCCGTAAT TCCCGTAAT TCCCGTAAT TCCCGTAAT TCTATGAGCC CATTAAGCAC CATTTAAGCGT GAAAACCGTA GGACCTCCAT GTTTCTCTT GATAAGTGAT ANTOGOAL	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1560
50 55 60 65 70 75	ELLARGALGM FGTDYPFHD LHHVVTLILI DLGCLSFGFS YIVAFARKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequit GCCGCCTGC GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGCTGC GCACGGTGTGC GCACGGCTGC GCACGGTTGG GGGTGGTCC TTAAAGACCA ATTCCTTTGG GTGGAGAGCA GACTTCCAGA AGCTTGCAGGG GGATTGCAGGG GGATTGCAGG GAGTCGTCA AGGGAATCCA AGGGAATCCA GCACTCTCA AGGGAATCCA GCACTCTTCA AAGGAATCA GCACTCTTCA AAGGAATCA GCACTCTTCA AAGGAATCTTA GCACTCTTCA AAACTGTTTG GAACACTGTTTA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WFWFRLYWF VSSYAPRYHN WFWFRLYWF TGQVHELRDL E 10 epidermal nber: Hs.77 id Accession lence: 187- 11 GCCGGAGTCC GTCGGCGTCC GTCGGGGTCC GTCGGGTCC GTCGGGTCT GACCTTCGG GTCCGTGGGTCT GACCTTCGG GTCGGGTCT GACTTTTGA TTGGGAATT TCCAGGGG GCCCCGGGG ACACCTGCC AGGGCAAATA CAGATCACG GCCTCCGCAA TTGGTGAATT GCACTTCCC CAGGGTTTT CACAGGTTTT CACAGGTTTT ACCTAGAAT GCCTGACAT TAATTTCAGG GGACCTCCCG GGGACTTTTAC TAATTTCAGG	LFRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci /432 GGAGGTAGCC GGAGGGAGAAA GGAGGACAGG GGACATAGTC GGCTGGTTAT GGACATAGTC CAGCTGCCAA GAACTGCCAG CAAGTCCCCC GAGGGACTGC CAGCTGCCAC CAGTGCCAG CAAGTCCCCC CAGTGCCAG CAAGTCCCCC CCCACTCATG CACCTTTAGAAA TAAGAAAA TCCTCTGGAT GCTGATTCAG GCTGATTCAG GCTGATTCAG GCTGATTCAG GCTGATTCAG CATACAGCAG AACATCCTTG AAAGAAAAA TCAGAAAAAA TCAGAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAA TCAGAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAA TCAGAAAAAA TCAGAAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAA TCAGAAAAAAA TCAGAAAAAA TCAGAAAAAAA TCAGAAAAAAAA TCAGAAAAAAAAAA	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL TO recepto: 5228 31 CCGGCGCCGC CCGCCTCGCC CCGCGCTCCCC ARAGTTTGCCC TATGTGCACA AGTCATCACC GCCACTGCC CCGCTCGCC CARAGGTGACT ARACTGACC AGTCACTGCC CCTCACACC GCCACTGCC CCACAGGAC CTCCACATGC AGTCACTGCC CCACAGGAC CTCCACATGC AGTCACTGCC CCACAGGAC CTTTCCACATC GCCACATGC GCTTGCCT AGGCTTGCC CCACAGGAC CTTTCCACATC AGGACCAGGC GCTTGCCT AGGCTTGCCT AGGACCAGC GCTTGCCT AGGACCAGC GCTTGCCTACA CTCCACATC AGGACCACAG AGGACCAAGC GCTTGCCTATA AGTTGCCTACACC CCACAGGAC CTTTGCCTACACC AGGACCAAGC GGATTACGCT TTGTGCTATA	ESAWKPLFYIL HSIYATLYMD LNIYPKSRGG YFFFNALLLL RNGLVKDKRF (avian erg (avian er	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL 51 ACCGGACGAC CAACACCGC CAACACCGC TCTTCGGGGA GGCTGCGCT TAACAAGCTC CAATAACTGT TCTTTCCTTC AGTGGAGGCA TCCTTGCATG CCATTAGGAG CCTGTGCAAC CCAGTGCAC TCCCAGCAG GTGTGCTGCA AGACGAAGCAC TCCCAGTAGA TCTATGAGATG TCTATGAGATG TATTAGAGTT AGTGTGAAC TATTAGAGTT AGTTTCTCTT CATTAGAGTT AGTTTCTCTT TCTTTCTTT TCTTTCTTT TCTTTCTTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT TATTAGAGTT AGACTCCAT TTTTTCTCTT TATTAGAGTT AGAACTGGAAA TTTTTTCTTTT TATTAGAGTT AGAACTGGAAA TTATTAGAGTT TATTAGAGTT TATTAGAGTT AAACTGGAAA TTATAACGGAAA TTATAACGGAAA TTATAACTGGAAA TTATAACTGAAA TTATAACTGAAAA TT	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1020 1020 1020 1020 1020 1140 1260 1320 1380 1440 1560 1560 1620
50 55 60 65 70 75	PETIDIPPEMD LHHVVTLILI DLGCLSFGS YIVAFAAKVL DNA SEQUENC Gene name: Unigene num Nucleic Ac: Coding sequil GCCGCGCTGC AGGCCACCTC GCACGGCCC GCAGCGATGC AGGCCACTTC GACGGCTGC AGGCTGCTGC AGGCTGTGG GAGGTGGTCC TTAAGACCC TTAAGACCC GTGCAAGG GTGCAAGG GTGCAAGG GTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GGTGCACAG GTGCACAG GGTGCACAG GCTTCAGAACC GCTTTCAGAAACT TTCAAAAACT TTCAAAAACT GCCTTTGAGA AGGAAATCA GCACTTTGAG AAACTGTTGA AAACTGTTGA AAACTGTTGA AAACTGTTGA TGCAAGGCCA GGAATGTGA AAACTGTTGA AAACTGTTGA TGCAAGGCCA TGCAGGCCA GAAGTGTGA AAACTGTTGA AAACTGTTGA TGCAAGGCCA TGCAGCCA TGCAGCCA TGCAGCACAG TGCAGCACAG TTTGAGAAACTGTTGA TTCAAAACTGTTGAGAACCGCTTTGAGA AAACTGTTGA TGCAAGGCCA TGCAGCCACAG TGCAGCACAG TGCAGCACAG TGCAGCACAG TTTTGAGAAACTGTTGAGAACCGCTTTGAGA AAACTGTTGAGAACTGTTGAGAACCGCTTTGAGAACTGTTGAGAACCGCAGAGCCA TGCAAGGCCA TGCAGCACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACACAC TGCACACAC TGCACACAC TGCACACAC TGCACACAC TGCACACAC TGCACACAC TGCACACAC TGCACACAC TCCACACAC TCCA	TALRSAATAR PRSVPTDWTP VSSYAPRYHN WEWFRLYWFP TGQVHELRDL EE 10 epidermal nber: Hs.7' Id Accession lence: 187' II GCCGGAGTCC GTCGGCGTCC CTGACTCCGT GACCTCCGG GTCGGCGTCC CTGACTCCGT GACCTTCGG TTGGGATTT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT TCCAGGAGTT TACTAACTA AAATCCTGCA TATCTAACTA AAATCCTGCA ACACTGGG GCCCCCGGGA ACACCTGGG GCCCCCGGGA ACACTGCC AGGGCAATTA CAGATCACGC CAGGTATTT CACATGCC CAGGTTTT ACCTAGAATT ACCTAGAAAT TAATTTCAGG GGACCTCCGG GCAGCTCCGGG TAATTTCAGG GGACCTCCGG GCAGCTCCGAA TTATTTCAGG GGACCTCCGG GCAGCTCCGAG TAATTTCAGG GCAGCTCCGGG CAGGCTCCGGG CAGCTCCGGG CAGGCTCCGGG CAGGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGCTCCGGG CAGGCTCCGGG CAGCTCCGCG CAGGCTCCGCG CAGGCTCCGCG CAGGCTCCGCG CAGGCT CAGGCT CAGGCTCCGG CAGCTCCGCG CAGGCT	LFRPLAKRCC GMAVPRDIAA VGILVLPHD LKVLYATSHC REYDTAEAQS growth faci //432 i #: NM_00: -3819 21 GAGGTAGCC GCCGAGTACC GCCGAGTACC GCAGTATTGA GAAATTACC GGCTGGTAT GGAAATTACC GGCTGGTAT TGATCATCAGA TGATCACAGA TGATCACCAG GAACTGCCAC GAGCGACTCC CAGCTGCTAG TGATCACCAG TGATCCCC GAGCGACTCC CAGCTGCTAG TAAGAAA TCATCAGAA TCCTCTGGT TCCTTCTGGT TCCTGCTCC TCCTGCATCCC CTCCTTGTAAAAAAT TCCTGAAAAACT TCAGAAAACC TCCTGCATCCC TCCTGGATCCC TCCTGGAAACC TCCTGCATCCC TCCTGGAAAACC TCCTGCATCCC TCCTGAAAAACC TCCTGCATCCC TCCTTCTGCAC TCCTTCTTCCC TCCTTCTTCCC TCCTTCTTCCC TCCTTCTT	LOPRDAAKMP AYLLOGSPYG 1SDVQLEFTK SLRTVPDIPF LKPSKAEKPL COF receptor 5228 31 CCGGCGCCCGC CCGCCCCGCC TCGGGAGAGC GCAGCCTCC TATGTGCAGA GTCCTCATTG AGAATATGT AAACCGGAC AGGGTCACC CTCAGCCTC CTCAGCCTC CTGCCTCATAG CCGCTCAGCC CTCAGCCTC CTGCCCCTCGC CTCCCAGACC CTCCCATAA CTGCCAGAGC CCACTGCG CGAGCCTGCG CGCACCTGCG CGCACCTGCG CGCACCTGCG CGCACCTGCG CGCACCTGCG CGCACCTGCG CGCACCTGCG CGAGCCAGCA CTCCCATAA CTCCACATCC CTACCAGAAC CTCCCATAA CTCCACATCC CTATCAGCAC CTTCTCATAA CTCCACATCC CTACCAGACC CTTCTCATAA CTCCACATCC CTTCTCATAA CTCCACATCC CTTCTCATAA CTCCACATCC CTTCTCATAA CTCCACATCC CTTCTCATAA CTTCCACATCC CTTCTCATAA AAAATTATAA AAAATTATAA AAAATTATAA AAAATTATAA AAAATTATAA AAAATTATAAA ATTGTCTCACATCC CTTCTCACTCACATCC CTTCTCTCATCA CTTCTCCTCATCA CTTCTCCTCATCA CTTCTCTCACTCA	ESAWKPLFYIL HSIYATLYMD LNIYFKSRGG YFFFNALLLL RNGLVKDKRF (avian er) (GCCGGCCAG GCCAACGCCA GGCAACGCCA CGGAGCGAG GCCAACGAG AGAGGATTATGA AGAGGATTATGA CCCTCAACAC TGCAACAC GCAACCA GCAACCA GCAACTGTCC AAATCATCTG GCCACAACCA GCAAATTACGAA TGAAGGAGT TGCAGGAA ATGATACGAC GCACACGTA TGAAGAGT TGCAGGAG TGCAGGTGC CCTCAAGGC CCTCACGTA AAACTGTC CCACCTCAACGC ACACCA GCAAATTCAGAA TGCAGGTGC CCTCAAGGA AGCTGTCC CACTCAAGGA ACCTCAAGGAC ACCTCAAGGAC ACCTCAAGGAC ACCTCAAGGAC ACCTCAAGGAC ACCTCAAGGAC ACCTCAAGGAC CCCTCAAGGAC CCCTCAAGGAC CCCTCAAGGAC CCCACACGTC CCAACACACA CCCTCAAGGAC CCCACACGTC CCACACGTC CCACACGTC CCCACACGTC CCCACACCAC CCCACACCAC CCCACACCAC CCCACACCAC	GSWSYSAYLL TWRKDSVVML SYHRLHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA LTLMNLYWPL STHREHALAA ACCGGACGAC CAACCACCGC TCTTCGGGGAC GGCTGGGAC TCTTCGGGGAC TCTTCGGGAC TCTTTCGTTC AGTGGAGCAT TCCTATGCAC GCCCATGGAG TCCATGGAAC CCAGGTGGAAT CCATGTGCAAC CCAGGTGGAT TCCCCGTAGT AGTGGAGC TCCCCAGGAGG TCCCCAGGAGGAT TCCCCGTAAT CTATGAGATG AATTTAGGGGT GAAAACCTTA GGTTTTCTCTT GATAAGTGAAA TGAAAACAGC	120 180 240 300 leukemia 60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1020 1140 1200 1320 1340 1200 1340 1200 1340 1200 1340 1200 1360
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	TGCAAGCTTC TO	CCACCCTCA	CCC2 ACCCAG	TTTCTCTCACA		CATACACTIC	1860
	CACCCAGAGT G						1920
	TGTATCCAGT G						
-	GTCATGGGAG A						
5	CTGTGCCATC C						
	AATGGGCCTA A						
	GTGGTGGCCC TO						
	CCCAACCAAG C						
10	GGCTCCGGTG O						2400
	AAAATTCCCG T						
	ATCCTCGATG A						
•	GGCATCTGCC T						
15	CTGGACTATG T GTGCAGATCG C						2640
	GCAGCCAGGA A						
	GCCAAACTGC T						
	AAGTGGATGG C						
20	AGCTACGGGG T						
20	CCTGCCAGCG A						3000
						CCAGCGCTAC	3060
						CAACTTCTAC	
						GTACCTCATC	
25	CCACAGCAGG G	CTTCTTCAG	CAGCCCCTCC	ACGTCACGGA	CTCCCCTCCT	GAGCTCTCTG	3300
	AGTGCAACCA C						3360
	CCCATCAAGG A						3420
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	CTCAACACTG 1	TCCAGCCCAC	CTGTGTCAAC	AGCAÇATTCG	ACAGCCCTGC	CCACTGGGCC	3660
	CAGAAAGGCA (3CCACCAAAT	TAGCCTGGAC	AACCCTGACT	ACCAGCAGGA	CTTCTTTCCC	3720
						AGAATACCTA	
35						AGTATGAGCC CCATCCCAAC	
55						ACACCGACTA	
						GTCTTCAAAC	
						TATTTAAADA	4080
40						TTTATTGATT	
40						TCTTCCAACA	
						ACTGTGAGCA GCTTCAAGGC	4260 4320
						GCCGGATCGG	
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45						TCCCCACGGT	
						GACTTGTTTG	
						CATGAAATCA GATTCATCAG	
						ACCECTTTTE	
50						GTCCTTTGGG	
						CCATCACCCC	
						TACTTCACTT	4920
						CAAACCCCCT	
55						AGCACTTACA GAGTAGTGTG	
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						TGGAAGATTG	
	GAAGATTCAG	CTAGTTAGGA	GCCCATTTT	TOTANTOTO	G TGTGTGCCC	GTAACCTGAC	5280
60						T ATCCACCCA	
00						TATGTTCAGT	
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	ATATTCATTT				. 010100110		3320
65	Protein sec						
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	Signal sequ		NP_005219				
70			L domain [S	7-190. 372-	4921		
			B: 646-66B				
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75						S LORMFNINCEV	
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						S DFLSNMSMDF D CCHNQCAAGO	
	TGPRESDCLV	CREPRDEAT	C KDTCPPLML	Y NPTTYOMOV	N PEGKYSFOL	T CVKKCPRNYV	300
00						S INATNIKHPK	
80	nctsisgdlh	ILPVAFRGD	S PTHTPPLDP	G ELDIFKIAK	E ITGFLLIQA	W PENRTOLHAF	420
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	rgregoktki t.t.gg=ppp===	TENEGENSC	K ATGOVCHAL	C BPEGCWGPE	F KUCVSCRNV	S RGRECVDKCK H CVKTCPAGVK	540
						H CVKTCPAGVM M VGALLLLLVV	

5	ALGIGLPMRR RHIVRKRILR RILQERELVE PLTPSGEAPN QALLRILKET EPKKIKVIGS GAFGTVYKGL WIPEGEKVWI PVAIKSLREA TSYKANKEIL DEAYVMASVD NPHVCRLLGI 780 CLTGTVQLIT QLMPFSCLLD YVREHKDNIG SQYLLMNCVQ IAKGMYLED RRLVWRDLAA RNVLVKTPQH VKITDFGLAK LLGAEEKEYH AEGGKVPIKM MALESILHRI YTHQSDWSY 900 GVTVWELMTF GSKPYDGIPA SEISSILEKG ERLPQPPICT IDVYMIMVKC WHIDADSRPK 960 PRELIIEFSK MARDPQRYLV IQGDERMHLP SPTDSNFYRA LMDEEDMDDV VDADEYLIPQ 1020 QGFFSSPSTS RTPLLSSLSA TENNSTVACI DRNGLQSCPI KEDSFLQRYS SDPTGALTED 1080 SIDDTFLPVP EYINQSVPKR PAGSVQNFVY ENQPLNPAPS RDPHYQDPHS TAVGNPEYLN 1140 TVQPTCVNST FDSFAHWAQK GSHQISLDNP DYQQDFFPKE AKPNGIFKGS TAENAEYLKV 1200	
15	DNA sequence 11 Gens name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Probeset Accession #: AW245805 Nucleic Acid Accession #: NM_003277 Coding sequence: 121-777	
20	1 11 21 31 41 51 1 AGGGGACTGG GGCCAAAGG CACCAGGGC CGCCCAGGGC GGCCAAAGG CACCAGGCC CGCCCAGGGC AAGGGACTCG GGCTTCTGG GGCTTCTGGG CTCCTAGCC CACCGTTCGA GATCCTGGGC CTGGTGCTT GCCTGTGGG CTGGGGGGT 180	
25	CREATCCTGG CGTGCGGGCT GCCCATGTGG CAGGTGACCO CCTTCCTGGA CCACAACATC GTGACGGCGC AGACCACCTG GAAGGGCCTG TGGATGTCGT GCGTGGTGCA GAGCACCGGG GACACACGAGCT GCAAAGTGTA CGACTCGGTG CTGGCTCTCA GCACCAGAGT GCAGGCGGCG CGGGCGCTCA CCTGGAGGGC CGTGCTGCTG GCGTCTGGTTG CACCCTGCGC GGCGGCGCAGT GCACCACCTG CGTGCCCCCG GGCCCGGCCA AGGCGCGTGT GGCCCTCACC GGAGGCGTGC TCTACCTGTT TTGGCGGCTG TGCCACTCTG CTGGTTCGCC 540	
30	GANGGOTGC TCTACCTGTT TTGGGGGCTG CTGGGSCTGG TGCCACTCTG CTGGTTCGCC 540 AACATTGTCG TCCGCAGAT TTACGACCGG TCTGTGCCCG TGTCGCAGAA GTACGAGCTG 600 GGCGCAGCGC TGTACATCGG CTGGGCCGCC ACCCCGCTGC TCATGGTAGCG CGGCTGCCTC 660 TTGTGCTGCG GGCGCCTGGGT CTGCACCGGC CGTCCCGACC TCAGCTTCCC CGTGAAGTAC 720 TCAGGGCCCG GGCGCCCCAC GGCCACCGC GACTACGCCTC AGAGGACTA CGTCTGAAGGG 780 OGCTGGGGCAC CGCCTGCCAGC CACACCGCC CACGCCTCC AGAGGCTTCG ATAAGCCTGG 840	
35	GGAGCCCCGC ATGGACCGCG GCTTCCGCCG GGTAGCGCG CGCGAGGCT CCTCGGAACG 900 TCCGGCTCTG CGCCCCTCGA ATCCGCCCC GCAGCTGACC 960 TTCTCCTGCC ACTAGCCCGG CCCTGCCCTT AACAGACGGA ATGAAGTTTC CTTTTCTGTG 1020 CGCGGCGCTG TTTCCATAGG CAGAGCGGGT GTCAGACTGA GGATTTCGCT TCCCCTCCAA 1080 GACGCTGGGG GTCTTGGCTG CTGCCTTACT TCCCAGAGGC TCCTGCTGAC TTCGGAGGGG 1140	
40	CGGATGCAGA GCCCGGGGCC CCCACCGGAA GATGTGTACA GCTGGTCTTT ACTCCATCGG 1200 CAGGCCCGAG CCCAGGGACC AGTGACTTGG CCTGGACCTC CCGGTCTCAC TCCAGCATCT 1260 CCCCAGGCAA GGCTTGTGGG CACCGGAGCT TGAGAGAGGG CGGGAGTGGG AAGGCTAAGA 1320 ATCTGCTTAG	
45		
	<u>Protein sequence 11</u> Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession #: NP_003268)
50	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903)
55	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession \$: NP_003268 Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane	
55 60	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession \$: NP_003268 Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane 1 11 21 31 41 51	
55	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession #: NP_003268 Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane 1 11 21 31 41 51 MSSAALEILG LVLCLVGWGG LILACGLPHW VYTAFLDHNI VYTAGTTWKGL WMSCVVQSTG 60 HMQCKVYDSV LALSTEVQNA RALTVSAVLL AFVALFVTLA GAQCTTCVAP GPAKARVALT 120 GGVLYLPCGL LALVPLCWFA NIVVREPYDP SVPVSQKYEL GAALYIGWAA TALLMVGGCL 180 LCCGAWVCTG RPDLSFPVKY SAPRRFTATG DYDKKNYV DNA sequence 12 Gene name: vascular endothelial junction-associated molecule Unigene number: Hs.54650 Probeset Accession #: AA410345 Nucleic Acid Accession #: AF255910 Coding sequence: 241-1137 1 12 131 41 51 TTACCATTGT GTTGGGCTGC GAGAAGAGGGA ACCGGCCTCT TGGCAGCCAG 60	
55 60	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession %: NP_003268 Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane 1 11 21 31 41 51	,
55 60 65	Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome) Unigene number: Hs.110903 Protein Accession #: NP_003268 Signal sequence: none found Pfam domain: PMP22 Claudin [4-181] Transmembrane domains: 5-27, 74-96, 123-145, 164-186 Cellular Localization: plasma membrane 1 11 21 31 41 51	

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Gene name: Vascular endothelial junction-associated molecule
Unigene number: Hs.54650
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                      Unique number: HS.54050
Protein Accession S: AAF81223
Signal sequence: 1-22
Igc2 domain: 41-116, 146-221
Transmembrane domains: 239-261
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                       Cellular Localization:
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LEWKKLGREV SFVYYQQTLQ GDFKNRAEMI DFNIRIKNVT RSDAGKYRCE VSAPSEQGQN
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                        IAAVVVVALV ISVCGLGVCY AQRKGYFSKE TSFQKENSSS KATTMSENDF KHTKSFII
25
                       DNA sequence 13
                        Gene name: solute carrier family 11 (proton-coupled divalent metal ion
                       Unigene number: Hs.182611
Probeset Accession #: D50402
Nucleic Acid Accession #: NM_000578
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                        Coding sequence: 1-1653
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CCTCTACTTCG TGGTCAGCTA TCTGGCCCAGC CTGCCCACC CTGCCTACT CGGCCTTGCA
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GAAGAGGACC ACAAAGGGGA GACCTGTGGC TAG
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                        Protein sequence 13
Gene name: solute
                       Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 Unigene number: Hs.182611
65
                        Protein Accession #: NP_000569
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Transmembrane domains: 58-80, 88-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523

Cellular Localization: plasma membrane

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                        LYPVVSYLPS LPHPAYPGLA ALLAAAYLGL STYLVWTCCL AHGATPLAHS SHHHPLYGLL
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                      DNA sequence 14
                       Gene name: solute carrier family 7 (cationic amino acid transporter, y+
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Unigene number: Hs.184601
Probeset Accession #: AP104032
Nucleic Acid Accession #: NM_003486
Coding sequence: 53-1576
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CCTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT
TATCGGCTCG GGCATCATCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG
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CGCGGAGCTC GGCACCACCA TCCCAAATC CGGCGCGCAC TACGCCTACA TGCTGGAGGT
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TGTGCTGGCA TTATCAGCG GCCTCTTTCCT CTACAGGAG TGGAATTACT TGGGGAACAT
CTGTGCTGGCA TTATCAGCG GCCTCTTTCC CTACAGAAA CCTGCCCCTG GCCATCATCA TGAATTTCCT
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TGAATTTCCT
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                                Protein sequence 14
                                Gene name: solute carrier family 7 (cationic amino acid transporter, y+
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Unigene number: Hs.184601
Protein Accession #: NP_003477
Pfam domain: as permeases [46-481]
Transmembrane domains: 52-74, 82-104, 120-142, 145-167, 169-191, 200-222, 237-259, 275-297, 323-345, 371-393,
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Cellular Localization: plasma membrane
1 11 21 31
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                                DNA sequence 15
                                Gene name: Glutamate receptor subunit
Unigene number: Hs.249141
                                Nucleic Acid Accession #:
Coding sequence: 1-2943
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	Unigene number: Hs.249141	
	Protein Accession #: AAB22591	
	Signal sequence: 1-27	
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33	Transmembrane domains: 297-319, 544-566, 624-646, 803-825	
	Cellular Localization: plasma membrane 1 11 21 31 41 51	
	1 11 21 31 41 51	
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	1.61	

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	CCATGTTTGG	CTGGAACATG	AAACTGACCT	CAGAGTACCA	CAGAAATGTC .	ACCTICCTII	1260
	CATGCCAATT	TGTTTCCGTC	ATGAGAATGG .	ACTACATGGT .	DDADTTDATA	TTCCTCACCT	1320
	GGATTTTCAT	CCCCCTGGTT	GTCATGTGCG	CCATCTATCT	TGACATCTTT	TACATCATTC	1380
5	GGAACAAACT	CAGTCTGAAC	TTATCTAACT	CCAAAGAGAC .	AGGTGCATTT	TATGGACGGG	1440
3	AGTTCAAGAC	GGCTAAGTCC	TTGTTTCTGG '	TTCTTTTCTT	GTTTGCTCTG	TCATGGCTGC	1500
	CTTTATCTAT	CATCAACTGC .	ATCATCTACT '	TTAATGGTGA	GGTACCACAG	CHTGTGCTGT	1560
	ACATGGGCAT	CCTGCTGTCC	CATGCCAACT	CCATGATGAA	CCCTATOGTC	TATGCCTATA	1620
	AAATAAAGAA	GTTCAAGGAA .	ACCTACCTTT	TGATCCTCAA	AGCCTGTGTG	GTCTGCCATC	1680
	CCTCTGATTC	TTTGGACACA	AGCATTGAGA	AGAATTCTGA	GTAGTTATCC	ATCAGAGATG	1740
10	ACTCTGTCTC .	ATTGACCTTC	ACATTYCYCA	TCABCABACA	CHROCOCC		
	GGCCAAGGGA	TTTTTACATC	CTTCATTACT.	TOTACTORO	TOTOLOGGE	TOTALOCCIO	1800
	CCCAATTATA	TOTOCOCO	CITONITUCI	TCCACIGAGG	COCCACCATC	TCCAGTGCTC	1860
	ALCOUNT TUTY	TTCACCCCCCCC	ICCACIACIC	TOTTOCICOA	CITCATTTTT	CCTTTGTCCT	1920
	TTCTCTCTAA	TICAGIGITI	TGGAGGCCTG	ACTTGGGGAC	AACGTATTAT	TGATATTATT	1980
15	GICTOTITIC	CITCTTCCCA	ATAGAAGAAT	aagtcatgga	GCCTGAAGGG	TGCCTAGTTG	2040
13	ACTTACTGAC	AAAAGGCTCT	AGTTGGGCTG	AACATGTGTG	TGGTGGTGAC	TCATTTCCAT	2100
	GCCATTGTGG	AATTGAGCAG	AGAACCTGCT	CTCGGAGGAT	GCCTAGAAGA	TOTTGGGAAC	2160
	agaagaaata	AACTGAGTTT	aagggggact	TAAACTGCTG	AATTCACCTG	TETTOTADDT	2220
	TGAGTAAATA	AAAGCTAATA	G				
20							
20	Protein seg	uence 16					
	Gene name:	adenosine	A3 receptor				
	Unigene num	ber: Hs.25	8				
	Protein Acc						
	Signal sequ						
25	Pfam domain						
	Transmembra			-22 06 100	100 150		
			12-34, 50	-/2, 80-108	1, 120-150,	179-201, 22	9-251
	Cerrarat IV		plasma_me				
	t	11	21	31	41	51	
30	Montro	1	<u></u>	<u></u>	1	1	
20	MPNNSTALSL	ANVTYITMBI	PIGLCAIVGN	ATAICAAKTM	PSLQTTTPYP	IVSLALADIA	60
	VGVLVMPLAI	VVSLGITIHP	YSCLFMTCLL	Lifthasims	LLAIAVDRYL	RVKLTVRYKR	120
	VTTHRRIWLA	LGLCWLVSFL	Voltempown	MKLTSEYHRN	VTFLSCOFVS	VMRMDYMVYP	180
	spltwipipl	VVMCAIYLDI	PYIIRNKLSL	NLSNSKETGA	FYGREFKTAK	SLFLVLFLFA	240
2.5	LSWLPLSIIN	CITYFNGEVP	QLVLYMGILL	SHANSMMNPI	VYAYKIKKFK	BTYLLILKAC	300
35	VVCHPSDSLD	TSIEKNSE					
•	DNA sequence	e 17					
	Gene name:	glypican 1					
		mber: Ha.26					
40		cession #:					
			#: NM 002	רפת			
		1ence: 222.	.1898				
		lence: 222-		21	43		
	1	lence: 222- 11 !	·1898 21	31	41	51	
45	1	11	21 	1	ŀ	1	
45	1 GGCTGCCCGA	11 GCGAGCGTTC	21 GGACCTCGCA	 ccccccccccc			60
45	1 GGCTGCCCGA GGCTTTTGTT	11 GCGAGCGTTC GTCTCCGCCT	21 GGACCTCGCA CCTCGGCCGC	CCCCGCGCGC CGCCGCCTCT	CCCGCGCCGC GGACCGCGAG	COCCECCCCC COCCECCCCCCCCCCCCCCCCCCCCCCC	60 120
45	1 GGCTGCCCGA GGCTTTTGTT CGGGACCTTG	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT	21 GGACCTCGCA CCTCGGCCGC TCGCGGGCGG	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA	CCCGCGCCGC GGACCGCGAG GGACCCGGCC	CGCCGCCGCC CCGCGCGCGC	
45	GGCTGCCCGA GGCTTTTGTT CGGGACCTTG AGAGGCGCGG	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGGTGGCC	21 GGACCTCGCA CCTCGGCCGC TCGCGGGCGG GGGGGCGCCG	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC	CCCGCGCCGC GGACCGCGAG GGACCGGGCC CATGGAGCTC	CGCCGCGCC CCGCGCGCC AGGATCCGAG CGGGCCCGAG	120
	GGCTGCCCGA GGCTTTTGTT CGGGACCTTG AGAGGCGCGG GCTGGTGGCT	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGGTGGCC GCTATGTGCG	21 GGACCTCGCA CCTCGGCCGC TCGCGGGCGC GGGGGCGCCG GCCGCAGCGC	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGCGCCGCC CCGCGCGCGC AGGATCCGAG CGGGCCCGAG	120 180
45 50	1 GGCTGCCCGA GGCTTTTGTT CGGGACCCTG AGAGGCCCG GCTGGTGGCT GCAAGAGCCG	11 GCGAGCGTTC GTCTCCCCT GCTCTGCCCT GCGGGTGGCC GCTATGTGCG GAGCTGCGGC	21 GGACCTCGCA CCTCGGCCGC TCGCGGCGGC GGGGGCGCCG GCGCAGCGC GAGGTCCGCC	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG AGATCTACCG	CCCGCGCCGC GGACCGCGAG GGACCGGGCC CATGGAGCTC CGCCGCGGG AGCCAAGGGC	CGCCGCCGCC CCGCGCGCGC AGGATCCGAG CGGCCCGAG GACCCGGCCA TTCAGCCTGA	120 180 240 300
	1 GGCTGCCCGA GGCTTTTGTT CGGGACCTTG AGAGGCGCG GCTAGTGGCT GCAAGAGCCG GCGACGTGCC	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC CCAGGCCGAG	21 GGACCTOGCA CCTOGGCGGC TCGCGGGCGG GGGGGCCCG GCCGCAGCGC GAGGTCCGCC ATCTCGGGTG	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG AGATCTACCG AGCACCTGCG	CCCGCGCCGC GGACCGCGAG GGACCGGGC CATGGAGCTC CGCCGCGGG AGCCAAGGGC GATCTTTCCC	CGCCGCCGCC CCGCGCGCGC AGGATCCGAG CGGGCCCGAG GACCCGCCCA TTCAGGCTCACA	120 180 240 300 360
	1 GGCTGCCCGA GGCTTTTGTT CGGGACCTTG AGAGGCGCG GCTAGTGGCT GCAAGAGCCG GCGACGTGCC	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC CCAGGCCGAG	21 GGACCTOGCA CCTOGGCGGC TCGCGGGCGG GGGGGCCCG GCCGCAGCGC GAGGTCCGCC ATCTCGGGTG	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG AGATCTACCG AGCACCTGCG	CCCGCGCCGC GGACCGCGAG GGACCGGGC CATGGAGCTC CGCCGCGGG AGCCAAGGGC GATCTTTCCC	CGCCGCCGCC CCGCGCGCGC AGGATCCGAG CGGGCCCGAG GACCCGCCCA TTCAGGCTCACA	120 180 240 300 360 420
	GGCTGCCGA GGCTTTGTT CGGGACCTTG AGAGGCGCG GCTGGTGGCT GCAAGAGCCC GCGACGTGCC CCTGCTGCAC	11 GCGAGCGTTC GCTCTGCCCT GCGGGTGGCC GCTATGTGCG GAGCTGCGGC CCAGGCGGAG CCAGGCGAGATG	21 GGACCTCGCA CCTCGGCGGC TCGCGGGCGG GGGGGCGCCG GCGCAGCGC GAGGTCCGC ATCTCGGGTG GAGGAGAACC	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG AGATCTACCG AGCACCTGCG TGGCCAACCG	CCCGCGCCGC GGACCGCGAG GGACCGGGCC CATGGAGCTC CGCCCGCGGG AGCCAAGGGC AGCCATGCC CAGCCATGCC	CGCCGCCGC CCGCGCGC CCGCGCGCG AGGATCCGAG CGGGCCCGAG GACCCGGCCA TTCAGCCTGA CAGGGCTACA GAGCTGGAGA	120 180 240 300 360 420 480
50	1 	11 GGGAGCGTTC GTCTCCGCCT GCTGTGCCC GCTGTGGCC GAGCTGCGG CAGGCGGAG CAGCGGAGTG GGACAGCAGC	21 GGACCTCGCA CCTCGGCCGC TCGCGGGCGCCC GCCGCAGCGC GCCGCAGCGC GCGCTAGCGC ATCTCGGGTG GAGGAGACC CGCGTCCTGC	CCCCGCGCGC CGCCGCCTCT GAACTGCGCA CCGGCCCGC TGGTCGCCTG AGATCTACCG AGCACCTGC TGGCCAACCG	CCCGCGCCGC GGACCGGGG GGACCGGGC CATGGAGCTC CGCCGCGGG AGCCAAGGGC GATCTGTCCC CAGCCATGCC TGCCACCAGG	CGCCGCCGC CGCGCGCCC CGCGCGCAG CGGGCCCAAG GACCCGGCAA TTCAGCCTGA CAGGGCTACA GAGCTGGAGA CTGCGCAGCT	120 180 240 300 360 420 480 540
50	1 	11 GCGAGCGTTC GCTCTGCCCT GCTGTGCCCT GCTATGTGCG GAGCTGCGGC CAGGCGGAG CAGCAGCAGC CAGCAGCAGC CTTCCAGCAC	21 GGACCTCGCA CCTCGGCCGC TCGCGGCCGG GGGGGCCCG GCGCAGCGC GAGGTCCGCC ATCTCGGGTG GAGGAGAACC CGCGTCCTGC CTGCTGAACG	CCCCGGGGGG CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCTGCA AGACTACGG AGCACCTGCG AGCCATGCT AGCCCATGCT AGCCCATGCT	CCCGCGCCGC GGACCGCAG GGACCGCAGG GGACCGCGGGG CATCGGCCACCAGGG AGCCAACGGC CAGCCATGCC TGCCACCCAG GACCTGCAG	COCACCTTCC	120 180 240 300 360 420 480 540
	1 	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGGTGGCC GCTATGTGCG GAGCTGCGGC CAGCGAGATG GGACAGCAGC CTTCCAGCAG CTTCCAGCAG CGGAGAGCTG	21 GGACCTOGCA CCTCGGCGGC CCGCAGCGC GCGCAGCGC GAGGTCCGCC GAGGAGAACC CGGTCCTGC CTGCTGAACC TACACGCAGA	CCCCGGGGGG CGCCGCCTCT GAACTGCGCA CCGGCCCCGC TGGTCGCCTG AGATCTACGG AGCACCTGCG TGGCCAACCG AGGCCATGCT ACTCGGAGGG	CCCGCGCCGC GGACCGCGAG GGACCGGGGC CATGGAGCTC CGCCGCGGGG AGCCAAGGGC GATCTGTCCC CAGCCATGCC TGCCACCAG GACGCTGCAG GACGCTGCAG	COCCOCCCC COCCCCCCCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 540 600
50	1 	11 GCGAGCGTTC GTCTCCGCCT GCTCTGCCCT GCGGGTGGCC GCTATGTGCG GAGCGGGAG CAGCGAGAGCAGC CGACAGCAGC CTTCCAGCAC CGGAGAGCTG GTACTACCGC	21 GGACCTOGCA CCTOGCOGC TCGCGGCGG GGGGGCGCCG GCGCTCAGCGC ATCTCGGGTG GAGGAGAACC CGCGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC	CCCCGGGGGG CGCCGCCTCT GAACTGCGCA CCGGCCCGGC	CCCGCGCCGC GGACCGCGAG GGACCCGGGC CATGGAGCTC CGCCCGCGGG AGCCAAGGGC GATCTGTCCC CAGCCATGCC TGCCACCAG GACGCTGCAG CTCCCGGGCC	CGCCGCCGCC CCGCCGCGCC AGGATCCGAG CGGCCCGAG GACCCGGCCA TTCAGCCTGA CAGGCTGAGA CTGCGCAGCT GCCACCTTCC CTGTACTCAG	120 180 240 300 360 420 480 540 600 660 720
50	1 	11 GCGAGCGTTC GTCTCCCCT GCTGTGCCCT GCGGGTGGCC GCGATGCGG GACAGCAGC CAGGCGGAG GGCAGCAGCAGC GGACAGCAGC GGCAGCAGCAGC GGTCCAGCAC GGTCCAGCAC	21 GGACCTOGCA CCTOGGCGC CCTOGGGGGG GGGGGCGCG GCGCAGCGC ATCTCGGGTC GAGGAGAACC CGCGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC	CCCCGGGGGG CGCCGCCTCT GAACTGCGCA CCGCCCCCGC TGGTCGCCTG AGATCTACGG AGCACTGCG TGGCCAACCG AGGCCATGCT ACTCGGAGGG ACGCGAGGGG ACGCGAGGGC ACGCGAGGGG ACGCGAGGGGACCTGGA AGCTGCAACCTGGA	CCCGCGCCGC GGACCGCGAG GGACCGGGGG CGCCGCGGGGG AGCCAAGGGC GATCTGTCCC CAGCCATGCC TGCCACCAG GACGTGCAG CATCCGGGAC CAGCCAGGAC CTTCCGGGAC GGAGACGCTGC	CGCCGCCGCCCCCCCGCGCGCCGCGCCGAGGCCCGAGGCCCAACACCCCCC	120 180 240 300 360 420 480 540 660 720 780
50	1 	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGATGTGCG GAGCTGCGGC CAGCGAGAGT GGACAGCAGC CTCCAGCAC GGGAGAGCTG GTACTACCGG GCTGAGCGGC	21 GGACCTCGCA CCTCGCCGC CCTCGCCGC GCGGGCGCCC GCGCAGCGC ATCTCGCGTG GAGGTACCGC ATCTCGGGTG GGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AGCAGCCCAACC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGGGGCGG GGACCGGGG GGACCGGGC CATGGAGCTC CGCCGGGGG AGCCAAGGG GATCTGTCCC CAGCCATGCC TGCCACCCAG GAGCTGCAG GAGCTGCAG GAGCTGCTG CCAGCTGCTG	CGCCGCCGCC CCGCGCGCCC AGGATCCGAG CGGGCCCGAG TTCAGCCTGA CAGGGCTACA CAGGCTACA CTGCCAGCT GCCACCTTCC CTGTACTCAG CCGCAGTTCT CTGCCTGATC CTGCCTGATC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	1 	11 GCGAGCGTTC GTCTCCCCT GCGGTGGCC GCTGTGCCCT GCGGTGGCC GCTATGTGCG GAGCTGCGG CAGCCGAG CAGCCGAG CAGCCGAG CTTCCAGCAC CGAGAGCTG GTACTACCGC GTCTGAGCGC CTCCTGAGCGC CTCCTGAGCGC CTCCTGAGCGC CTCCTGAGCGC CTCCTGAGCGC	21 GGACCTOGCA CCTOGCOGC CCTOGCOGC GGGGGCGCCG GCGGTCAGCGC AACTCCGGTG GAGGAAACC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCG AAGCAGGCGC	CCCCGGGGG CGGCGCTCT GAACTGGGA CCGCCCGG TGGTCGCTG AGACCTGGA AGACCTGGA AGGCCATGCT ACTCGGAGGG ACGCGGGGGG AGGCGCTGGA AGCTGGA AGCTGGA AGCTGGA AGCTGGA AGCTGGA AGCTGGA AGCTGGA	CCCGCGCCGC GGACCGGGG GGACCGGGG ATTGAGGCT CACCGCGGG GATCTGTCC CAGCATGCA GACCATGCA GACCATGCA GACCATGCA GACCATGCA GACCTTCCGGAC CCAGCCTTCCGGCAC GCCCTTCCGG GCCCTTCCGG	CGCCGCCGCCCCCCGCGCGCCAGGATCCGAGCCCGAGGCCCGAGGCCCAGAGCTGCAGAGCTGCAGAGCTCCCCGCAGCTCCCCGCAGTCCCCGCAGTCCCCGAGCCCGCAGTCCCCGAGCCGCAGCCGAGTCCCCGAGCCGAGTCCCAGCAGCCGCAGCCGAGTCCCAGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCCCAGCCGCAGCCCCAGCCGCAGCCCCAGCCCCAGCCCCCAGCCCCCC	120 180 240 300 360 420 480 540 600 660 780 840 900
50	1 	11 GCGAGCGTTC GTCTCCCCT GCTCTGCCCT GCTGTGCCCT GCGGTGGCC GCAGTGGGC GCAGGCGGAG CAGCGGAGATC GGACAGCAGC CTTCCAGCAC CGGAGAGCTC GTACTACCGC CTCCAGGAC CTGCCTGCGC CTGCCTGCGC CCTGCCTGCGC CCAGGACGTG	21 GGACCTOGCA CCTOGGCCGC CCTOGGCCGC GGGGGCGCCG GCGCAGCGC ATCTOGGGTC GAGGAGAACC CGCGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT ACCCGTGCCT ACCCGTGCAACG	CCCCCGCGCGC CCCCCGCGCCCCCGC CCGCCCCCCCC	CCCGCGCCGC GGACCGGGG GGACCGGGC CATTGGAGCTC CGCCCGCGGG AGCCAAGGGC CAGCCATGCC TGCCACCAG GACGCTGCAG GAGGCTGCAG CCTCCGGGAC GGAGACGCTG CCAGCTGCTG GCCCTTCGGG TCCGCTCCTGGG	COSCOGCCGCC CCGCGCGCCCAAGATCCGAG CCGGGCCCAAG TTCAGCCTGA CAGGGCTAACA CAGGCTAACA CAGGCTAACA CAGGCTAACA CAGGCTAACA CAGGCTACACA CAGGCTACACA CAGGCTACACAC CTGTAACTCAG GCCAGGTTCT CTGCCTGATC CAGGCCCCGA GTGCAGGGCC CCCCAAGTCCC	120 180 240 360 420 480 540 660 720 780 840 960
50 55	1 	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGATGTGCGG GAGCTGCGGC CAGCGAGAG CAGCGAGAGCAGC CTCCCAGCAC GTACTACCGG GCTGAGCGGC CTCCAGCAC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CAGGAGAGT CATGAAGCTG	21 GGACCTCGCA CCTCGGCGC CCTCGGCGG GCGGGGCGCCG GCGGAGGCC ATCTCGGGTG GAGGTACCG GGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC CTCTTCAAGC AGCAGGCCG ACCCGTGCCT GTCCGGAAAG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGG GGACCGGGG CATTGGAGCTC CGCCCGCGGG AGCCAAGGGC CAGCCATGCC TGCCACCCAG GAGGTGCAG CTTCCGGGAC GGAGACGCTG GCCTTCGGG TCCCTTCGGG TCCCCTGGGG TCGCTCCTTT CCCCCTGGGG TCGCTCCTTT	COCCOGACTEC COCCOCACC COCCOGACTEC COCCOCACC COCCOGACTEC COCCOCACC COCCOCACC COCCOCACC COCCOCAC COCOCAC COCCOCAC COCCOC COCCOCAC COCCOC COCOCAC COCCOC COCCOC COCCOC COCCOC COCCOC COCCOC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55	1 	11 GCGAGCGTTC GTCTCCCCT GCGGTGGCC GCTGTGCCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC CAGGCGGAG CAGGCAGAC GGAGAGCTG GTACTACCGC GCTCGAGCC CCTCCGGGC CCTCCTGGGC CCTGCGGCC CAGCGACTG CATGAAGCTG CATGTCCGAA	21 GGACCTOGCA CCTOGCOGC CCTOGGCGCG GGGGGCGCCG GCGGTCAGCGC GAGGTCCGC GAGGTCCGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCCG AAGCAGGCCG GTCCGGAAAG GTCTACTGCCT GTCCGGAAAG	CCCCGGGGGG CGCGCCTCT GAACTGGGA CCGGCCCCGG TGGTCGCCTG AGATCTACGG AGCACTGCG TGGCCATCCT ACTGGGAGGG ACGGAGGGG TGCACCTGGA AGCTGCACC AGGGGTCGG TGGTCACGG TGGTCACGG TGGTCACGGT TGGCTCACGGT TGGCTCACGGT TGGCTCACGGT TGGCTCACGGT TGGCTCACGGT	CCCGCGCCGG GGACCGGGG GGACCGGGGG AGCCAAGGGC CATGGAGCTC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCG GGACTGCAG CTTCCGGGAC GGAGACGCTT CCCCCTGGGG GGGAGTCCCT TGCCAGCAG CTGCCTGGGG TCGCTCCTTT CCCCCTGGGC GGGAGTCCCA	CGCCGCCGCC CCGCCGCCGC AGGATCCGAG GACCCGGCCA TCAGCCTGA GACCTGAG CAGGCTACA CAGGCTACA CAGCTTCC CTGTACTCAG GCCACTTCC CTGTACTCAG GCCACGTTCC CTGCTGATG GAGGCCCGGA GTGCAGGGCC CCGGAGTTCC GCCGCCAGGC GCCGCCAGGC GCCGCCAGGC GCCAGCCTGC	120 180 240 360 420 480 540 660 720 780 840 960
50 55	1 	11 GCGAGCGTTC GTCTCCCCT GCTGTCCCT GCGGTGGCC GCGATGGCC GCAGCGCGAG CAGCAGCAGC GCAAGCAGC GCTCCAGCAC GGAGAGCTG GTTCCAGCAC GCTCCAGCAC GCTCCAGCAC GCTCCAGCAC GCTCCAGCAC GCTCCAGCAC GCTCCAGCAC CTTCCAGCAC CTTCCAGCAC CTTCCAGCAC CTTCCAGCAC CTTCCAGCAC CAGCAACCTTG CAGCAACCTG CAGGAACCTG CAGGAACCTG	21 GGACCTOGCA CCTOGGCGC CCTOGGGGGG GGGGGCGCG GCGCAGCGC ATCTCGGGTC GAGGAGAACC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCACTGGAAAG GTCTACTGAACG CTCTTACTCAACTCAACTCCAACTCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTC	CCCCCGCGCGC CCCCCGCGCGC CCCCCGCCCCGC CCCCCC	CCCGCGCCGC GGACCCGAG GGACCCGAG GGACCCGGG AGCCAAGGGC CATTGAAGGTC CAGCCATGCC TGCCACCAG GACGCTGCAG GACGCTGCAG GAGACCTGCAG CCAGCCAGGC TCCAGCCAG GAGACCTGCAG CCAGCCGGGC GGAGACCCTTCCGGGC TCCCCCTTTCGGGGC GGGAGTCCCC TGCCAACCAG CACCGAGCAA	CGCCGCCGCC CCGCGGCCGC AGGATCCGAG GAGCCCGAG GACCCGGCCA TCAGCCTGA CAGGGCTACA CAGGCTACA CAGGCTACA CAGGCTACA GAGCTGGAGA CTGCACCTTCC CTGTACTCAG GCCAGCTTC CTGCCAGT CTGCAGGCC CGGAGTGCT GCCCCAACTGC GCCGCAGGGCT CCCGACCTGC CCCGACCTGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50 55 60	1 	11 GCGAGCGTTC GTCTCCGCCT GCTGTGCCC GCGGTGGCC GCGGTGGCC GCAGGCGGAG CAGGCGGAG CAGGCAGAG CTTCCAGCAC GTACTACCAG GCTGAGGAGCT GTACTACCAG CCTGCAGGAG CTTCCAGGAC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGAC CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGATGCCGA GAGGAACCTC CAGGAACTTG CGAGAAGTTT	21 GGACCTCGCA CCTCGGCGC CCTCGGCGG GGGGGCGCCG GCGGAGGGC ATCTCGGGTG GAGGTACCTC CTCCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGTAAGC ATCGGAAAGA ATCGGAACA ATCGGAACAC ATCGGAACAC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGCGCCGCC CGGCGCGCC AGGATCCGAG AGGATCCGAG AGGATCCGAG ACCGGCCAA ACCGGCCAA ACCGGCCAA ACGGCTACA ACGGCTACA ACGGCTACA ACGGCTACA ACCTTCC ACGCAGCTTCC ACGCAGCTTCT ACGCAGCTTCT ACGCAGGT ACGCAGGC AGGCAGGC ACGCAGCTGATG ACGCAGGC ACGCAGCTGATG ACGCAGGC ACGCAGCTGATG ACGCAGAGC ACCGAACTGG ATTCTGGGGTA	120 180 240 300 360 420 480 660 720 840 900 900 900 1020
50 55	1 GGCTGCCGGA GGCTTTGTT CGGGACCTTG AGAGGCGGG GCTGGTGGCC GCGACGTGCC CCTGCTGCAC CCGGCCCTCG TCGATGACCA CCGGCCCTCG TCGATGACCA GGGCCGCCT ACTACCTGGA AGAGAGCTGC CGGCCGCT TCGAGAGCTGC CCTGCCTGA ACGCCGAGTG CCTCCCTGA ACGCCGAGTG CCTCCCTGA	11 GCGAGCGTTC GTCTCCGCCT GCGGTGCGCC GCGGTGCGCC GCGAGCGCGGGCC GCAGCCGGAGATG GGACAGCAGC CTTCCAGCAC CGGAGATG GTACTACCGC GCTGAGGGC CTCCAGGCC CCTCGAGGGC CTGCAGGGC CTGCAGGGC CAGCGAGTTC CATGAAGCTTG CATGAAGCTTG CATGAAGCTTG CAACAGGGAC CAACAGGGAC CAACAGGGAC CAACAGGAAGTTTC CAACAGGGAC CAACAGGGAC	21 GGACCTOGCA CCTOGCOGC CTCGCGGCGG GGGGGCGCCG GCGGCAGCGC GAGGTCCGC GAGGTCCGC CTGCTGAACG CTGCTGAACG CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGT GTCCACTGCC CTCTTACTGCA ATCGGCAGCA	CCCCCGCGCGC CCCCCGCGCGC CCCCCCGCCCCGC CCGCCCCCC	CCCGCGCCCGC GGACCGCGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGGGGCCGAGGGCCGAGGGCCGAGGGCCGAGGGCCGAGGGCGAGGGCGAGGGGGAGAGGGCCCGAGGGCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCGAGCCCGAGGGCAGGCCCGAGGGACCCGAGGGACCCGAGGGAGGCCCGAGGGACCCGAGGGACCCGAGGGACCCGAGGCCAGGCCAGGCACCAGACCGAGGCACACACACGGAACCCCAGACCCGAGGGAACCCCAGACCCGAGGGAACCCAACACCAACACCAACACCAACACCAACACCAACAC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140
50 55 60	1 GGCTGCCGGA GGCTTTGTT CGGGACCTTG AGAGGCGGG GCTGGTGGCC GCGACGTGCC CCTGCTGCAC CCGGCCCTCG TCGATGACCA CCGGCCCTCG TCGATGACCA GGGCCGCCT ACTACCTGGA AGAGAGCTGC CGGCCGCT TCGAGAGCTGC CCTGCCTGA ACGCCGAGTG CCTCCCTGA ACGCCGAGTG CCTCCCTGA	11 GCGAGCGTTC GTCTCCGCCT GCGGTGCGCC GCGGTGCGCC GCGGTGCGCC GCGGCGGGGCC GCAGGCGGAGATG GGACAGCAGC CTTCCAGCAC CGGAGATG GTACTACCGC GCTGAGGGC CTGCAGGGC CTGCAGGGC CAGCGAGTTG CATGAAGCTTG CATGAAGCTTG CATGAAGCTTG CAACAGGGAC CAACAG	21 GGACCTOGCA CCTOGCOGC CTCGCGGCGG GGGGGCGCCG GCGGCAGCGC GAGGTCCGC GAGGTCCGC CTGCTGAACG CTGCTGAACG CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGT GTCCACTGCC CTCTTACTGCA ATCGGCAGCA	CCCCCGCGCGC CCCCCGCGCGC CCCCCCGCCCCGC CCGCCCCCC	CCCGCGCCCGC GGACCGCGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGGGGCCGAGGGCCGAGGGCCGAGGGCCGAGGGCCGAGGGCGAGGGCGAGGGGGAGAGGGCCCGAGGGCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCCGAGGGCAGGCCGAGCCCGAGGGCAGGCCCGAGGGACCCGAGGGACCCGAGGGAGGCCCGAGGGACCCGAGGGACCCGAGGGACCCGAGGCCAGGCCAGGCACCAGACCGAGGCACACACACGGAACCCCAGACCCGAGGGAACCCCAGACCCGAGGGAACCCAACACCAACACCAACACCAACACCAACACCAACAC	120 180 240 300 360 420 540 660 720 780 900 900 900 1080 1140 1260
50 55 60	1 	11 GCGAGCGTTC GTCTCCGCCT GCTGTGCCC GCGGTGGCC GCTATGTGCG GAGCTGCGGC CAGGCGAGA CAGGCAGAG CTCCAGCAG CTTCCAGCAC CTGAGCAGC CTGCTGGGC CTGCCTGGGC CTGCCGGAGAGCTG CTGCCTGGGC CAGGAACTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CAAGGAACTTC CAACAGGAACTC CAACAGGAACTC CAACAGGGAC ACCTTCAGGC ACCTTCAGGC ACCTTCAGGC	21 GGACCTCGCA CCTCGGCGG CCTCGGCGG GCGGGGCGCCG GCGGAGGTCGC ATCTCGGGTG GAGGAGACC CTCTGAACG AGCAGCACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGTGACCC ACCCGTGCCT ACCCGGAAAG GTCTACTGGAAAG ATCTGGACAC ATCTGACTCA ATCTGACTCA ACCCTCGACAG ACCCTCACAG GGGCCTGACAG ACCCTGAGAAA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	COGCCGCCCA COGCCGCCCCA COGCCCAC COGCCCCAC COGCCCCAC COGCCCCAC COGCCCCAC COGCCCCCCCCCC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320
50 55 60	1 GGCTGCCGA GGCTTTGTT CGGGACCTTG AGAGGCGCG GCTGGTGGCT GCACAGAGCG CCGCGCTCCA TCGATGACCA CCGGGCCTCG TCGATGACCA CCGGGCCTCG ACTACCTGGA AGAGACTGC TCGGCGTGC CGAGAGCTGC CCTCCAGGA ACGCCGAGT ACTCCCGGA ACGCCAGTG CCTCCAGGA ACGCCAGTG CCCCCGGAGAGCGC GGGAGAGCC GCGAGAGCC	11 GCGAGCGTTC GTCTCCCCT GCGTTGCCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC GAGCTGCGGC GAGCTGCGGC GAGCAGCAGC CAGGCAGAG GTACTACCGG GTACTACCGG GCTCGAGCGC CAGCGAGAGT GTACTACCGG CTTCCAGGAG GTACTACCGG GTACTACCGG CAGCGACGT CATCAGAGCT CATCAGAGCT CAGCGACTT CAACAGGGACT CAACAGGACT CAACAGGAC CAACAGGACT CAACAGGAC CAACAGAC CAACAGAC CAACAGAC CAACAGCAC CAACAC CAACAC CAACACC CAA	21 GGACCTCGCA CCTCGCCGC CCTCGCGCGC GCGGCGCCG GCGGTCAGCGC GAGGTCCGC GAGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC AAGAGGCCG GTCCGGAAAG GTCTACTGTG GTCCGGAAAG GTCTACTGTG ATCGGCAGC ATCGGCAGC ATCGGCAGCA ACGCTCACGA ACGCTCACGA ACGCTCACGA ACGCTCACGA ACGCTGAGA ACGCTCGAGAAA	CCCCCGCGCGC CCCCCGCGCGC CCCCCGCCCCC GAACTGCGCA GAACTGCGCA GGCCATCCT TGGCCAACCG AGGCCATCCT AGGCCATCCT AGGCGACGG ACGCGAGGG ACGCGAGGGC TGCACCTGGG TGGCTCACC AGGCGCTCCC TGGTCTCCC TGGTCTCCC TGGTCCCT TGGTCTCCC TGGTCTCACT TGCACACTTCCA TCCACACTTCCA TCCACACTTCCAC TCCACACTTCCACAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCACAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCACAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCAC TCCACACTTCCACTTCCACAC TCCACACTTCCACTTCCAC TCCACACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCA	CCCGCGCCGC GGACCGGGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGGGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGGCCAAGGCCCAAGGCCCACCCCCC	120 180 300 360 420 480 540 660 720 840 960 1020 1140 1260 1320 1340
50 55 60 65	1 GGCTGCCGA GGCTTTTGTT CGGGACGTG GCACGAGCG GCACGTGCC CCTGCTGCAC CCGCGCTCCG TCGATGACCA CCGGCGCTT AGCTGCGCT AGCTGCGCT AGCTGCGCT AGCTGCGCT AGCTGCGGTGC CGAGAGCTGT CCTGCCCTGA ACGCCAGGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGGTGT CCTCCAGGA ACGCCAGCTCCA GCGACGTCCA GCGACGTCCA TGAGCACTGC	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GAGCGGAGA CAGCGAGAGCAGC CTCCAGCAC CGGAGAGCAGC CTCCAGCAC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTC CACAGGGAC CACGGACTTCAGGC CGACTTCAGGC CGACTTCAGGC CGACTTCTAGGC CACTTCTAGGC CGACTTCTAGGC CGACTTCTAGGC CGACTTCTAGGC CACTTCTAGGC CGACTTCTAGGC CACTTCTAGGC CGACTTCTAGGC CACTTCTAGGC CGACTTCTAGGC CACTTCTAGGC CACTTCTAGGC CGACTTCTAGGC CACTTCTAGGC CACTTCTAGC CACTTAGC CACTTCTAGC CACTTCTAGC CACTTCTAGC CACTTCTAGC CACTTCTAGC CA	21 GGACCTCGCA CCTCGGCGC CCTCGGCGCG GCGGGGCGCCG GCGGGGCGCCG ATCTCGGGTG GAGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCCAACC CTCTTCAAGC CTCTTCAAGC TCCGGAAAG GTCTACTGTG AAGCAGCCG ACCCGTGCCT ACCGGAAAG ACCCGTGCCG ACCCGTGCCG ACCCGTGCCG ACCCTCACGG ACCCTCACGG ACCCTCACGG ACCCTCACGG ACCCTGAGA ATCAGCCTCC ACCGTGCTGAGA ATCAGCCTCCGAGA ACCCTGCGGAGA ACCCTGCAGGA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGGG GGACCGGGG GGACCGGGG AGCCAAGGGC CATGGAGGC CAGCCATGGC TGCCACCAG GACGTGAG CCTTCCGGGAC GGAGACGCT TCCGCTCTT CCCCTTCGGG GCGGATCCCT TCCCACCAG GCAGCTCCT TCCCACCAG TCCCACCAG TCCCACCAG CCAGCGACAAG GCAGCGACAAG GCAGGACCAG TGAGGCGAAG TGAAGCCAAG TGAAGCCAAG TGAAGCCAAG TGAAGCCAAG	COSCOGCOGC COGCOGCOGC AGATCOGAG COGGCCCAGA CAGGCCCAA CAGGCCCACA CAGGCCCACA CAGGCCCACA CAGGCCCACA CAGGCCCACA CAGGCCACAC CAGGCCACAC CAGGCCACAC CAGGCCCACAC CAGGCCCACAC CAGGCCCACAC CAGGCCCACAC CAGGAGCCCACAC CAGGCCACACAC CAGGCCCACACCCCCACACACCCCAC CAGGAGCCCCACCCCCCAAGATGCCCAAAAAACCCCAACACCCCAACACCCCAAAAAAACCCC	120 180 300 360 480 600 600 780 900 900 1080 1180 1260 1380 1440
50 55 60	1 	11 GCGAGCGTTC GTCTCCCCCT GCGGTGGCCC GCTGTGGCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC CAGGCGAA CAGGAGAGC GGACAGCAGC GTACTACCGC GCTCCAGCAC CCTGCCTGAGCCC CCTGCCTGGGC CAGGAACTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CAACAGGAACTTC CAACAGGAACTTC CAACAGGAC CCAGGGCCTT CCAACAGGAC CCAGGGCCCT CATGACTGGC CATGATGAC CAACAGGAC CCAGGACTTCTGG CAACAGGAC CATGATGAC CATGAGGAC CATGATGAC CATGAGGAC CATGATGAC CATGAGGAC	21 GGACCTCGCA CCTCGCCGC CCTCGCGCGG GCGGGCGCCG GCGGAGGTCGGC ATCTCGGGTG GAGGAAACC CTGCTGAACG TACACGCAGA AGCAGCCA ACCCTGCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGTG AATCTGCAACC CTGTACTGTG AATCTGCAACC CTGACTCACGG GGGCCTGACG ACCCTTCACGC GGGCCTGACG ACCCTGACGA ACCCTGACGA ACCCTGCACGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA	CCCCGGGGGG CGCGCCTCT GAACTGGGA GACTGGGCA GGGCATCT GGCCAACG AGGCCATCCT TGGCCAACG AGGCGATGGG TGGACGA AGGCGCTGGG TGGACGA AGGCGCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCAGTG TGGACTCAGT TGGACACTTG TGGACACTTG TGGACACTTG TGGACACTTG TGAGGGCTCAC TGGACACTTG TGGACACTTG TGAGGACACT AGAAGCGGG AGGCGACACT AGGAGACACT AGGGGACACT ACGAGGACACT	CCCGCGCCGG GGACCGGGGG GGACCGGGGG GGACCGGGGG AGCCAAGGGC CATGGAGCTC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCG GCACTGCAG CTTCCGGGAC GGAGACGCTT CCCCCTGGGC GGGAGTCCCC CAGCCATGCGG CAGCAGGGCGGGCAAG CCAGCGGGCAAG TGAAGCCAAG CACGGGCAAG CACGGGCAAG CACGGGGCAAG CAGGGGGGAAG CAGGGGGGAAG CAGGGGGAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGCGAAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGCCCATGCAG CAGGCCGAG CAGCCCATGCAG CAGCCATGCAG CAGCCCATGCAG CAGCCATGCAG CAGCCAG CAGCCATGCAG CAGCCAG CAGCCA	CGCCGCCGCC CCGCGGCGCC AGGATCCGAG AGGATCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGCCC	120 180 300 360 420 480 540 560 720 960 1020 1140 1260 1320 1340 1560
50 55 60 65	1 	11 GCGAGCGTTC GTCTCCCCCT GCGGTGGCCC GCTGTGGCCT GCGGTGGCC GCTATGTGCG GAGCTGCGGC CAGGCGAA CAGGAGAGC GGACAGCAGC GTACTACCGC GCTCCAGCAC CCTGCCTGAGCCC CCTGCCTGGGC CAGGAACTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CAACAGGAACTTC CAACAGGAACTTC CAACAGGAC CCAGGGCCTT CCAACAGGAC CCAGGGCCCT CATGACTGGC CATGATGAC CAACAGGAC CCAGGACTTCTGG CAACAGGAC CATGATGAC CATGAGGAC CATGATGAC CATGAGGAC CATGATGAC CATGAGGAC	21 GGACCTCGCA CCTCGCCGC CCTCGCGCGG GCGGGCGCCG GCGGAGGTCGGC ATCTCGGGTG GAGGAAACC CTGCTGAACG TACACGCAGA AGCAGCCA ACCCTGCAACC CTCTTCAAGC AAGCAGGCCG ACCCGTGCCT GTCCGGAAAG GTCTACTGTG AATCTGCAACC CTGTACTGTG AATCTGCAACC CTGACTCACGG GGGCCTGACG ACCCTTCACGC GGGCCTGACG ACCCTGACGA ACCCTGACGA ACCCTGCACGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA	CCCCGGGGGG CGCGCCTCT GAACTGGGA GACTGGGCA GGGCATCT GGCCAACG AGGCCATCCT TGGCCAACG AGGCGATGGG TGGACGA AGGCGCTGGG TGGACGA AGGCGCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCAGTG TGGACTCAGT TGGACACTTG TGGACACTTG TGGACACTTG TGGACACTTG TGAGGGCTCAC TGGACACTTG TGGACACTTG TGAGGACACT AGAAGCGGG AGGCGACACT AGGAGACACT AGGGGACACT ACGAGGACACT	CCCGCGCCGG GGACCGGGGG GGACCGGGGG GGACCGGGGG AGCCAAGGGC CATGGAGCTC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCG GCACTGCAG CTTCCGGGAC GGAGACGCTT CCCCCTGGGC GGGAGTCCCC CAGCCATGCGG CAGCAGGGCGGGCAAG CCAGCGGGCAAG TGAAGCCAAG CACGGGCAAG CACGGGCAAG CACGGGGCAAG CAGGGGGGAAG CAGGGGGGAAG CAGGGGGAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGGCAAG CAGGGCGAAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGGCCGAG CAGCCCATGCAG CAGGCCGAG CAGCCCATGCAG CAGCCATGCAG CAGCCCATGCAG CAGCCATGCAG CAGCCAG CAGCCATGCAG CAGCCAG CAGCCA	CGCCGCCGCC CCGCGGCGCC AGGATCCGAG AGGATCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGCCC	120 180 300 360 420 480 540 560 720 960 1020 1140 1260 1320 1340 1560
50 55 60 65	1	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGATGTGGCC GCGGGCGAGCCGCAGCCGCAGCCGCAGCAGCAGC GCTACACCAC GCGAGAGATG GCTCCAGCAC GCGAGAGATG GCTCGAGCAC GCGAGAGTGC CTCCAGGCC CAGCGAGATG CATGAAAGCTG CATGAAAGCTG CAACAGGAC CAACACC CAACCC CAACACC CAACACC CAACACC CAACACC CAACACC CAACACC CAACACC CAACC CAACACC CAACCC CA	21 GGACCTCGCA CCTCGCGCGC CCTCGCGCGC GCGGCACCGC GCGGCACCGC GCGCTCCTGC CTGCTGAACG CTGCTGAACG CTCTTCAAGC AAGCAGCACA CTCTTCAAGC ACCGTACCA ATCAGCAGCA ATCAGCAGCA ATCAGCTCA ATCAGCAGCA ACCCTGCACCA CTGCTACTGCA ACCCTCACCAGCA ACCCTCACCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCTGCAGCA ACCCCTGCAGCA ACCCCTGCAGCA ACCCCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	CCCCCGCGCGC CCCCCGCGCGC CCCCCGCGCCCCGC CCGCGCCCCGC CCGCCCCCGC CCGCCCCCGC TGGTCGCCTA AGATCTACGG AGCACCTGCA AGGCCATCCT AGACCACCG AGGCCATCCT AGGCCAACCG AGGCCATCCT AGGCCACCG AGGCCACCG AGGCCACCG AGCCCTGCA AGCCCTGCA AGCCCTCCA AGCCCTCCA AGCCCTCCA AGCCCTCCA AGCCCTCCA AGCCCTCCC AGGCCTCCCT CCACGCCACC AGCTCCCT CCACGCCACC AGCTGTCTC CCAGGCACTCC CCAGGCACTGC CCAGGCACTGC CCAGGCACTGC CCAGGCACTGC CCAGGCACTGC CCAGGCACTGC CCAACCACCC CCACCACACCC CCCCCC CCCCCC CCCCCC	CCCGCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGCGCCGCCGCCGCGCCGCGCCGCGCCGCG	120 180 300 360 480 540 660 720 840 960 1020 1140 1200 1320 1380 1450 1500
50 55 60 65	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCAGCGGAG CAGCGAGAGCAG CAGCGAGAGCAG CTCCAGCAC CGGAGAGCTG GTACTACCGC CTGCCTGGGC CTGCCTGGGC CAGCAGAGTTC CAATAAGCTG CAATAAGCTG CAACAGGAAC CCAGGGCCCT ACCTTCAGGC GGACTTCTAGGC GGACTTCTAGGC GGACTTCAGGC CAGTGAGTTTC CAACAGGAC CAGTGACTCTGG CAGTGACTCTGG CAGTGACTCTGC CAGTGACTCTC CATGACCAC CTTACAACGGC CTTACAACAGGC CTTACAACACGGC CTTACAACAGGC CTTACAACAGGC CTTACAACAGGC CTTACAACAGGC CTTACAACGGC CTTACAACAGGC CTTACAACAGGC CTTACAACAGC CTTACAACAGGC CTTACAACGGC CTTACAACAGGC CTTACAACAGGC CTTACAACAGGC CTTACAACAGC CTTACAACAGCAC CTTACAACAGC CTTACAACACACACACAC CTTACAACACACACACACA	21 GGACCTCGCA CCTCGGCGC CCTCGGCGG GGGGGCGCCG GCGGAGGGC ATCTCGGGTG GAGGTCCTGC GAGGTCCTGC TACACGCAGA GGTGCCAACC CTCTTCAAGC TACACGCAGA GTGCCAACC TCTTCAAGC TCCGGAAAG GTCTACTGT AATCTGCA ATCGGCAGCG ACCCTCACG ACCCTCACG ACCCTCACG ACCCTCACG ACCCTCACG ACCCTCACG GGCCTGACG ACCCTCACG GGCCTGACG ACCCTGACA ACCACCACA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGG GGACCGGGG GGACCGGGG AGCCAAGGC CATGGAGGC CAGCCATGCC TGCCACCAG GACCTGCA TGCCACCAG GAGGCTGCA TCCGGGAC TCCGCTCTT CCCCTTTCGGG TCCCACCAG GCCATCCCT TCCCACCAG TCCCACCAG TCCCTTCGGG CCAGCCATCCC TCCCACCAG TCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCCACCAG TCCAGCCCAC TCCAGCCAC TCCAGCCCAC TCCACCAC TCCA	COSCOGCOGC COGCOGCOGC AGGATCOGAG AGGATCOGAG ACOGGCCCAA ACAGGCTCAA ACAGGCTAACA GAGCTGGAGA CTGCGCAGCT CCACCTTCC CTGTACTCAG GCGAGTTCT CTGCCTGAT GAGGCCCGA GTGCAGGCC CCGGAGTGCT GCCACCTCC AGGATCCT ACCACCACC AGGAGCCCCAA ACCAACCGG GCCAACCCC AAGATGGCCC AAGATGGCCC AAGATGGCCC AAGATGGCCC AAGATGACCAACCG ACCAACCAACCG ACCAACCAACCGC AACAACCGG ACCAACCA	120 180 300 360 480 540 660 720 840 960 1020 1140 1260 1320 1340 1560 1560 1680
50 55 60 65	1	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCTGTGGCCT GCGGTGGCC GCTATGTGCG GAGCTGCGC CAGGCGAA CAGGAGAGC GGACAGCAGC GTATCACGG GTACTACCGC GCTGAGCGC CTGCCTGGGC CAGGAGACTG CATGAAGCTG CATGAAGCTG CAACAGGAACTTC CAACAGGAC CCAGGGCCTT CAACAGGAC CAGGACTTCCAGGAC GAGAACTTC CAACAGGAC CCAGGACCT CAACAGGAC CATGAACACT CAACAGGAC CATGAACACT CAACAACGGC CATGAACACT CAACAACGGC CATGAACAT CTACAACGGC CATGAACAT CTACAACGGC CAGTGAATGAC CAGGACTT CAACAACGGC CGGTGATGACCAC CGGTGATGACCAC CGGTGATGATGAC CAGGACTT CTACAACGGC CGGTGATGATGAC CGGTGATGACCAC CGGTGATGATGAC CAGGACTT CTACAACGGC CGGTGATGATGAC CGGTGATGACAC CGGTGATGACAC CGGTGATGACAC CGGTGATGAC CGGTGAC CGGTGAC CGGTGATGAC CGGTGATGAC CGGTGAC CGGGCC CGGTGAC CGGTGAC CGGGCC CGGTGAC CGGTGAC CGGTGAC CGGTGAC CGGGCC CGGTGAC CGGTGAC CGGGCC CGGTGAC CGGTGAC CGGGCC CGGTGAC CGGGCC CGGTGAC CGGGCC CGGGCC CGGGCC CGGGCC CGGGCC CGGGCC CGGGCC CGGGCC CGGGCC C	21 GGACCTCGCA CCTCGCCGC CCTCGGCGCG GCGGGCGCCG GCGGAGGTCCGC ATCTCGGGTG GAGGAAACC CTGCTGAACG TACACGCAGA AGGAGACC CTCTTCAAGC AAGCAGGACA ACCGTGCCTG GTCGGAAAG GTCTACTGTG AATCTGCAACC GTCTACTGTG AATCTGCAACC CTCTTCAAGC AATCAGCTCA CTGGACAGC ACCCTTGCTGAA ATCGGCAGCA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAGA ACCCTGCTGAAA ACCACTACCG GGCCTTGAGG ACCCTGCTGAGA ACCCTGCTGAGA ATCAGCCTCC CCTTGCTGAA ACCACTACAGA CCGCACCAGA ACCACTACAGA CCGCACCAGA AACGACTGCG CTGCTGGGAA AACGACTGCG CTGCTGGGAA AACGACTGCG CTGCTGGGAA AACGACTGCG CTGCTGGGAGA AACGACTGGGAGA AACGACTGGAGA AACGACTGGGAGA AACGACTGGAGA AACGACTGAGA AACGACTGAGA AACGACTGGAGA AACGACTGAGA AACGACTGAGAA AACGACTGACAA AACGACTGACAA AACGACTGACAA AACGACTGACAACAA AACGACTGACA	CCCCGGGGGG CGCGCCTCT GAACTGGGA GGCGCCTCT GAACTGGGCA GGGCCATCCT TGGCCAACGG AGGCCATCCT TGGCCAACGG AGGCGCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGG TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCTGGA TGGACCACTTG TGGACCACTTG TGGACCACTTG TGGACCACTTG TGGACCACTTG TGAGGACACT TGAGGACACT CAGGGACACT TCAGCAGACACT TCAGCACACTG TCAGCACACTG TCAGCACACTG TCAGCACACTG TCAGCACACC TCATCAGCA ACTTCCAGGA	CCCGCGCCGG GGACCGGGG GGACCGGGGG GGACCGGGGG AGCCAAGGGC CATGCACCAG AGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCG GCACCAGGGC CCTCCGGGAC GGAGACCCTT CCCCCTGGGC GGGAGTCCCC CAGCCATGCG CAGCAGGCAG CACCGACAAG CACCGACAAG CACGGGGCAAG TGAAGCCAAG CACGGGGCAAG TGAAGCCAG CAGGGGTGAG CAGGGGTGAG CAGGGTGAG CAGGGTGAG CAGGGTGAG CAGAGGCCAG CAAGGCCAGTGAG CAAGAGCCAG CAAGAGCAG CAAGAGCCAG CAAGAGCAG CAAGAGCCAG CAAGAGCACAAAAAAAA	CGCCGCCGCC CCGCGGCGCC AGGATCCGAG AGGATCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGCC CTGTACTCAG AGCCGGCTCC CTGTACTCAG AGGCCCGAG AGGCCCGAG AGGCCCGAG AGCCCGC ACCCCC ACCCAGCCCC ACCCACCC	120 180 300 300 420 480 540 560 720 780 960 1020 1140 1260 1320 1340 1500 1500 1562 1620
50 55 60 65 70	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGATGCGGC GCAGGCGGAGATG GGACAGCAGC CCAGGCGGAGATG GGACAGCAGC GCTCCAGCAC GCGAGAGCAGC GCTCCAGGCC CCTCCAGCAC GCTCAGCAC GCTCAGAGCAC CCTCCAGGC CTCCAGGC CTCCAGGC CTCCAGGC CAGGAGATTC CATAAAGCTG CAACAGGAC CCAGGGCCCT ACCTTCAGGC CAGGACTTC CAACAGGAC CCAGGGCCCT CACTAGGCC CAGGACTTC CAACAGGAC CCAGGGCCCT CACTAGAGCTG CAGGACTTCTGG CAGTATTGCC CAGTGATGAC CTGACACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGGC CGTGAACGCC CGGCCCT CTGAACGGC CGTGAACGCC CGCAGCCC CGCAGCCC CGCACCC CGCACC CGCACCC CCCC CGCACCC CCCC CGCACCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	21 GGACCTOGCA CCTOGGCGC CCTGGGGGGG GGGGGGCCCG GCGGCAGCGC GAGGTCCGC ATCTCGGGTG GAGGAACC CTGCTGAACG CTGCTGAACG CTCTTCAAGC AAGCAGCAGA ACCGTGCCA ATCAGCAGA ACCGTGCCA ATCAGCAGA ACCCTGGAAA ACCCTGGAAA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ACCCCAGCACA ACCCAGCACA ACCCCAGCACA ACCCCAGCACA ACCCCAGCACA ACCCCAGCAGA ACCGCAGCAGA AACGACCAGA AACGACCAGA AACGACCAGG	CCCCCGCGGGG CCCCCGCGGGGCCCGCGCGCGCCCGGGGCCCGGGCCCGGGCCCGGGG	CCCGCGCCGC GGACCGGGGGGGGGACCCATGGACGGGGGGGGGG	CGCCGCCGCCCCCCCGCGCCCAGGCCCAGGCCCAGAGCCCAAGAGCCCAACGGCCCAAGAGCCCAACGAGCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCCCCAAGAGCACCCAACCAACACGGCAACCAACACGGCAAGAGCAGC	120 180 300 360 480 540 660 720 840 900 1020 1140 1200 1320 1380 1440 1560 1560 1680 1780
50 55 60 65	1	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGATGTGCCG GCGAGGCGAG	21 GGACCTCGCA CCTCGCCGC CCTCGGCGG GGGGCGCCCG GCGGAGGCCC ATCTCGGGTG GAGGTCGCC ATCTCGGGTG GAGGACACC CTCTTCAAGC AACCAGAA ACCAGAACC ATCTCGGATAC ATCTCGGATAC ATCTCGGATAC ATCTCGGATAC ACCCTGCCAACC ACCCGTGCCC ACCCGTGCCC ACCCGGACAC ACCCGGACAC ACCCTGGAGA ACCCTGGAGA ACCCTGGAGA ATCAGCCTC CGCTGCTGGA ACCCTGGAGA ATCAGCCTC CGCTGCTGGA ACCCTGGAGA ATCAGCCTC TTCAGCTCC TTCACCCATG TTCACCCCATG TTCACCCATG TTCACCCCATG TTCACCCATG TTCACCATC TTCACCATC TTCACCCATC TTCACCCATC TTCACCCATC TTCACCCATC TTCACCCATC TTCACCCATC TTCACCATC TTCACCCATC TTCACCCATC TTCACCATC TTCACCATC TTCACCATC TTCACCATC TTCACCATC TTCACCATC TTCACCCATC TTCACCCATC TTCACCCATC TTCACCCATC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCCG GGACCGCGGGGGGGGGGGGGGGGGGGGG	COCCAGCTCC CAGGAGCCAGA COCCAGGCCAGA COCCACACTTCAGCCTGA COCCACCTTCC COCCACCTCC COCCACCTCC COCCACCTCC COCCACCTCC CAGCTCC CAGCTCC CAGCTCC CAGCTCC CACCACCCCC CACCTCC CACCACCCCC CACCACCCCC CACCTCC CACCACCCCC CACCACCCCC CACCACCCCC CACCAC	120 180 300 360 420 480 540 660 780 900 900 1080 1180 1260 1380 1440 1560 1620 1680 1740
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCTGTGCCCT GCGGTGGCC GCTATGTGCG GCAGGCGGAG CAGGCGGAG CAGGCAGAC CAGGCAGAC GCAGAGCTG GTACTACCGC GCTCCAGCC CTCCAGCC GCTCAGCCG CTCCAGCC CTCCAGCC CTCCAGCC CTCCAGCC CTGCCTGGC CAGGACTTC CATGAACTTC CAACAGGAC CCAGGGCCT CAACAGGAC CCAGGGCCT CATGAACTTC CAACAGGAC CCAGGGCCT CATGAACTC CAACAGGAC CATGAACTC CAACAGGAC CCAGGCCCT CATGAACCT CAACAGGC CGTGATAATGC CAGGACT CTACAACGGC CGTGAATGAC CCAGGCCT CATGACCAC CGCTGCCAGC CCGGTCCCAGC CCTCCCAGC CCTCCAGC CTCCAGC CCTCCAGC CTCCAGC	21 GGACCTCGCA CCTCGCCGCA CCTCGGCGCG GGGGGCGCCG GCGGTCAGCGC GAGGTCCGC GAGGTCCGC GAGGTCCGC CTGCTGAACG TACACGCAGA AGGAGAACC CTCTTCAAGC AAGCAGGAGA ACCCGTGCCT GTCCGGAACA GTCTACTGCA AATCTGCTGA AATCTGCTCA AATCTGCAGA ACCCTCACAG ACCCTTCACAG GGGCCTGAGG ACCCTGAGA ACCCTCACAGA ACCCCCAGC AGCCAGCAGA AACCAGCA CCCCAGCAGA AACCACCAGA ACCACCAGA CCCCAGCAGA AACCACCAGA ACCCCCAGC TTGACCCCCAGC TTGACCCCAGC AGCCCCCAGC AGGCCCCAGC	CCCCGGCGGC CCCCGGCGGC CCCCGCGCGCC CGCGCCCCGC CGGCGCCCCGC CGGCGCCCCGC CGGCGCCCGC CGGCCCACC CGGCCACCG CGGCGCACCG CGGCGACG CGGCGCGC CGGCGCGC CGGCGCC CGGCGCC CGGCGCC CGGCGCC CGGCGCC CGGCGCC CGGCGCC CCCCCGGGCC CCCCCC	CCCGCGCCGC GGACCGCGG GGACCGGGG GGACCGGGG GGACCGGGG AGCCAAGGGC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC GGACTGCAG CTTCCGGGAC GGAGACGCTG GCCTTCGGG CCGGGCAG CCGGGGCAAG CCGGGGCAAG CCGGGGCAAG CCAGCGAG CCAGCGGG CAAGCCAG CAGGGGGGA CCAGCGGGCAAG CCAGCGGGCAAG CCAGCGGGCAAG CCAGCGGGCAAG CCAGCGGGCAAG CCAGCGGGCAAG CCAGCGGCCAAC CCAGCAGGCCAG CCAGCAGGCCAG CCAGCAGGGCCAG CCAGCAGGGCCAG CCCAGCAGGGCCAG CCCAGCGGGCCAG CCCAGCGGGCCAG CCCAGCGGGCCAG CCCAGCGGCCAGGGCCAG CCCAGCGGGCCAG CCCAGCGGGCCAG CCCCTGCGGCCCGGGGCCAG CCCTGCGGGCCAGGGCCCCTGCGGGCCCCTGCGGGCCCCGGGGCCCCGGGGCCCCCGGGGCCCCCGGGGCCCC	CGCCGCCGCCCCCCGCGCGCCAGGACCCCGCGCCAGGCCCACCCCCC	120 180 300 300 420 480 540 540 960 1020 1140 1260 1320 1340 1500 1680 1740 1560 1680 1780 1800 1800 1800
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCAGCCGGAGATG GGACAGCAGC CTCCAGCAC GGAGAGATG GTACTACCGC GCTGAGCGC CTCCAGCAC GCGAGAGAGC CTCCAGGCC CAGCGAGATG GTACTACCGC CAGCGAGCTG CATGAAGCTG CATGAAGCTG CAACAGGGAC CAACAGGAC CAACAACAGC CAACAACAGC CAACAACAGC CAACAACAGC CAACAACAGC CAACAACAACAAC CAACAACAAC CAACAACAAC CAACAA	21 GGACCTCGCA CCTCGCGCGC CCTCGCGCGC GCGGCGCCG GCGGCGCCG GCGGCGCCG GCGGCG	CCCCCGGGGG CCCCCGGGGGCCTCT GAACTGCGCA GACTGCCCTG GAACTGCGCA AGGTCACCTGCG AGGCCATCCT TGGCCAACCG AGGCCATCCT AGGCCACCT AGGCCTCACT AGGCCACCT AGGCCTCACT AGGCCACCT AGGCCTCCACC AGGCACTC CCCAGGCACCT CCACCC ACCTCCCAGG ACCTCTCACGG ACCTCTCACGG ACCTCTCAGGA ACCTCCCAGG CCCCCACCTT GCCGGACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGCACCTT GCCGGACCTT GCCGACCTACACACCC CCCGACCTT GCCGACCTACACACCC CCCGACCTACACACACACACACACACACACACACACACAC	CCCGCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	120 120 240 300 360 480 540 660 720 1020 1140 1200 1140 1320 1380 1440 1560 1680 1740 1860 1920
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCGCCT GCTGTCCCCCT GCGGTGGCC GCTATTGTGCG GAGCTGCGC GCAGGCGAG CAGGCGAG CAGGCGAG CTCCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTTCAGCA CTGAGCAG CTTCAGCA CAGGAGATT CATTACCGC CAGGAGATT CATTACCGC CAGGAGACTC CATGAGCAG CATGAGCTC CATGAGCAG CAGGACTCT CATGACGAC CAGGACTCT CATGACCAC CAGGACTC CAGGACTC CAGGACTC CAGACACC CAGGACT CAGACACC CAGGACT CAGCACC CAGCACC CAGCACC CAGCACC CAGCACC CAGCACC CAGCACC CAGCACC CAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	21 GGACCTCGCA CCTCGCCGC CCTCGGCGG GGGGCGCCCG GCGGAGGTCCGC ATCTCGGGTG GAGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCAACC CTCTTCAAGC AAGCAGGCC AACCAGGAGAACCAGA AACAGCCCA ACCCTGCTGAACG TCTACTGGATCA ACCTGCGAAAAATAC CTGCAGAAAAAAAACACCCCCCCACCAGGCCCAGGCCCAGGCCCAGCCAGCACCAGA ACCCCCCCTTCCTGGATG ACCCTGCAGAAAAAAAACCACCCCCCACCAGCACCAGAAAAAAACCCCCC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCCGCGCGGGGGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCC CCGCGGCGCC AGGATCCGAG AGGATCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGCC CTGTACTCAG ACCCGGCCAG ACCCCGAG ACCCCGAG ACCCCAGCC CCGAGCTCC ACCCCCC ACCCCCC ACCCCCC ACCCCCC ACCCCCC	120 180 300 360 420 480 540 660 780 900 900 1030 1140 1260 1320 1440 1500 1620 1620 1620 1840 1840 1840 1840 1840 1840 1840 184
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCGCT GCGTGGCCT GCGGTGGCC GCTATGTGCG GCAGGCGGAG CAGGCGGAG CAGGCGGAG CAGGCAGC GCAAACCAG GCTCAGCAG GCTCAGCAG CCTCCAGCA GCAGAGCTG GTACTACCGC GCTCAGAGCG CCTCCAGGCC CAGCGAGCTG CATGAGCTG CATGAGCT CATGAGCT CAACAGGACTT CAACAGGAC CAACAGGACTT CAACAGGAC CAACAGGACT CAACAGGAC CAACACGC CCGAACACC GCTGACACC GCTGACACC GCTGACACC GCTGACACC CCGAACACC GCTGACACC CCGAACACC CCGACC CCGAACACC CCGACC CCGACC CCCAACACC CCCAACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACACC CCCAACC CCCAACACC CCCAACACC CCCAACAC	21 GGACCTCGCA CCTCGCCGCA CCTCGCCGCG GGGGGCGCCCG GCGGTCAGCGC GCGGTCAGCGC GAGGTCCGC GAGGTCCGC CTGCTGAACG TACACGCAGA AGCAGCGCG GTCTTCAAGC AAGCAGGCGG GTCACTGC GTCACTGCAACA ATCAGCAGA AATCAGCAGA ATCAGCTCA ATCAGCAGC GGGCCTGAGA ACGCTGAGA ACGCTGAGA ACGCTGAGA ATCAGCTTCC CGCTGCTGAA ATCAGCCTCC CGCTGCTGAA TCAGCCTCC CGCTGCTGAA ACGCTCACGG GGCCTGAGA ACGCTCACGG ACGCTGAGA ATCAGCTCC CGCTGCTGAA ACGCCCCAGC AGCCCCAGC AGCCCCAGC AGGCCCCGGT CCCAAACATAC CAGGGAGGGAG ACGCCCCGGT CCCAAACATAC CAGGGAGGGAG ACGCCCGGT CCCAAAAATAC CAGGGAGGGAGC CCCAAACATAC CAGGGAGGGGC CCCAAAAATAC CAGGGAGGGGC CCCAAACATAC CAGGGAGGGGC CCCAAAAATAC CAGGGAGGGGC CCCCAAGC AGGCCCCGGT CCCAAAAATAC CAGGGAGGGGC CCCAAAAATAC CAGGGAGGGGC CCCCAAGC CCCCAAGC AGGCCCCGGT CCCAAAAATAC CAGGGAGGGGC CCTCATTCCCCCTCC CCTCATTCCCCCTCCC CCTCATTCCCCCCCC	CCCCCGCGCGC CCCCCGCGCGC CGCGCCTCT GAACTGCGCA GACTGCGC TGGTCGCCTG AGATCTACCG AGGCCATCCT TGGCCAACCG AGGCCATCCT AGATCACCG AGGCCATCCT AGGCCACCT AGGCCACCT AGGCCACCT AGGCCACCT AGGCCTACCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC TCGTGCTCC TCGAGGTCTCC TCAGGCACCT TCAACGCCT ACTCCTCCAGG ACTTCCAGGACACT ACTCCAGGACACT ACTCCAGGACACT ACTCCAGGACACT ACTCCAGGACACT ACTCCAGGACCT ACTCCAGGACCT ACTCCAGGACCT ACTCCAGGACCT ACTCCAGGACCT ACCGGACCT ACCGACCT ACCGCACCT ACCGCACCT ACCGCACCT ACCGCACCT ACCCACACACC ACCGCACCT ACCGCACCT ACCGCACCT ACCCACACACAC ACCCACACACAC ACCCACACACA	CCCGCGCCCGC GGACCCGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGCGCCAGGACGCCCAAGAAGGCCCAAGAGGCCCAAGAGGCCCAAGAGACCCAAGAGACCCAAGAGACCCACCCCCGCGCCAGACCCCCC	120 180 300 300 480 540 660 720 840 960 1020 1140 1200 1320 1340 1560 1560 1740 1860 1980 1980
50 55 60 65 70	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGGGGAG CAGCGGAGCGC CAGCGAGAC GCAGCGAGC GCTCCAGCAC GCGAGAGCT GTACTACCGC GCTGGGCC CAGCGAGCT CATGAGGGC CTGCCTGGGC CATGAAGCTG CATGAAGCTG CATGAAGCTC CATGAGCT CAGCAGC CAGGACTT CACCAGGAC CAGGACT CAGGACC CAGGACT CAGGACC CAGGACT CAGGACC CAGGACT CAGGACC CAGCAC CAGGACC CAGCAC CACC CAGCAC CAGCAC CACC	21 GGACCTCGCA CCTCGGCGC CCTCGGCGCG GGGGGCGCCG GCGGGGCGCCG ATCTCGGGTG GAGGTCCTGC CTGCTGAACG TACACGCAG TACACGCAG TACACGCAG ACCCTTCTCAAGC TCTCTCAAGC ACCCGTGCCT GTCCGGAAAG ACCCGTGCCT AACAGCAGA ACCACTCACG ACCCTCACG ACCCTCACG ACCCTGAGA ATCAGCCTCA CGCTGCTGAGA ATCAGCCTCCA ATCAGCTCCA ATCAGCTCCA ATCAGCTCCA ATCAGCTCCA ATCAGCTCCA CGCTGCTGGA TCTCTGGATG GCCAACCAGA TCGCAGCAGA ACCACTGAGA TCGCCCCAGC ACGCCCCAGC TGCCCCAGC ACGCCCCAGC CCAGCAGAAAAAC CCAGAGAGAG	CCCCGGCGCC CCCCGGCGCC CGCGGCCTCT GAACTGCGCA CCGGCCCCGC CGGCGCCTCT GGATCTACGG AGATCTACGG AGACCTGCG AGACCACGG AGGCCATCCT AGACCACGGA AGGCCATCCC AGGCCATCCC AGGCCATCCC AGGCCTACGC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCTCCC AGGCCTCC CCAGGCACCT CCAGGCACCT CCCCAGGC CCCCCACCT ACTCCCAGG CCCCCACCT ACCCCCAGGC CCCCACCT ACCCCAGGC CCCCACCT CCCCAGGC CCCCACCT CCCCAGGC CCCCACCT CCCCAGGC CCCCACCT CCCCACGC CCCCACCT CCCCACGC CCCCACCT CCCCACGC CCCCACCT CCCCACGC CCCCACCT CCCCACGC CCCCACCT CCCCACGC CCCCACCT CCCCACCT CCCCACCT CCCCACCT CCCCCACCT CCCCCACCT CCCCACCT CCCCACCT CCCCCACCT CCCCACCT CCCCCACCT CCCCCACCT CCCCCACCT CCCCCACCT CCCCCACCT CCCCCACCT CCCCCACCT CCCCACCT CCCCCACCT CCCCACCT CCCACCT CCCCACCT CCCCCCCC	CCCGCGCCCG GGACCCGGGGGGGGACCCATGGACGGGGGGGGGG	CGCCGCCGCCCCCCCCGCGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCC	120 180 300 360 480 660 780 960 1080 1140 1260 1380 1440 1560 1620 1740 1860 1920 1980 1980 1980 1980 1980 1980 1980 198
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCGCCT GCTGTCCCCCT GCGGTGGCC GCTATTGTGCG GAGCTGCC GCGAGCGAG CAGGCGAG CAGGCGAG CTCCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTCAGCAG CTGAGCAG CTGAGCAG CTGAGCAG CAGGAACTC CATAAGCTA CAACAGGAAC CAACAGGAAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAGGAC CAACAACGGAC CAACAACGCAC CTACAACGGAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACGCAC CAACAACCAC CAACAACCAC CAACAACCAC CAACAA	21 GGACCTCGCA CCTCGGCGC CCTCGGCGGCGCGGGGGCGCCCG ATCTCGGGTG GAGGTCCTGC CTGCTGAACG TACACGCAGA GGTGCAACC CTCTTCAAGC CTCTTCAAGC AAGCAGGCCC AACCAGAGA AACCAGTGCCT GTCCGGAAAG ATCAGCTGA ACGCTGCC GGCTGCTGA CGGGACCAGA ACGCTGCCGAACCAGA ACGCTGCCGAACCAGA ACGCTGCCGGAAAATAC CCCAGCTCCCGGC CCAGCAGGGGCCCAGCGGTCCCAGC CCCAGCAGAGACCAGA CGCAGCAGCAGAAAAAAC CCCAGCTCCCGGT	CCCCGGCGGC CGCGCCCTCT GAACTGCGCA CGGCGCCCCGC CGGCGCCTCT GAACTGCGCA AGACCTGCG TGGCCAACCG AGGCCATCCT TGGCCAACCG AGGCGACGGC TGGCCACCTGGA AGCTGCACCTGGA AGCTGCACCTGGA AGCTGCACCTGGA AGCTGCACCTGGA AGCTGCACCTGGA AGCTGCACCT TGGCTCACTGCT TGGCTCACTGCT TGGCTCACTGCT TGGCTCACTGCT TGCACGAGGTCAT AGAAGCGGC TCATGCACT TCATGCACT TCATGCACT TCATGCACT TCATGCAGGACACT ACTTCCAGGA CCCCGACCTT AACACAGAC TCATGCACT TCATGCACT TCATGCACT CCCGGACCTT AACACAGAC TCTCCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGG CCTCCCAGC TCTCCAGCT TCTCTCTCTCT TCTCTCTCTCT TCCATGCATT TCTCTCTCT TCCATGCATT TCTCTCTCT TCCATGCATT TCTCTCTCT TCCATGCATT TCTCTCTCT TCCATGCATT TCTCTCTT TCTCTTCTT TCTCTTCTCT	CCCGCGCCCG GGACCGGGG GGACCGGGG GGACCGGGG GGACCGGGG AGCCAAGGGC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCC CAGCCATGCG GCACTGCAG CTTCCGGGAC GGAGACCGTT CCCCCTTGGG CCCTTCGGG CGGGCAAG CACCGACAAG GCTGCCGGGCAAG CACCGACAAG CACCGACAAG CACCGACAAG CACGGGCTAGC CAGGGGCTAG CAGGGGTGGA CAGGGGTGGA CAGGGGTGGA CAGGGGTGAG CAGGGGTGAG CAGGGGCTAG CAGGGGCTAG CAGGGCTGAG CAGGGCTAGAG CAGGGCTAGAG CAGGGCTAGAG CAGGGCTAGAG CAGGGCTAGAG CAGGGCTAGAG CAGGAGGCC CCCCAAGGC ATATTTAATT TGAGCAGGGGC TTAATTTTGT TCAGGGACCG CAGGGGGCAGC CAGGGGGGGGGC CAGGGGGGGG	CGCCGCCGCC CCGCGCGCC AGGATCCGAG AGGATCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGCC CTGTACTCAG ACCCGGCAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG AGCCCGAG TTCTGGGAGCC AGCCACCTC ACCACCAC AGCAGCCC ACCACCAC AGCAGCCC ACCACCAC ACCACCAC ACCACCAC ACCACCAC ACCACC	120 180 300 300 420 480 540 660 780 900 1030 1140 1260 1320 1440 1500 1620 1620 1620 1620 1980 2040 2060 2100 2100 2100 2100 2100 2100 210
50 55 60 65 70	1	11 GCGAGCGTTC GTCTCCCCT GCGGTGGCC GCTGTGCCCT GCGGTGGCC GCTATGTGCG GCAGGCGGAG CAGGCGGAG CAGGCGGAG GCAGACAG GCAGACAG GCTCAGCAG GCTCAGCAG GCTCAGCAG GCTCAGCAG GCTCAGCAG GCTCAGCGG CTCCAGGGC CAGCAGCGGC CAGCGAGCTG CATGAGCTG CATGAGCTG CATGAGCTG CAACAGGACTTC CAACAGGACTTC CAACAGGACTT CAACAGGAC CAGGCCCT CAGCACAC CAGGCCCT CAGCACAC CAGCACAT CTACAACGGC CCGGACCTT CAGCCCT CAGCACCCC GCTTGCAGG CCGGACCCT CAGCACCCT CAGCACCT CAGCACCT CAGCACCT CAGCACCT CAGCACCT CAGCCCT CAGCACCT CAGCCCT CAGCACCT CAGCCCT CAGCCCCT CAGCCCCT CAGCCCC CACCCC CACCCC CACCCC CACCC CAC	21 GGACCTCGCA CCTCGCCGCA CCTCGCCGCC GCGGCGCCCG GCGGCGCCCG GCGGCCCGC GCGGCCCGC GCGGCCCGC GCGGCCCGC CCGCCCAAC CCCCCCACCC GCGCCCCCCCC	CCCCCGCGCGC CCCCCGCGCGC CCCCCGCGCGCC CGCGCCCCGC CGCGCCCCGC CGGCGCCCCGC CGGCGCCCCGC TGGTCGCCTG AGATCTACGG AGCACCTGGA AGGCCATCCT AGGCCATCCT AGGCGACGG ACGCGAGGG ACGCGAGGG ACGCGAGGG ACGCGAGGC AGGCCTCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCCTCCC AGGCGCTCC TCATCCAGG ACTTCTCCAGG ACTTCCAGG ACTTCCAGG ACTTCCAGG ACTTCCAGG CCCCCAGGCACCT ACGCGCCCC TCATCCAGG CCCCCCAGC CCCCCAGCCT TTCTCCAGG CCCCCACCTT TCTCCAGG CCCCCACCTT TCTCCAGG CCCCCCCCC CGCCGCCCT TTTCTCCCTCC CCCCAGCCCT TTTCTCCCTCC CCCCACCTT TCTCCCCCCCCCC	CCCGCGCCCGC GGACCCGGGGGGGGGGGGGGGGGGGGG	CGCCGCCGCCCCCCGAGGAGAACCCAAGAGGACCCAAGAGGACCCCCC	120 180 300 300 420 480 540 960 1020 1140 1200 1320 1340 1560 1560 1740 1860 1980 2040 2220 2220
50 55 60 65 70	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGGGGGAG CAGGCGGAG CAGGCGGAG CTCCAGCAG GTACTACCGC GCTACTACCGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAACATC CAGGGCCTT CACAGGGCCTG CATGAACATC CATGAACATC CATGAACATC CATGAACATC CAGGGCCTG CATGAACATC CAGGGCCTG CATGAACATC CAGGGCCTG CATGAACATC CAGGGCCTG CAGGACTGGGA CCGGCCTGAAGCCCC GGCTCCAAGGCCAGT TAGCCCTCCC GGCCTCCAAGGCCAGGCC	21 GGACCTCGCA CCTCGCCGCA CCTCGGCGGC GGGGGCGCCCG GCGGAGGCCCC ATCTCGGGTG GAGGTCGCC ATCTCGGGTG GAGGTCGCC ATCTCGGAACG CTCTCAAGC CTCTTCAAGC AAGCAGGCCC AACCAGAAG GCCACACAGA GCCACCAGA ACGCTGCCG ACCCGGGCCC CCTCTGGAACG GGGCCTGAACA ATCGGCAGA ACGCTGCAGA ACGCTGCAGA ACGCTGGAGA ATCAGCCTCC CCAACAAGA CCCAGCTCCCG CCGAAAAATAC CAGGAGGGGC CCCAAAAATAC CAGGAGGGGC CTCCCCAAAA CCCAGCTCCC CAACCAGA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGGGGGGGACCCGGGGGGGGGG	COSCOGCOGC COGCOGCOGC AGGATCOGAG AGGATCOGAG AGGATCOGAG ACAGGGCCCAG ACAGGGCTAA CAGGGCTAAC AGAGCTGAAC AGAGCTGAAC AGAGCTGAAC AGAGCTCAC AGAGCTCAC AGAGCTCAC AGAGCCCCAC AGAGCCCCAC AGAGCCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC ACCAACCGC ACCAACCA	120 180 360 480 540 660 780 960 1080 1140 1260 1320 1440 1560 1680 1680 1740 1800 1680 1740 1800 1680 1740 1800 1800 1800 1800 1800 1800 1800 18
50 55 60 65 70	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGGGGGAG CAGGCGGAG CAGGCGGAG CTCCAGCAG GTACTACCGC GCTACTACCGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAACATC CAACAGGAACTTC CAACAGGAC CTGCCTGGGC CATGAACATC CATGAACATC CATGAACATC CATGAACATC CATGAACATC CTTACACATC CATGAACATC CTGCCTGGGC CCTGCAGGC CCTGCAGGC CCTGCAGG CCTGCAGG CCTGCAGG CCTGCAGG CCTGCAGG CATGACTTC GGCTGCAGC CATGACCTTC GGCTCCAGG CAGGCCCTG CAGGCCCTG CAGGCCCTG CGCCTCCAAGG CACTCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCC CGCCTCCAAGG CACCCCCC CGCCTCCAAGG CACTCCCCC CCCCC CCCCC CCCCCC CCCCC CCCCC CCCC	21 GGACCTCGCA CCTCGCCGCA CCTCGGCGGC GGGGGCGCCCG GCGGAGGCCCC ATCTCGGGTG GAGGTCGCC ATCTCGGGTG GAGGTCGCC ATCTCGGAACG CTCTCAAGC CTCTTCAAGC AAGCAGGCCC AACCAGAAG GCCACACAGA GCCACCAGA ACGCTGCCG ACCCGGGCCC CCTCTGGAACG GGGCCTGAACA ATCGGCAGA ACGCTGCAGA ACGCTGCAGA ACGCTGGAGA ATCAGCCTCC CCAACAAGA CCCAGCTCCCG CCGAAAAATAC CAGGAGGGGC CCCAAAAATAC CAGGAGGGGC CTCCCCAAAA CCCAGCTCCC CAACCAGA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGGGGGGGACCCGGGGGGGGGG	COSCOGCOGC COGCOGCOGC AGGATCOGAG AGGATCOGAG AGGATCOGAG ACAGGGCCCAG ACAGGGCTAA CAGGGCTAAC AGAGCTGAAC AGAGCTGAAC AGAGCTGAAC AGAGCTCAC AGAGCTCAC AGAGCTCAC AGAGCCCCAC AGAGCCCCAC AGAGCCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC AGAGCCCAC ACCAACCGC ACCAACCA	120 180 360 480 540 660 780 960 1080 1140 1260 1320 1440 1560 1680 1680 1740 1800 1680 1740 1800 1680 1740 1800 1800 1800 1800 1800 1800 1800 18
50 55 60 65 70	1	11 GCGAGGCTTC GTCTCCGCCT GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGTGGCC GCGGGGGGAG CAGGCGGAG CAGGCGGAG CTCCAGCAG GTACTACCGC GCTACTACCGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CTGCCTGGGC CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAAGCTG CATGAACATC CAACAGGAACTTC CAACAGGAC CTGCCTGGGC CATGAACATC CATGAACATC CATGAACATC CATGAACATC CATGAACATC CTTACACATC CATGAACATC CTGCCTGGGC CCTGCAGGC CCTGCAGGC CCTGCAGG CCTGCAGG CCTGCAGG CCTGCAGG CCTGCAGG CATGACTTC GGCTGCAGC CATGACCTTC GGCTCCAGG CAGGCCCTG CAGGCCCTG CAGGCCCTG CGCCTCCAAGG CACTCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCCC CGCCTCCAAGG CACTCCCCC CGCCTCCAAGG CACCCCCC CGCCTCCAAGG CACTCCCCC CCCCC CCCCC CCCCCC CCCCC CCCCC CCCC	21 GGACCTCGCA CCTCGCCGCA CCTCGGCGGC GGGGGCGCCCG GCGGAGGCCCC ATCTCGGGTG GAGGTCGCC ATCTCGGGTG GAGGTCGCC ATCTCGGAACG CTCTCAAGC CTCTTCAAGC AAGCAGGCCC AACCAGAAG GCCACACAGA GCCACCAGA ACGCTGCCG ACCCGGGCCC CCTCTGGAACG GGGCCTGAACA ATCGGCAGA ACGCTGCAGA ACGCTGCAGA ACGCTGGAGA ATCAGCCTCC CCAACAAGA CCCAGCTCCCG CCGAAAAATAC CAGGAGGGGC CCCAAAAATAC CAGGAGGGGC CTCCCCAAAA CCCAGCTCCC CAACCAGA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCGCGCCGC GGACCGGGGGGGGGACCCGGGGGGGGGG	CGCCGCCGCCCCCCGAGGAGAACCCAAGAGGACCCAAGAGGACCCCCC	120 180 360 480 540 660 780 960 1080 1140 1260 1320 1440 1560 1680 1680 1740 1800 1680 1740 1800 1680 1740 1800 1800 1800 1800 1800 1800 1800 18

5	TCTGAGATGA TGCATGATGC CCTCCCCTCA GCGCAGGCTG CAGAGCCCGG CCCCACCTCC 246 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGAGGCC TGAGACAGCA CCACTGCTGA 252 GGAGTCTGAG GACTGTCCTC CCACAGACCC TGCAGTGAG GGCCCTCCAT GCGCAGTGA 252 GGGGCCACTG ACCCACTGC GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG 264 GGAGGCAGC TGGGCTCTGC CAATGTGGC TGCCCCTGC ACACAGGGCC CACAGGGCAG 270 GCCTTGCTGG GGTCCAGGGC TGTTGGAGGA CCCGAGGGC TGAGGAGCAG CCAGGCCCG 270 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTC CTGTTCACCG TGACACAGGT 262 CAGGGCTCAG AGTGACCCTC GGCTGTCACC TGCTCACAGG GATGACGGG CCTGCAGGG CACAGGGAA TGCCTAGGTC CTTCCCCAAC CCAGCCAGCT GCACTGCAGG 286 CCCGCACTG CACACGGGAA TGCCTAGGTC CTTCCCCGAC CCAGCCAGCT GCACTGCAGG 286 GCACGGGGAC CTGGATAGTT AAGGGCTTT CCAAACATGC ATCCATTAC TGACACTTCC 30 TGTCCTTGTT CATGGAGAGC TGTTGCGCCC TCCCAGATGG CTCCGAGGCC 306	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
15 20	CACCITIGAC CITEGITACC TICTITICACT CACTIGAGGCC ATCAGGGCC TIGCCCAGGC 312 CTIGACGGC CITCCITCC TICTITICACE CAGTIGACGG GGAGGGTTG 324 TOTIGITITITIC GGAAGGGTTC CTICAACGGG AGAGGACTTG GGGGCAGCTTG 324 TICTIGAACGG ACTGACCCTG AGAGGCCCG TIAGTGCCC CATGACTTTT ATCACCGTCC 334 CCACACTTGG ACGGGGTCC CCGGTTGCTG GTCAGGTCCC CATGACTTGT TICTIGAACG 334 CCTGACTTTAG ATGTTTTGGG ATCAGGAGC CCCAAACACAG GCAAGTCCAC CCCATAATAA 344 CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GACCCCAC CCTACACTAG CCACACTCCC GCTTCACACA GACGGCCTAG GGGTGGCCCT CAGACCCCAC CCTACGCTCA TCTCTGGAAG GGGCAGGCCTG GAGTGGCCAAG CTGCTGTGT 366	20 30 10 50 50 80
25	CCTTCCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGAG 36 TCCTTGTATG AATAAAAGGC TGGAAACCTA AA Protein_sequence_17	60
30	Gene name: glypican 1 Unigene number: Hs.2699 Protein Accession #: NP_002072 Signal sequence: none found Pfam domain: Glypican protein [2-490] Transmembrane domains: none found Cellular Localization: plasma membrane	
35	1 11 21 31 41 51	60 20 .80
40	TDKPWGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 3 RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA	180 130 160
45	DNA sequence 18 Gene name: NY-REN-24 antigen Unigene number: Hs.128425 Nucleic Acid Accession #: AF155102 Coding sequence: 27-908	
50	1 11 21 31 41 51 1 CGGAGGGGG GGGCGAGGGG GTGCTCATGG AGGAGGACCT GATCCAGCAG AGCCTGGACG ACTACGACGC CGGCAGGTAC AGCCCGGGC TGCTCACGG GCACGAGCTG CCACTGGACG CGCACGTGCT GGAACCGGAT GAGGACCTGC AGCGCCTGCA GCTCTCGCGC CAGCAGCTCC	60 120 180
55	GCATGGGCCA GGACGAGGCG CAGTTCAGCG TGGAGATGCC ACTCACCGGC AAGGCCTACC TGTGGGCCGA CAAGTACCGG CCACGCAAGC CGCGCTTCTT CAACCGCGTG CACAGGGCT TCGAGTGGAA CAAGTACAAC CAGACGCACT ACGACTTTGA CAACCCACCG CCAACGCACCT TGCAGGGATA CAAGTTCAAC ATCTTCTTACC COGACCTCAT GGACAAGGCGC TCCAAGGCCG	240 300 360 420 480
60	GCCGCCTACG AGGACATCGC TITICAAGATC GTCAACCGC AGTGGGAATA CTCGCACCGC CACCGCTTCC GCTGCCAGTT TGCCAACGGC ATCTTCCAGC TGTGCTTTCA CTTCAAGCGC TACCGCTATC GCCGGTGACG GCCCTGGGGA ACGGCAGGC AGGACGACCACG GGGTGCCACA GCCCAGGTC AGCGCCACCC GCGTGCCACA GCCCAGGC TTGTTCTTCA GCATCCGACG	540 600 660 720 780
65	GGAACATCTC CAACAGAAGC AAAACGGAAA GTGCCTCCCG GACCCCCAGA GGGCCACCCA ACCTCACCAG TCACCAGCCC CAGACCACCC ACAGCCCCC CCAGACACCC CGCCCCATCT CGGAAATAGTT CCGTTTGTTT CTCTAAAAAG ACTTGTAGGT GGGAAAAAAA ATCTTTTGTT CTCATGGAAT TGGCCTATTG GCAAGATCGC ATGTTTTTTT AATAAACGTT GTATTTTAGA ATAAAA	840 900 960 .030
70	Protein sequence 18 Gene name: NY-REN-24 antigen Unigene number: Hs.128425 Protein Accession #: AAD42868	
75	Signal sequence: none found Transmembrane domains: none found Cellular Localization: plasma membrane 1 11 21 31 41 51	
80	GEGEAVLME EDLIQQSLDD YDAGRYSPRL LTAHELPLDA HVLEPDEDLQ RLQLSRQQLQ TGDASESAE DIPPRRAKEG MGQDEAQFSV EMPLIGKAYL WADKYRPRKP RPFNRVHTGF WNKYNQTHY DEDNPPPKIV QQYKFNIFYP DLIDKRSTPE YPLEACADNK DPAILRFTRG LRGHRFQDR QPRVGILAPP RLPLPVCQRH LPAVLSLQAL PLSAVTALKN GRPGGPRATR	60 120 180 240 300

	DNA sequenc	-a 10					
	Gane nime: tumor necrosis factor receptor superfamily, member 1A						
	Unigene number: Hs.159 Probeset Accession #: BE295782						
5	Nucleic Ac	cession #: ld Accession	BB295782	065			
	Coding sequ	ence: 256	.1623	.005			
	1	11	21	32	41	51	
	OGGCCCAGTG	ATCTTGAACC	(C) 2 2 CC (C)	Charmon	1	!	
10	GAAAATTAAA	GCAGAGAGGA	GGGGAGAGAT	CACTGGGACC	ACCOMMAN	CTYCERSTON	60 120
	GAGTETCAAC	CCTCAACIGT	CACCCCAAGG	CACTTGGGAC	GTCCTCGACA	CACCCACTCC	180
	COMMINANCE	CAGCACTGCC CTGGCATGGG	GCTGCCACAC	TGCCCTGAGC	CCABATGGGG	CACTCACACC	240
	CTGGAGCTGT	TGGTGGGAAT	ATACCCCTCA	GGGGTTATTG	GACTGCTGCC	GCTGGTGCTC	300 360
15	GACAGGGAGA	AGAGAGATAG	TOTGTGTCCC	CAAGGAAAAT	スマルサイベート	ポーシストルマスステ	420
	TOGATTTGCT	GTACCAAGTG	CCACAAAGGA	ACCTACTTOP	ACAATGACTG	TOTAGGGGGGG	480
	CTCAGACACT	CGGACTGCAG GCCTCAGCTG	CTCCAAATGC	CGADAGGAAA	TYRESTYCACCET	CCACA TOTAL	540 600
20	TUTTUCACAG	TGUACCEGGA	CACCGTGTGT	GGCTGCAGGA	ACABACCAGEA	COCCO CO CONTRACTOR OF THE PARTY OF THE PART	660
20	TOWNSTWARK	ACCITITICCA	GTGCTTCAAT	TGCAGCCTCT	GCCTCAATGG	GACYCOTOCAC	720
	UAMAACGAGT	AGGAGAAACA GTGTCTCCTG	TACITALCTORT		かんしゅう いっとり へんしゅう	CL LOWINGORGO	780
	CIACCCCAGA	TIGAGAATGT	TARGGGGCACT	GAGGACTCAG	CALCA CALCA CACA	CONCERNOOS	840 900
25	CIGGICATIT	TCTTTGGTCT	TIGOCITITA	TCCCTCCTCT	TCATTCGTTT	AATGTATOGC	960
~~	INCOMEGGI	GGAAGTCCAA TTGAAGGAAC	GCTCTACTCC	STRUCTURE	COLDANTOCOCO	ACCTY20 N N N N	1020
	ACTCCAGGCT	TCACCCCCAC	CCTGGGGCTTC	AGTCCCCGTCC	CCAGTTCCAC	CALLOS CARGOS	1080 1140
	WOC ! COVEC!	ATACCCCCCC	TGACTGTCCC	AACTTTGCGG	CTCCCCGCAG	ACACCITOCOCA	1200
30	CONCOCINIC	AGGGGGCTGA AGAAGTGGGA	CCCCATCCTT	GCGACAGCCC	TOTOTOTO	CCCCATCCC	1260
	CELTACONCOC	TUTACUCCUT	GGTGGAGAAC		TO CONTRACTOR A	CONSTRUCTO	1320 1380
	CGGCGCCTAG	GGCTGAGCGA	CCACGAGATC	GATCGGCTGG	AGCTYTCAGAA	CCCCCCCCCC	1440
	GCCACGCTGG	CGCAATACAG AGCTGCTGGG	ACCCUTACTO	ACCTGGAGGC	GGCGCACGCC	GCGGCGCGAG	1500
35	GACATCGAGG	AGGCGCTTTG	CGGCCCCGCC	GCCCTCCCCC	CCCCCCCCCC	TOTALOGO	1560 1620
	TGAGGCTGCG	CCCCTGCGGG	CAGCTCTAAG	GACCGTCCTG	CCAGATCCCC	THE COLOR	1680
	GGTGCTMACC	GGAAAGGAGG CCTCGATGTA	CATAGCTTTT	CTCAGCTGCC	TATELLATION	CCDCDCCCCC	1740
40	CGCTGTGCGC	GCCGAGAGAG	GTGCGCCCTG	GGCTCAAGAG	CCTGAGTGGG	TYPETERSON	1800 1860
70	GGATGAGGGA	CCTATCCCT	CATGCCCCTT	TTCCCTCTCC	TCACCAGCAA	CCCCCCCCC	1920
	1111611116	TITOTCCCTG	AAATCAATCA	TGTTACACTA	TTAGGAAACT-C	COURT CONTRACTOR	1980 2040
	ICCCCICIOC	CIGGACAAGC	ACATAGCAAG	CTGAACTGTC	CTARGGCAGG	CCCGRCCRCC	2100
45	GAACAATGGG	GCCTTCAGCT	GGAGCTGTGG	ACTITITAC	ATACACTAAA	ATTCTGAAGT	2160
	-						
	Protein sec	ruence 19					
	Cene name: Unigene nu	tumor nec doer: Hs.1	rosis facto: 59	r receptor	superfamily,	member 1A	
50	Protein Acc	cession #:	NP_001056				
	Signal sequ		9 _				
	TNPR domain	n: 44-81, ene domains	84-125, 127.	-166, 168-1	95		
55	Cellular L	calization	: plasma m	embrane			
23	1	11 .	21	31	41	51	
		LPLVLLELLV	GIVPSQUIGI.	UDDI CIDDEVD	Dencio	I DOINIGE COS	
	MCHROT I LYN	DCPGPGQDTD	CRECESGSFT	ASENHLBHCT.	RCRKCOKPMO	CURTROCER	60 120
60	KUT V CGCKKN	OYKHYWSENL	FOCENCSI CT.	NGTWILECTE	CONTRACTOR AND A	ADDI DOMONO.	180
	SKTARIACCK	CTKLCLPQIE STPEKEGELE	GTTTKPLAPN	PRPRPTPRPT	DTTATECTUDE	DTTTT DO COVE	240 300
	PODCENERAL	KKEAVBBAOG	ADPILATALA	SDPIPNPIOK	MED CANKDOO	LOTTODDATEV	360
_	WA A DULA D. D. P. P.	WKEPVRRLGL LGCLEDIBEA	SUBBIDRLEL	QNGRCLREAG	YSMLATWRRR	TPRREATLEL	420
65			INGPARLIPPA	PSULK			
	DNA sequen		_				
	Unicene nu	prominin mber: Hs.1:	(mouse)-lik	e 1			
70	Probeset A	cession #1	R40057				
70	Nucleic Ac	id Accession	#: NM_00	6017			
	coging seq	uence: 38-: 11	2635 21	••			
	1	1	1	31 	41 	51 	
75	CCAAGTTCTA	CCTCATGTTT	GGAGGATCTT	GCTAGCTATG	GCCCTCGTAC	TOGGCTCCCT	60
, 5	GLIGGIGGIG	GGGCTGTGCG TGGAATTATG	GGAACTCCTT	TTCAGGAGGG	CAGCCTTCAT	CCACACATCA	120
	ACC. LOCALCEL	ATTGGCATTC	TCTTTGAACT	AGTGCATATC	TITTE TO THE	TOOTACACCO	180 240
	GCGTGATTTC	CCAGAAGATA	CTTTGAGAAA	ATTCTTACAG	አልርርርር አጥል ጥ ር	DATCCBBBBB	300
80	TUATTATUAC	AAGCCAGAAA TGCTGTGTCC	CTGTAATCTT	AGGTCTAAAG	ATTICTOR OF	ATTONACONCO	360
•	1117111161	AIGIGICUTT	GCTYTTAACAA	ATY:TY:/ZTY:/A	Chhammanaa	100010000	420 480
	COMMUTUGG	CUCITCUTGA	CGAAAATGCTT	TOTALTOT	CALCALANA VANCON		540
	WATWAGE ATT	GGCATCTTCT AAACTGGCAG	ATGGTTTTGT	GGCAAATCAC	<u> የ</u> መርረም የተመሰመ አ	~~~	600
					CONNETETE	▼OWNIGHER	660

	TCCAGAGCAA ATCAAATATA TATTGGCCCA GTACAACACT ACCAAGGACA AGGCGTTCAC 72	
	AGATCTGAAC AGTATCAATT CAGTGCTAGG AGGCGGAATT CTTGACCGAC TGAGACCCAA 78	
	CATCATCCCT GTTCTTGATG AGATTAAGTC CATGGCAACA GCGATCAAGG AGACCAAAGA 84	
_	GGCGTTGGAG AACATGAACA GCACCTTGAA GAGCTTGCAC CAACAAAGTA CACAGCTTAG 90	0
5	CAGCAGTCTG ACCAGCGTGA AAACTAGCCT GCGGTCATCT CTCAATGACC CTCTGTGCTT 96	
	GGTGCATCCA TCAAGTGAAA CCTGCAACAG CATCAGATTG TCTCTAAGCC AGCTGAATAG 102 CAACCCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTTGACAACG TTAATAACGT 108	
	TCTTAGGACA GATTTGGATG GCCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC 114	
• •	TGACAGAGTA CAACGCCAAA CCACGACTGT CGTAGCAGGT ATCAAAAGGG TCTTGAATTC 120	
10	CATTOGITCA GATATCGACA ATGTAACTCA GCGTCTTCCT ATTCAGGATA TACTCTCAGC 126	0
	ATTCTCTGTT TATGTTAATA ACACTGAAAG TTACATCCAC AGAAATTTAC CTACATTGGA 132	
	AGAGTATGAT TCATACTGGT GGCTGGGTGG CCTGGTCATC TGCTCTCTGC TGACCCTCAT 138 CGTGATTTTT TACTACCTGG GCTTACTGTG TGGCGTGTGC GGCTATGACA GGCATGCCAC 144	
	CCCGACCACC CGAGGCTGTG TCTCCAACAC CGGAGGCGTC TTCCTCATGG TTGGAGTTGG 150	
15	ATTAACTTTC CTCTTTTGCT GGATATTGAT GATCATTGTG GTTCTTACCT TTGTCTTTGG 156	
	TGCAAATGTG GAAAAACTGA TCTGTGAACC TTACACGAGC AAGGAATTAT TCCGGGTTTT 162	0
	GGATACACCC TACTTACTAA ATGAAGACTG GGAATACTAT CTCTCTGGGA AGCTATTTAA 168	
	TARATCARAR ATGRAGCTCA CTTTTGRACA AGTTTACAGT GACTGCARAR ARATAGAGG 174 CACTTACGGC ACTCTTCACC TGCAGARCAG CTTCRATATC AGTGRACATC TCRACATTAR 180	
20	TGAGCATACT GGAAGCATAA GCAGTGAATT GGAAAGTCTG AAGGTAAATC TTAATATCTT 186	
	TCTGTTGGGT GCAGCAGGAA GAAAAACCT TCAGGATTTT GCTGCTTGTG GAATAGACAG 192	
	ARTGARTTAT GACAGCTACT TGGCTCAGAC TGGTAAATCC CCCGCAGGAG TGAATCTTTT 198	0
	ATCATTTGCA TATGATCTAG AAGCAAAAGC AAACAGTTTG CCCCCAGGAA ATTTGAGGAA 204	
25	CTCCCTGAAA AGAGATGCAC AAACTATTAA AACAATTCAC CAGCAACGAG TCCTTCCTAT 210 AGAACAATCA CTGAGCACTC TATACCAAAG CGTCAAGATA CTTCAACGCA CAGGGAATGG 216	
	AGAACAATCA CTGAGCACTC TATACCAAAG COTCAAGATA CTTCAACGCA CAGGGAATGG 216 ATTOTTOGAG AGAGTAACTA GGATTCTAGC TTCTCTGGAT TTTGCTCAGA ACTTCATCAC 222	
	AAACAATACT TCCTCTGTTA TTATTGAGGA AACTAAGAAG TATGGGAGAA CAATAATAGG 228	
	ATATTTTGAA CATTATCIGC AGTGGATCGA GTTCTCTATC AGTGAGAAAG TGGCATCGTG 23	10
30	CAAACCTGTG GCCACCGCTC TAGATACTGC TGTTGATGTC TTTCTGTGTA GCTACATTAT 240	
30	CGACCCCTTG AATTTGTTTT GGTTTGGCAT AGGAAAAGCT ACTGTATTTT TACTTCCGGC 246 TCTAATTTTT GCGGTAAAAC TGGCTAAGTA CTATCGTCGA ATGGATTCGG AGGACGTGTA 257	
	CGATGATGTT GAAACTATAC CCATGAAAAA TATGGAAAAT GGTAATAATG GTTATCATAA 250	
	AGATCATGTA TATGGTATTC ACAATCCTGT TATGACAAGC CCATCACAAC ATTGATAGCT 264	
25	GATGITGAAA CIGCITGAGC ATCAGGATAC TCAAAGIGGA AAGGATCACA GATTITIGGI 270	00
35	AGTITCIGGG TCTACAAGGA CTTTCCAAAT CCAGGAGCAA CGCCAGTGGC AACGTAGTGA 270	
	CTCAGGCGGG CACCAAGGCA ACGGCACCAT TGGTCTCTGG GTAGTGCTTT AAGAATGAAC 28: ACAATCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGACTCCCTC CCTTCCTGTC 28:	
	ACANTCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGACTCCCTC CCTTCCTGTC 28 TATTTTTGTT TTTTACTTTT TTACACTGG TTTCTATTTA GACACTACAA CATATGGGGT 29	
40	GTTTGTTCCC ATTGGATGCA TTTCTATCAA AACTCTATCA AATGTGATGG CTAGATTCTA 30	
40	ACATATTGCC ATGTGTGGAG TGTGCTGAAC ACACACCAGT TTACAGGAAA GATGCATTTT 30	60
	GTGTACAGTA AACGGTGTAT ATACCTTTTG TTACCACAGA GTTTTTTAAA CAAATGAGTA 31	
	TTATAGGACT TTCTTCTAAA TGAGCTAAAT AAGTCACCAT TGACTTCTTG GTGCTGTTGA 31 AAATAATCCA TTTTCACTAA AAGTGTGTGA AACCTACAGC ATATTCTTCA CGCAGAGATT 32	
	TTCATCTATT ATACTITATC AAAGATTGGC CATGTTCCAC TTGGAAATGG CATGCAAAAG 33	
45		60
	GAGAGAGAAA TGCTGTTCGT TCAAAAGTGG AGTTGTTTTA ACAGATGCCA ATTACGGTGT 34	20
		80
		40
50		60
		20
		80
	AAAAAGGAAC TTGGC	
55	Protein sequence 20	
	Gene name: prominin (mouse)-like 1	
	Unigene number: Hs.112360	
	Protein Accession #: NP_006008	
60	Signal sequence: 1-21 Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806	
	Cellular Localization: plasma membrane	
	1 11 21 31 41 51	
65	MALVLGSLLL LGLCGNSFSG GQPSSTDAPK AMMYELPATN YETQDSHKAG PIGILFELVH IPLYVVQPRD PPEDTLRKFL QKAYESKIDY DXPETVILGL KIVYYEAGII LCCVLGLLFI 1	60
UJ		120 180
		240
		300
70		360
70		120
		180 540
		500
75	LKVNLNIFLL GAAGRKNLQD FAACGIDRWN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS (660
75		720
		780
	VFLCSYIIDP LNLFWFGIGK ATVFLLPALI FAVKLAKYYR RMDSEDVYDD VETIPMKNME 1 NGNNGYHKDH VYGIHNPVMT SPSQH	B4¢
00		
80	DNA sequence 21	
	Gene name: G protein-coupled receptor 39	
	Unigene number: Hs.85339 Nucleic Acid Accession #: NM 001508	
	Coding sequence: 1-1362	
	-	

	1	ii	21	31	41	51		
	PASCETTON	C CCAGCCTCC	COCACAGA		1	1		
_	CCCGAGTTT	G AGGTGGCCA	GGGCAGTGAC CTGGATCAAA	ATCACCCTTA	TOTTGGTGTA	COTGATCATC	60 120	
5	TTCGTGATG	G GCCTTCTGG	GAACAGCGCC	ACCATTOGGG	TCACCCAGGT	GCTGCAGAAG	180	
	AAAGGATAC	t tgcagaaggi	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240	
	ACCITCACC	C TCATCGGCA:	GCCCATGGAG CTGCAAGCTG	TTCTACAGCA	TCATCTGGAA	TCCCCTGACC	300	
	GCTACGCTG	C TGCACGTGC	GACACTCAGC	TTTGAGGGCT	ACATORCOAT	CTGCAGCTAC	360 420	
10	TTCAGGTAC	A AGGCTGTGT	C GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480	
	GTCACCTCO	G CCCTGGTGG	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCCTG	540	
	CACCCCCA	C CCAGCCACC	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCACGAG	600	
			CITOGIGGIC				660 720	
15	ATGTGCTGG	A ACATGATGC	A GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780	
	ACGCGGCCT	C CGCAGCTGA	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840	
	ACCATCATC	A TOUTGAGGE	GGCCAAACCC	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900 960	
			CTTCTCGGAG					
20	CCGCTCCTG	T ACACGGTGT	CTCGCAGCAG	TTTCGGCGGG	TGTTCGTGCA	GGTGCTGTGC	1080	
	TGCCGCCTG	T CGCTGCAGC	A CGCCAACCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140	
			r TGTGCAGCGC A GATTTTCTTA					
3.5	TCTAAGTCC	C AGTCATTGA	G TCTCGAGTÇA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1320	
25	AATTCTGCT	G CAGAGAATG	G TTTTCAGGAG	CATGAAGTIT	GA			
	Protein o	equence 21						
			n-coupled re	ceptor 39				
20	Unigene n	umber: Hs.	8533 9	-				
30	Protein A	ccession #:	NM_001508,	NP_001409				•
		quence: no	ne found (72-172, 22	4-2441				
	Transmemb	rane domain	B: 32-54, 6	8-90. 111-1	33. 151-173	. 221-243.	280-301.	320-342
25	Cellular	Localizatio	n: plasma n	embrane		,, .	,	300 010
35	1	11	21	ą1	41	51		•
	MASPELPGS	D CSOIIDHSH	V PEPEVATWII	TTLILVYLII	Į FVMGLLŒNSA	TTPUTOULOR	60	
	KGYLQKEVI	D EMVSLACED	I LVFLIGMPME	PYSLIWNPLT	TSSYTLSCKL	HTPLPEACSY	120	
40	atllhylti	.9 PERYIAICH	P PRYKAVSGPO	: QVKLLIGFVW	VTSALVALPL	LPAMGTEYPL	180	
40			B QPETSNMSIO G TRPPQLRKSI					
			R AYMILLPFS!					
			S TTDSARFVQ					
45	SKSQSLSLI	es Lepnegakp	a nsaaengfoi	3 HEV				
77								
	TABLE 8A: AE	OUT 1260 GENES	SUP-REGULATED	IN GLIOBLASTO	AA COMPARED T	O NORMAL ADUL	THISSUES	
	1 Bible BA lists	about 1260 genes	up-redulated in disc	blasioma comoare	i Uubs Isamon ol b	issues. These wer	a eplacted for	om 59680 probesets on the Affymetrix/Eos Hu03 GeneChip
50	array such the	il the ratio of "avera	ige" glioblastoma to	average" normal	adult tissues was	areater than or eou	albo 2.5. Th	e "average" gliobiastoma level was set to the 75th percentil.
20	sonorific backe	ius guodiasioma iu: imind levels of nor	mors. Ine "averago Lenecific butwidised	e" normai eduil liss Ion, lho 10th norm	us level was set to	the 85th percentik	amongsi va	rious non-malignant tissues. In order to remove gene- s subtracted from both the numerator and the denominator
	before the rati	o was evaluated.	- opcome ny ontoice	ion, tro roar perce	iluo valuo eliking:	or nes investigables	II USSUES WAS	suddenied from ooth the mining rate of the demonthings.
	Pkey:		probeset identifier					
55	ExAcon: UnigenelD:	Exemplar A	ccession number, (Genbank accesslo	number			
JJ	Unigene Tide:	Unigene nu Unigene ge						
	R1:		h percentile tumor	to 85th percentile r	ormal body tissue			
	M			-	,			
60		xAcon Uniq 016181 Hs.2	teneiD Unigene	Tille Il myelin protein 2			R1	
00				nase C binding on	tein 2		75.2 74.6	
	455601 A	1368680 Hs.6	16 SRY (see	determining regio			74.2	
		J699994 Hs.2		i myelin protein 2	•		71.6	
65			129911 ESTs 315369 Homosa	DMA- F1 10	2075 64 1		70.7	
05				piens cDNA: FLJ2 rosine phosphetes			68.3 64.3	
	413472 E	E242870 Hs.1	75379 solute ca	rrier family 1 (glial			60.1	
			127792 delta (Dr	osophila)-like 3			52.3	
70			1774 Homo sa 159623 NK-2 (Dr	plens mRNA; cDN osophila) homolog	A DKFZp761C171	2 (f	46.7	
. •			74554 KIAA008		В		40.1 39.0	
	418375 N	M_003081 Hs.	34389 synaptos	comal-associated p			38.7	
				x determining regio			37.2	
75				piens mRNA; cDN		4 (f	36.8	
				t growth factor 1 (a cadherin-associate			32.8 31.8	
	431941 /	AK000106 Hs.	272227 Homo sa	piens cDNA FLJ2			31.8	
			47448 ESTs				31.4	
80				ssociated oligoden scute complex (Or			30.9	
-5			12450 protocad		Asochura) LIGUIOL		30.4 30.2	
	439415	F05538 Hs.	12825 ESTs				28.3	
	430838	N46664 Hs.	169395 hypothe	lical protein FU12)15		26.9	

	400.400				
	429466 447004	M85835	Hs.12827	ESTS	25.9
	424581	AW296968 M62062	Hs.157539 Hs.150917	ESTs	25.3
_	452744	Al267652	Hs.30504	catenin (cadherin-associated protein), a Homo sapiens mRNA; cDNA DKFZp434E082 (fr	24.8
5	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.8 24.3
	453642	AI370936	Hs.34074	dipeptidyipeptidase Vi	24.3
	424140	Z48051	Hs.141308	myelin oligodendrocyte głycoprotein	24.2
	450133 408562	AW969769 Al436323	Hs.105201	ESTs	24.2
10	448672	AI955511	Hs.31141 Hs.225106	Homo sapiens mRNA for KIAA1568 protein, ESTs	23.3
	435708	Al362949	Hs.75169	ESTs	22.7 22.0
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	21.9
	407168	R45175	Hs.117183	ESTs	21.7
15	431019	NM_005249	Hs.2714	forkhead box G1B	21.5
13	409049 433896	AV423132 AW294729	Hs.146343	EST ₆	21.4
	445041	T64183	Hs.274461 Hs.282982	ESTs solute carrier	21.1
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	21.0 20.4
20	444378	R41339	Hs.12569	ESTs	20.0
20	411305	BE241596	Hs.69547	myelin basic protein	19.9
	437414 441016	AW894071	Hs.48448	hypothetical protein DKFZp547C176	19.8
	440435	AW138653 AL042201	Hs.25845 Hs.21273	ESTs	19.6
	438209	AL120659	Hs.6111	transcription factor NYD-sp10 aryl-hydrocarbon receptor nuclear transl	18.5
25	452461	N78223	Hs.108106	transcription factor	18.4 18.1
	409395	U46745	Hs.54435	dystrobrevin, alpha	18.1
	417183 409638	R52089	Hs.172717	EST ₈	18.0
	428392	AW450420 H10233	Hs.21335 Hs.2265	ESTs	18.0
30	449611	AI970394	Hs.197075	secretory granule, neuroendocrine protei ESTs	18.0
	446692	Z44514	Hs.156829	Homo saplens mRNA for KIAA1763 protein,	17.0 16.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9
	444471	A8020684	Hs.11217	KIAA0877 protein	16.8
35	421659 431725	NM_014459 X65724	Hs.106511 Hs.2839	protocadherin 17	16.7
	429276	AF056085	Hs.198612	Norrie disease (pseudoglioma) G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.6 16.5
	441440	AI807981	Hs.30495	EST8	15.7
40	449433	A1672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	15.7
70	421264 415910	AL039123 U20350	Hs.103042 Hs.78913	microtubule-associated protein 18	15.5
	413597	AW302885	Hs.117183	chemokine (C-X3-C) receptor 1 ESTs	15.3
	424945	Al221919	Hs.173438	hypothetical protein FLJ10582	15.1 14.9
15	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	14.9
45	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
	416857 419721	AA188775 NM_001650	Hs.292453	ESTs	14.7
	411078	AI222020	Hs.288650 Hs.182364	aquaporin 4 CocoaCrisp	14.6
	453924	R49295	Hs.24886	ESTS	14.4 14.4
50	409389	A8007979	Hs.3012B1	Homo sapiens mRNA, chromosome 1 specific	14.3
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
	410909 412266	AW898161 N59006	Hs.53112 Hs.26133	ESTs, Moderately similar to ALUB_HUMAN A	14.0
	412986	X81120	Hs.75110	ESTs cannablnoid receptor 1 (brain)	14.0
55	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	14.0 14.0
	439239	AJ031540	Hs.235331	ESTs	14.0
	441497	R51084	Hs.23172	ESTs	14.0
	445495 414245	BE622641 BE148072	Hs.38489 Hs.75850	ESTs, Weakly similar to I38022 hypotheti	14.0
60	429900	AA460421	Hs.30875	WAS protein family, member 1 ESTs	13.7
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6 13.6
	449605	AW138581	Hs.198416	ESTs	13.6
	452526 420547	W38537	Hs.280740	hypothetical protein MGC3040	13.6
65	441350	AF155140 AB020690	Hs.98738 Hs.7782	gonadotropin-regulated testicular RNA he	13.3
•-	420077	AW512260	Hs.87767	pareneoplastic antigen MA2 ESTs	13.3
	424120	T80579	Hs.290270	ESTs	13.2 13.2
	456965	AW131888	Hs.172792	ESTs, Wealdy similar to hypothetical pro	13.2
70	423361	AW170055	Hs.47628	ESTs	13.1
70	428409 417160	AW117207	Hs.98523	ESTs	12.9
	451621	N76497 A1879148	Hs.1787 Hs.26770	proteolipid protein 1 (Pelizaeus-Merzbac fatty acid binding protein 7, brain	12.6
	411379	Al816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5 12.5
75	436954	AA740151	Hs.130425	ESTs	12.5 12.4
75	430691	C14187	Hs.103538	ESTs	12.4
	433551 422544	A1985544 AR018260	Hs.12450	protocadherin 9	12.4
	427540	AB018259 R12014	Hs.118140 Hs.20976	KIAA0716 gene product ESTs	12.2
00	435624	AF218942	Hs.24889	formin 2	12.1
80	415849	R20529	Hs.6806	ESTs	12.1 12.1
	428845	AL157579	Hs_153610	KIAA0751 gene product	11.9
	442671 444396	AI005668 T65213	Hs.134779	EST	11.9
	444350	103213	Hs.4257	ESTs	11.8
				. 100	

	452752	AW044058	Hs.33578	KIAA0820 protein	11.8
	425523 416072	AB007948	Hs.158244	KIAA0479 protein	11.8
	440184	AL110370	Hs.79000	growth associated protein 43	11.7
5	428976	AB002297 AL037824	Hs.7022	dedicator of cyto-kinesis 3	11.7
-	444783	AK001468	Hs.194695 Hs.62180	ras homolog gene family, member !	11.6
	448299	AA497044	Hs.20887	anillin (Drosophila Scraps homolog), act	11.6
	414214	D49958	Hs.75819	hypothetical protein FLJ10392 glycoprotein MSA	11.6
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
10	405238			The state of the s	11.5
	420352	U79734	Hs.97206	huntingtin interacting protein 1	11.4 11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs.169309	myelin-essociated oligodendrocyte basic	11.4
1.5	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
15	451952	AL120173	Hs.301663	ESTs	11.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTs	11.3
20	429918	AW873986	Ha.119383	ESTs	11.3
20	443912	R37257	Hs.184780	ESTs .	11.3
	448743 420092	AB032962	Hs.21896	KIAA1136 protein	11.3
	408081	AA814043 AW451597	Hs.88045	ESTs	11.2
	411642	NM_014932	Hs.167409 Hs.71132	ESTs	11.2
25	415170	R44386	Hs.164578	neuroligin 1 ESTs	10.9
	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.9
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8 10.8
20	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	10.7
30	400293	N51002	Hs.305480	Homo sepiens mRNA; cDNA DKFZp761E2112 (f	10.7
	447773	A1423930	Hs.36790	ESTs. Wealty similar to putative p150 [H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coti (ika	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
35	440684	Al253123	Hs.127358	ESTs, Highly similar to S21424 nestin [H	10.3
55	444017 438380	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
	440471	T05430 AA886146	Hs.6194 Hs.307944	chondroitin suffate proteoglycen BEHAB/b	10.3
	413063	AL035737	Hs.75184	EST8	10.2
	439978	BE139460	Hs.124873	chitinase 3-like 1 (cartilage glycoprote Homo sapiens cDNA FLJ11477 fs, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo seplens mRNA; cDNA DKFZp76111912 (I	10.1
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	10.1 9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AI538323	Hs.52620	integrin, beta 8	9.8
45	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
73	436511 414596	AA721252	Hs.291502	ESTs	9.8
	449539	AF002020 W80363	Hs.76918	Niemann-Pick disease, type C1	9.7
	412959	D87458	Hs.58446 Hs.75090	ESTs KIAA0282 prolein	9.7
	412811	H06382	Hs.21400	ESTs	9.6
50	449300	AJ656959	Hs.222165	ESTs	9.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.6 9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
55	451516	AI800515	Hs.12024	ESTs	9.4
"	422656	AI870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo saplens, Similar to RIKEN cDNA 5730	9.3
	414175 415279	Al308876	Hs.103849	hypothetical protein OKFZp761D112	9.3
	428784	F04237 Y12851	Hs.1447 Hs.193470	glial fibrillary acidic protein	9.2
60	429903	AL134197	Hs.93597	purtnergic receptor P2X, ligand-gated to	9.2
	424641	AB001106	Ha.151413	cyclin-dependent kinase 5, regulatory su glia maturation factor, beta	9.2
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	44944B	D60730	Hs.57471	ESTs	9,1
	408508	AI806109	Hs.135736	KIAA1580 protein	9.1 9.0
65	452785	AL359942	Hs.298434	erythrold differentiation and denucleati	9.0
	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	8.9
70	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
70	449825	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
	400292 417404	AA250737	Hs.72472	ESTs	8.7
	420345	NM_007350 AW295230	Hs.82101 Hs.25231	plackstrin homology-like domain, family	8.7
	429927	NM_001115	Hs.2522	ESTs	8.7
75	437528	N59648	Hs.169745	adenylate cyclase 8 (brain) crumbs (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	Interleukin 13 receptor, elpha 2	8.7
	400780				8.6
90	434891	AA814309	Hs.123583	ESTs	8.6 8.6
80	449277	AA001064	Hs.172976	ESTs	8.6
	415709	AA649850	Hs.278558	ESTs	8.5
	439947	AB005627	Hs.6788	astrotactin	8.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5

	433042	AW193534	Hs.281895	Homo sapiens cDNA FL/11660 fis, clone HE	8.4
	416370	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	8.4
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	8.4
5	415796	R87548	Hs.78854	ATPase, Na+/K+ transporting, beta 2 poly	8.3
,	426271 408947	AF028547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	8.3
	419863	AL080093 AW952691	Hs.49117 Hs.93485	Homo sapians mRNA; cDNA DKFZp564N1662 (f	8.3
	433447	U29195	Hs.3281	Homo septens mRNA; cDNA DKFZp761D191 (fr neuronal pentradn II	8.3
	431467	N71831	Hs.256398	Homo sepiens mRNA; cDNA DKFZp434E0528 (I	8.3 8.3
10	409327	L41162	Hs.53563	coflagen, type IX, alpha 3	8.3
	414300	AJ304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	EST8	8.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
15	419704 429007	AA429104 D80642	Hs.45057	EST8	8.2
10	442710	AI015631	Hs.23210	gb:HUM092E09B Human fetal brain (TFujiwa	8.1
	425048	H05468	Hs.164502	ESTs ESTs	8.1
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	8.1
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0 8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
	422728	AW937826	Hs.103262	ESTs, Wealty similar to 2N91_HUMAN ZINC	7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neuroligin	7.9
25	455384 446819	H72176 AU076643	Hs.4273	hypothetical protein FLJ13159	7.9
	435501	AW051819	Hs.313 Hs.129908	secreted phosphoprotein 1 (osteopontin,	7.9
	423600	Al633559	Hs.310359	KIAA0591 protein ESTs	7.8
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	7.8 7.8
20	415314	N88802	Hs.5422	glycoprotein M6B	7.7
30	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586i1823 (f	7.7
	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	AI982493	Hs.197647	ESTs	7.7
	419249 407896	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.7
35	419103	D76435 Z40229	Hs.41154 Hs.95423	Zic family member 1 (odd-paired Drosophi	7.7
-	438779	NM_003787	Hs.6414	hypothetical protein FLJ23033 nucleolar protein 4	7.6
	433532	AW976367		gb:EST387475 MAGE resequences, MAGN Homo	7.6 7.6
	448555	AI536697	Hs.159863	ESTs	7.5
40	439662	H97552	Hs.269060	ESTs	7.5
40	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	7.5
	410099	AA081630	Hs.169387	KIAA0036 gene product	7.5
	431592 409731	R69016 AA125985	Hs.213194	hypothetical protein MGC10895	7.4
	405819	AA123363	Hs.56145	thymosin, beta, identified in neuroblast	7.4
45	407886	AW969688	Hs.100826	ESTs	7.4
	437416	AL359605	Hs.283851	Homo sepiens mRNA; cDNA DKFZp547G036 (fr	7.4 7.4
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 catcl	7.4
	408604	D51408	Hs.21925	ESTS	7.4
50	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
50	447499 454036	AW262580 AA374756	Hs.147674	protocadherin beta 16	7.3
	409746	NM_004794	Hs.93560 Hs.56294	Homo seplens mRNA for KIAA1771 protein,	7.3
	410037	AB020725	Hs.58009	RAB33A, member RAS oncogene family KIAA0918 protein	7.2 7.2
	419318	AW969742	Hs.291005	ESTs	7.2
55	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.2
	442028	A1243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52620	integrin, beta 8	7.2
	436281 426429	AW411194 X73114	Hs.85195 Hs.169849	myeloid leukenia factor 1	7.2
60	407182	AA312551	Hs.230157	myosin-binding protein C, slow-type ESTs	7.2
	415293	R49462	Hs.106541	ESTs	7.1
	422764	AI767727	Hs.47522	ESTs	7.1 7.1
	451592	AI805416	Hs.213897	ESTs	7.1
65	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0
02	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
	434149	Z43829	Hs.19574	hypothetical protein MGC5469	7.0
	436726 417632	AA324975 R20855	Hs.128993 Hs.5422	ESTs, Wealdy similar to T00079 hypotheti	7.0
	422421	AA325138	Hs.235873	glycoprotein M6B hypothelical protein FLJ22672	7.0
70	435267	N23797	Hs.110114	ESTs	6.9 6.9
	437117	AL049256	Hs.122593	ESTs	6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070528	Hs.13429	Homo saplens clone 24787 mRNA sequence	6.9
75	445745	AB007924	Hs.13245	KIAAD455 gene product	6.9
, ,	424085 428588	NM_002914 F12101	Hs.139226 Hs.185701	replication factor C (activator 1) 2 (40	6.9
	421723	AA620400	Hs.300717	Homo saplens mRNA full length insert cDN sodium channel, vollage-gated, type til,	6.8
	447342	Al 199268	Hs.19322	Homo sapiens, Similar to RIKEN cONA 2010	6.8
00	443297	AI049884	Hs.133029	ESTs	6.7 6.7
80	443992	AW022228	Hs.322922	ESTs	6.7
	453098	AW294631	Ha.11325	ESTs	6.7
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	6.7
	443761	A1525743	Hs.160603	ESTs	6.6

	420cm0	ACTRO00.40			
	429609 435056	AF002246 AW023337	Hs.210863 Hs.5422	cell adhesion molecule with homology to	6.6
	453431	AF094754	Hs.32973	glycoprotein M6B glycine receptor, beta	6.5
_	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	6.5
5	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.5 6.5
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805	L10333	Hs.99947 •	relicution 1	6.4
	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypotheti	6.4
10	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407866 440700	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.3
	427701	AW952281 AA411101	Hs.296184 Hs.243886	guarrine nucleotide binding protein (G pr	6.3
	422949	AA319435	ITS.243000	nuclear autoantigenic sperm protein (his	6.3
	445102	AW204610	Hs.22270	gb:EST21657 Adrenal gland tumor Homo sep ESTs	6.2
15	452401	NM_007115	Hs.29352	tumor necrosts factor, alpha-induced pro	6.2
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2 6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	6.2
	416871	H98716		gb:yx13d08.s1 Soares metanocyte 2NbHM Ho	6.1
20	416702	AA186428	Hs.85591	EST8	6.1
20	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
	424997 438660	AL138167 U95740	Hs.96920	ESTs	6.1
	453649	Y07494	Hs.6349 Hs.34114	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	448444	AW818436	Hs.23590	ATPase, Na+fK+ transporting, alpha 2 (+) solute carrier family 16 (monocarboxylic	6.1
25	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.1
	425517	AF121179		gb:AF121179 Homo saplens liver (Chang L-	6.0 6.0
	427457	AW779105	Hs.164682	EST8	6.0
	437034	AA742643		gb:rry91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.0
30	444170	AW613879	Hs.102408	ESTs	6.0
50	457183 448999	H91882	Hs.118569	Dvl-binding protein IDAX (Inhibition of	6.0
	454048	AF179274 H05626	Hs.22791 Hs.6921	transmembrane protein with EGF-like and	6.0
	439772	AL365406	Hs.10268	ESTS	6.0
	448944	AB014605	Hs.22599	Homo sapiens mRNA full length insert cDN atrophin-1 interacting protein 1; activi	5.9
35	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
	415485	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	5.9 5.9
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9
	447350	Al375572	Hs.172634	ESTs	5.9
40	451783 447101	R42554	Hs.210862	T-box, brain, 1	5.9
40	440492	N72185 R39127	Hs.44189	ESTs	5.9
	440274	R24595	Hs.21433 Hs.7122	hypothetical protein DKFZp547J036	5.9
	438461	AW075485	Hs.286049	scraple responsive protein 1 phosphoserine aminotransferase	5.9
	418064	BE387287	Hs.83384	\$100 calcium-binding protein, beta (neur	5.9
45	437036	Al571514	Hs.133022	ESTs	5.8 5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070841	Hs.10684	Homo saplens clone 24421 mRNA sequence	5.7
50	445828 447198	F05802	Hs.81907	ESTs	5.7
50	427897	D61523 NM_017413	Hs.283435 Hs.303084	ESTs	5.7
	448499	BE613280	Hs.77550	spelin; pepiida ligand for APJ receptor hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	5.7
	412155	R38167	Hs.12449	Homo saplens transmembrane protein HTMP1	5.6 5.6
55	435718	R06569	Hs.269534*	ESTs	5.6
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW514021 AW749443	Hs.245510	ESTs	5.6
60	422411 438328	AW749443 Al492261	Hs.22511 Hs.32450	ESTS ESTS	5.6
	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo saplens clone 24461 mRNA sequence	5.6
	418677	\$83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5 5.5
65	400859				5.5
03	413625	AW451103	Hs.71371	ESTs	5.5
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.5
	434933 438702	R91095 A1879064	Hs.4276	KIAA1701 protein	5.5
	452055	Al377431	Hs.54618 Hs.141693	ESTS	5.5
70	430979	AJ479755	Hs.129010	hypothetical protein MGC10858 ESTs	5.5
	412709	AL022327	Hs.74518	KIAA0027 protein	5.5 5.5
	439920	H05430	Hs.288433	neurotrimin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
15	419235	AW470411	Hs.288433	neurotrimin	5.4
	418030 410330	BE207573 AW023630	Hs.83321	neuromedin B	5.4
	410781	A1375672	Hs.46786 Hs.165028	ESTs ESTs	5.4
00	420658	AW965215	Hs.336656	ESTS	5.4
80	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4
	443740	R56434	Hs-21062	ESTs	5.4 5.4
	426457	AW894687	Hs.169965	chimerin (chimaerin) 1	5.4
	450375	AAD09647	Hs.8850	a disintegrin and metalloproteinase doma	5.4

	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4
	426600	NM_003378 AB037821	Hs.171014	VGF nerve growth factor inducible	5.4
	424432 429250	H56585	Hs.146858 'Hs.198308	protocadherin 10 tryptophan rich basic protein	5.4 5.4
5	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
	436282 404584	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3 5.3
10	439845	AL355743	Hs.56663	Homo saplens EST from clone 41214, full	5.3
10	424001 425073	W67883 W39609	Hs.137476 Hs.22003	paternally expressed 10 solute carrier family 6 (neurotransmitte	5.3 5.3
	426625	178300	Hs.300642	serologically defined colon cancer antig	. 5.3
	428137	AA421792	Hs.170999	ESTs .	5.3
15	428879 438176	AA431765 AW138970	Hs.122113	gb:zw80c03.s1 Soares_testis_NHT Homo sap ESTs	5.3 5.3
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.3
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340 435244	N31772 N77221	Hs.79226 Hs.187824	fasciculation and elongation protein zet ESTs	5.3 5.3
20	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
	407748 430437	AL079409 Al768801	Hs.38176 Hs.169943	KIAA0606 protein; SCN Circadian Oscillat Homo sapiens cDNA FLJ13569 fls, clone PL	5.3 5. 3
25	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.2
25	453941 424998	U39817 U58515	Hs.36820 Hs.154138	Bloom syndrome chitinase 3-like 2	5.2 5.2
	423419	R55336	Hs.23539	EST8	5.2
	424922	BE386547	Hs.217112		5.2
30	447359 408206	NM_012093 AF041853	Hs.18268 Hs.43670	adenylate kinase 5 kinesin family member 3A	5.2 5.2
-	421013	M62397	Hs.1345	mutated in colorectal cancers	5.2
	429443 434367	AB028967	Hs.202687	potassium voltage-gated channel, Shal-re	5.2
	444861	AB020700 R46789	Hs.3830 Hs.76118	KIAA0893 protein ubiquitin carboxyl-terminal esterase L1	5.2 5.2
35	446142	A1754693	Hs.145968	ESTs	5.2
	448816 451050	AB033052 AW937420	Hs.22151 Hs.69662	KIAA1228 protein ESTs	5.2 5.2
	451108	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	5.2
40	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
40	416737 424800	AF154335 AL035588	Hs.79691 Hs.153203	LIM domain protein MyoD family Inhibitor	5.2 5.2
	443695	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	5.2
	415257	F03016	Hs.27513	ESTs	5.2
45	433929 415651	Al375499 Al207162	Hs.27379 Hs.3815	ESTs stathmin-like-protein R63	5.1 5.1
	451027	AW519204	Hs.40808	ESTs	5.1
	409172 423343	Z99399 AA324643	Hs.118145 Hs.246106	ESTs ESTs	5.1 5.1
~~	429172	AA447417	Hs.285491	ESTs	5.1
50	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.1
	451270 452904	AW341392 AL157581	Hs.235795 Hs.30957	ESTs Homo saplens mRNA; cDNA DKFZp434E0826 (f	5.1 5.1
	420560	AW207748	Hs.59115	ESTs	5.1
55	418097 442910	R45137 Al365130	Hs.21868 Hs.11307	ESTs ESTs, Weakly similar to T19326 hypotheti	5.1 5.1
	434849	AW292765	Hs.8053	ESTS	5.1 5.1
	413554	AA319146	Hs.75428	secretogranin (I (chromogranin C)	5.1
	414217 412068	A1309298 S72043	Hs.279898 Hs.73133	Homo sapiens cDNA: FLJ23165 fis, clone L metallothlonein 3 (growth inhibitory fac	5.1 5.0
60	413627	BE182082	Hs.246973	ESTs	5.0
	418661 422438	NM_001949 AA445925	Hs.1189 Hs.270896	E2F transcription factor 3 ESTs, Moderately similar to Z195_HUMAN Z	5.0
	423728	AW891294	Hs.132136		5.0 5.0
65	431431	AL096711	Hs.252953		5.0
03	435087 452097	AW975241 AB002364	Hs.23567 Hs.27916	ESTs a disintegrin-like and metalloprotease (5.0 5.0
	410434	AF051152	Hs.63668	toll-like receptor 2	4.9
	408692 407808	AL040127 AA663559	Hs.34074	dipeplidylpeplidase VI	4.9
70	418940	H17739	Hs.279789 Hs.288513		4.9 4.9
	425977	R15138	Hs.165570	Homo saplens clone 25052 mRNA sequence	4.9
	425814 447112	AF036943 H17800	Hs.172619 Hs.7154	myelin transcription factor 1-like ESTs	4.9 4.9
26	449574	F05048	Hs.175373	EST8	4.9
75	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	4.9
	423869 413248	BE409301 T64858	Hs.134012 Hs.21433	! C1q-related factor hypothetical protein DKFZp547J036	4.9 4.9
	449176	A1633545	Hs.198072	2 ESTs	4.9
80	448451 402604			gb:UI-H-Bi0p-abh-g-09-0-UI.s1 NCI_CGAP_S	4.8
-	436039		Hs.121070) ESTs	4.8 4.8
	448769		Hs.38173	ESTs	4.8
	423678	AW963357	Hs.7847	ESTs	4.8

	439451	AF088270	Hs.278554	heterochromatin-like protein 1	4.8
	425870	R13408		ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
5	413409	AI638418	Hs.78580	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	4.8
,	413823 417246	AA825721 Al760098	Hs.246973 Hs.21411	ESTs ESTs	4.8 4.8
	420900	AL045633	Hs.44269	ESTs	4.8
	424153	AA451737	Hs.141496	MAGE-like 2	4.8
10	443539	AJ076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
10	448750	U95020	Hs.21903	calcium channel, vollage-dependent, beta	4.8
	454030 424458	AW021429 M29273	Hs.231980 Hs.1780	ESTs myelin associated glycoprotein	4.8 4.8
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	4.8
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
	431103 429956	M57399	Hs.44 Hs.22542	pleiotrophin (heparin binding growth fac ESTs	4.7 4.7
	435060	AJ374651 AJ422719	Hs.233349	ESTs, Wealty similar to fork head like p	4.7
	438203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
	422222	A1699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733 449353	AW298410 AA001220	Hs.21475 Hs.271369	ESTs ESTs	4.7 4.7
	452022	AW072330	Hs.293875	ESTs	4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
	404541				4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125 458435	R17268 Al418718	Hs.259873 Hs.144121	exonal transport of synaptic vesicles ESTs, Wealdy similar to T46916 hypotheti	4.7 4.6
30	425745	U44060	Hs.14427	Homo saplens cDNA: FLJ21800 fis, clone H	4.6
	413492	D87470	Hs.75400	KIAA0280 protein	4.6
	419629	AB020695	Hs.91662	KIAA0888 protein	4.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.6
35	436140 439169	W87355 AJ912122	Hs.269587 Hs.41095	ESTs ESTs	4.6 4.6
55	443150	AID34467	Hs.34650	ESTs	4.6
	451073	AI758905	Hs.205063	ESTs	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
40	452106 451407	Al141031	Hs.21342 Hs.326401	ESTs	4.6 4.6
70	448765	AA131376 R15337	Hs.21958	fibroblast growth factor 128 Homo saplens mRNA; cDNA DKFZp547D088 (fr	4.6 4.6
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	4.6
	437204	AL110216	Hs.12285	ESTs, Wealdy similar to 155214 salivary	4.6
45	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.5
43	422175 407889	N79885 R34556	Hs.6382 Hs.30800	ESTs, Highly similar to T00391 hypotheti ESTs, Wealdy similar to S65657 alpha-1C-	4.5 4.5
	419343	AA456245	Hs.85603	down-regulated by Ctrinb1, a	4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
50	429399	AA452244	Hs.16727	ESTs	4.5
50	450149 453118	AW969781	Hs.132863	Zic family member 2 (odd-paired Orosophi	4.5
	443455	AW195849 AB001025	Hs.252757 Hs.9349	ESTs ryanodine receptor 3	4. 5 4.4
	442613	AI004002	Hs.130522	Ky channel-interacting protein 1	4.4
<i>E E</i>	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
55	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
	418845 435202	AA852985 AI971313	Hs.89232 Hs.170204	chromotox homolog 5 (Drosophila HP1 alph KIAA0551 protein	4.4 4.4
	437496	AA452378	Hs.170144		4.4
<i>c</i> 0	451254	AI571016	Hs.172967	ESTs	4.4
60	439039	A1656707	Hs.48713	ESTs	4.4
	439979 441607	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	424983	NM_005010 AJ742434	Hs.7912 Hs.169911	neuronal cell adhesion molecula ESTs	4.4 4.4
	410611	AW954134	Hs.20924	KIAA1628 protein	4.4
65	402605			•	4.4
	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222 454027	Al061301 R40192	Hs.164773 Hs.21527	ESTs Human DNA sequence from clone GS1-115M3	4.4 4.4
	454293	H49739	Hs.134013		4.4
70	442832	AW206560	Hs.253569		4.4
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279	AW959861	Hs.290943		4.3
	427194 419723	AA399018 AL120193	Hs.250835 Hs.92614		4.3 4.3
75	445810	AW265700	Hs.155660		4.3
	409734		Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 selivary	4.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.3
80	433024 453202		Hs.26549 Hs.26270	KIAA1708 protein hypothetical protein FLJ11588	4.3 4.3
	425264		Hs.20369		4.3
	416427	BE244050	Hs.79307	Rac/Cdc42 guarrine exchange factor (GEF)	4.3
	431789	H19500	Hs_26922		4.3

	AAAEOO	D41200	He coop	FCTA	
	444600 454042	R41398 H22570	Hs.6996 Hs.172572	ESTs hypothetical protein FLJ20093	4.3 4.3
	441899	Al372588	Hs.8022	TU3A protein	4.3
_	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
5	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
	430291 433597	AV660345 AA708205	Hs.238126 Hs.100343	CGI-49 protein ESTs	4.2 4.2
	444127	N63620	Hs.13281	EST8	4.2 4.2
10	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	4.2
10	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 nanci	4.2
	408577 409719	H50572 AI769160	Hs.19515 Hs.108681	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.2
	428538	AI143139	Hs.2288	Homo sapiens brain turnor associated prot visinth-like 1	4.2 4.2
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
15	432865	AI753709	Hs.152484	ESTs, Weakly similar to 138022 hypotheti	4.2
	447138 450648	A!439112 Al703366	Hs.93828 Hs.26766	ESTs, Wealdy similar to 2109260A B cell ESTs	4.2
	451459	AI797515	Hs.270560	ESTS, Moderately similar to ALU7_HUMAN A	4.2 4.2
~~	421686	AB011156	Hs.106794	KIAA0584 protein	4.2
20	452776	AA194540	Hs.13522	ESTs, Weakly similar to 138022 hypotheti	4.2
	436421 423858	A1678031 AL137326	Hs.122813 Hs.133483	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	434001	AW950905	Hs.3697	Homo sapiens mRNA; cDNA DKFZp434B0650 (f serine (or cysteine) proteinase inhibito	4.2 4.2
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.2
25	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
	439607	BE540565	Hs.159460	ESTs	4.1
	424028 446936	AF055084 H10207	Hs.153692 Hs.47314	Homo saplens cDNA FLJ14354 fis, clone Y7 ESTs	4.1
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent prolein kin	4.1 4.1
30	412448	A1768015	Hs.92127	ESTs	4.1
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220 419683	N49776 AA248897	Hs.170994	hypothetical protein MGC10946	4.1
	426071	AW138057	Hs.48784 Hs.163835	ESTs ESTs	4.1 4.1
35	428743	AL080060	Hs.301549	Homo sepiens mRNA; cDNA DKFZp584H172 (fr	4.1
	432809	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039 425905	AI922988 AB032959	Hs.172510 Hs.318584	ESTs novel C3HC4 type Zinc finger (ring finge	4.1
40	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1 4.1
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433932	AW954599	Hs.169330	neuronal protein	4.1
	436637 439231	AI783629 AW581935	Hs.26766 Hs.141480	ESTS	4.1
45	450530	NM_006668	Hs.25121	Homo sapiens mRNA; cDNA DKFZp434N079 (fr cytochrome P450, subfamily 46 (chotester	4.1 4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-0-sulfot	4.1
	410486 413916	AW235094 N49813	Hs.69233 Hs.75615	zinc finger protein	4.0
50	438703	A1803373	Hs.31599	apolipoprotein C-II ESTs	4.0 4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fls, clone HE	4.0
	405771				4.0
	418841 421764	NM_002332 AI681535	Hs.89137	low density lipoprotein-related protein	4.0
55	424176	AL137273	Hs.148135 Hs.142307	serine/threonine kinase 33 hypothetical protein	4.0 4.0
	425773	N21279	Hs.237749	ESTs	4.0
	427304	AA761526	Hs.163853	ESTs	4.0
	428882 452834	AA436915 AI838627	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	4.0
60	452654	AA952989	Hs.105685 Hs.63908	KIAA1688 protein hypothetical protein MGC14728	4.0 4.0
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429698	A1685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0
65	435854 439199	AJ278120 R40373	Hs.4996 Hs.26299	putative ankyrin-repeat containing prote ESTs	4.0
00	439450	R51613	Hs.125304	ESTs	4.0 4.0
	446782	AI653048	Hs.144006	ESTs	4.0
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9
70	402408 453362	H14988	Hs.107375	ESTs ·	3.9
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	3.9 3.9
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	3.9
	425010	T16837	Hs.4241	ESTs .	3.9
75	444230	H95537 AW292779	Hs.146067		3.9
, ,	441738 418951	F07809	Hs.169799 Hs.89506	ESTs paired box gene 6 (aniridia, keratilis)	3.9
	406311			house any Resis o fermions' vestifit?)	3.9 3.9
	408460	AA054726	Hs.285574		3.9
80	410658	AW105231	Hs.192035		3.9
50	414699 418849	AI815523 AW474547	Hs.76930 Hs.53565	synuclein, afpha (non A4 component of am	3.9
	429477	Al275514	Hs.6658	Homo saplens PIG-M mRNA for mannosyltran ESTs	3.9 3.9
	433766	AA609234	Hs.112669		3.9 3.9
			•	162	

	435400	ALCONOLOGO .		abiliana and an anna di tanan da ta	••
	436190 447891	AK001059 · R41754	Hs.6496	gb:Homo sapiens cDNA FLJ10197 fis, clone ESTs	3.9 3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9
_	404283			•	3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9
	429656 412754	X05608 AW160375	Hs.211584 Hs.74565	neurofilement, light polypeptide (68kD) amyloid beta (A4) precursor-like protein	3.9 3.9
	445314	AI689948	Hs.65489	Homo saplens cONA: FLJ21517 fis, clone C	3.9
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9
10	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.9
	438054	AA776826	Hs.62183	ESTS	3.9
	436420 445133	AA443966 AW157646	Hs.31595 Hs.153506	ESTs ESTs	3.9 3.9
	432590	Al609273	Hs.110783	ESTs	3.9
15	453331	Al240665	Hs.8895	ESTs	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	424635 451489	AA420887 NM_005503	Hs.115455 Hs.26468	Homo saplens cDNA FLJ14259 fis, clone Pt. amytoid beta (A4) precursor protein-bind	3.8 3.8
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.8
20	448302	Al480208	Hs.182906	Homo saplans mRNA for KIAA1872 protein,	3.8
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	3.8
	417355 446727	D13168	Hs.82002 Hs.16032	endothelin receptor type B	3.8
	424340	AB011095 AA339038	Hs.7033	KIAA0523 protein ESTs	3.8 3.8
25	423346	AI267677	Hs.127416	synaptojanin 1	3.8
	412788	AA120960	Hs.198416	ESTS	3.8
	404593	1107000	11- 000000	FOT- 141-11-1-11-1-1-11-11-11-11-11-11-11-11-	3.8
	416856 429896	N27B33 AA460367	Hs.269028 Hs.224223	ESTs, Weakly similar to 138022 hypotheti ESTs, Moderately similar to 138022 hypot	3.8 3.8
30	439619	AW975998	Hs.68595	ESTs, Weakly similar to I38022 hypotheti	3.8
	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
	440322	AA879430	11 40400	gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	447761 452453	AF061573 AI902519	Hs.19492	protocadherin 8	3.8
35	439671	AW162840	Hs.6641	gb:QV-BT009-101198-051 BT009 Homo sapien kinesin family member 5C	3.8 3.8
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278	AW294659	Hs.34054	Homo sepiens cDNA: FLJ22488 fls, clone H	3.8
	447028 449458	AI973128	Hs.167257 Hs.208261	brain link protein-1	3.8
40	445888	AI805078 AF070564	Hs.13415	ESTs Homo saplens clone 24571 mRNA sequence	3.8 3.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	3.8
	428841	AI418430	Hs.104935	ESTs	3.8
	430643	AW970065	Hs.287425	MEGF10 protein	3.8
45	422263 451625	AA307639 R56793	Hs.129908 Hs.106576	KIAA0591 protein alanine-giyoxytate aminotransferase 2-li	3.8 3.8
	439238	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN!	3.8
	441928	AJ370188	Hs.211454	ESTs	3.8
	441797	AI936933	Hs.214635	ESTs	3.7
50	414922 425588	D00723 F07396	Hs.77631 Hs.46751	glycine deavage system protein H (amino ESTs	3.7 3.7
••	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682	Al383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
55	425741 418211	AF052152 BE244746	Hs.159412 Hs.247474	Homo saplens clone 24628 mRNA sequence hypothetical protein FLJ21032	3.7 3.7
-	440080	AW051597	Hs.143707	ESTs	3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.7
60	409234 420489	AI879419 AA815089	Hs.27206 Hs.193513	ESTs ESTs	3.7 3.7
-	426890	AA393167	Hs.41294	ESTs	3.7
	438849	W28948	Hs.10762	ESTs	3.7
	441869	NM_003947	Hs.8004	hunlinglin-associated protein interactin	3.7
65	448796 459318	AA147829 NM_000038	Hs.301431	endothelial zinc finger protein Induced gb:Homo sapiens adenomatosis polyposis c	3.7 3.7
•••	459518	Al937419	Hs.294069	Homo saplens cONA FLJ13384 fis, clone PL	3.7
	434444	Al765276	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL135740	Hs.102447	TSC-22-like	3.7
70	410555 421637	U92849 AF035290	Hs.64311 Hs.106300	a disintegrin and metalloproteinase doma	3.7
, 0	418522		Hs.7149	Homo saplens clone 23556 mRNA sequence Homo saplens cDNA: FLJ21950 fis, clone H	3.7 3.7
	420807	AA280627	Hs.57846	ESTs	3.7
	449961	AW265634	Hs.133100	ESTS	3.7
75	422634				3.7
13	421030 427099		Hs.101174 Hs.173560		3.7
	452355		Hs.29202	odd Oz/ten-m hornolog 2 (Drosophila, mous G protein-coupled receptor 34	3.7 3.7
	440483	AI200836	Hs.150386	ESTs	3.7
90	429597		Hs.2442	a disintegrin and metalloproteinase doma	3.7
80	423756 425187		Hs.22509	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens ESTs	3.6
	434859		Hs.299315		3.6 3.6
	413199		Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.6

	445729	H21066	Hs.13223	Homo sepiens mRNA full tength insert cON	3.6
	416120	H46739	1.0.10225	gb:yo14h02.s1 Soares adult brain N2b5HB5	3.6
	429239	AA448419	Hs.45209	ESTs	3.6
5	419088 446659	NM_000216 AJ335361	Hs.89591 Hs.226376	Kallmann syndrome 1 sequence ESTs	3.6 3.6
5	426757	AW205640	Hs.158206	ESTs	3.6
	418819	AA228776	Hs.191721	ESTs	3.6
	458332	AI000341	Hs.220491	ESTs	3.6
10	408826 410343	AF216077 AA084273	Hs.48376 Hs.76561	Homo sapiens clone HB-2 mRNA sequence ESTs, Weekly similar to S47072 finger or	3.6 3.6
•	410507	AA355288	Hs.40834	transitional epithelia response protein	3.6
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo saplens	3.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.6
15	428002 428505	AA418703 AL035461	Hs.2281	gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi ctrromogranin B (secretogranin 1)	3.6 3.6
••	430530	AA480870	Hs.47660	EST8	3.6
	436425	Al913146	Hs.318725	CGI-72 protein	3.6
	438078 442927	A1016377 A1024347	Hs.131693 Hs.131519	ESTs ESTs	3.6 3.6
20	446242	N66336	Hs.7360	EST8	3.6
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.8
	450474	AW872844	Hs.201919	ESTs	3.6
	452198 455800	A1097560 R22479	Hs.61210 Hs.167073	ESTs, Weakly similar to 138022 hypotheti Homo sapiens cDNA FLJ13047 fis, clone NT	3.6 3.6
25	436443	AW138211	Hs.128746	ESTs	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.6
	456038	AA203285	Hs.294141	ESTs, Weakly similar to alternatively sp	3.6
	408902 442950	AW014869 Al500417	Hs.5510 Hs.46764	ESTs ESTs	3.6 3.6
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.6
	425478	AB007953	Hs.268840	ESTs	3.6
	453884 404721	AA355925	Hs.36232	KIAA0186 gene product	3.6 3.6
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycen 5 (neur	3.6
35	440553	AA889416	Hs_295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.5
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	3.5
	413999 421458	N4B124 NM_003654	Hs.34460 Hs.104576	ESTs carbohydrate (keratan sulfate Gal-6) sul	3.5 3.5
40	425017	AL119305	Hs.288405	ESTs	3.5
40	435958	H98180	Hs.117975	ESTs	3.5
	415101 451320	R45531 AW118072	Hs.144534 Hs.89981	ESTs diacylglycerol kinase, zeta (104kD)	3.5 3.5
	430290	A1734110	Hs.136355	EST8	3.5
4.5	416836	D54745	Hs.80247	cholecystokinin	3.5
45	414821	M63836	Hs.77424	Fc fragment of IgG, high affinity la, re	3.5
	419412 437860	AW161058 AA333063	Hs.90297 Hs.279898	synuclein, beta Homo sapiens cDNA: FLJ23165 fis, clone L	3.5 3.5
	452689	F33868	Hs.284176		3.5
50	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	3.5
50	427491 428037	R43279 N47474	Hs.22574 Hs.89230	ESTs, Wealdy similar to 138022 hypotheti potassium Intermediate/small conductance	3.5 3.5
	444584	Al168422	110.00200	gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.5
55	453775 412659	NM_002916 AW753865	Hs.35120 Hs.74376	replication factor C (activator 1) 4 (37	3.5 3.5
73	429077	AB028983	Hs.2352	olfactomedin related ER localized protel adenylate cyclase 2 (brain)	3.5 3.5
	436887	AW953157	Hs.193235		3.5
	450784	AW246803	Hs.47289	ESTs	3.5
60	44 <u>6</u> 827 436434	AW451243 N50465	Hs.157069 Hs.92927	ESTs putative 47 kDa protein	3.5 3.5
	412777	Al335773	Hs.270123		3.5
	436476	AA326108	Hs.33829	bHLH prolein DEC2	3.5
	408601 429401	U47928 AW296102	Hs.86122 Hs.99272	protein A ESTs, Weakly similar to S32567 A4 protei	3.4 3.4
65	448425	A1500359	Hs.233401		3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	451729 435910	AW160725 Al084152	Hs.312469 Hs.21782		3.4
	434577	R37316	Hs.179769		3.4 3.4
70	414598	AI094221	Hs.135150		3.4
	439627	BE621702	Hs.29076		3.4
	413293 423992		Hs.302499		3.4 3.4
	426249		Hs.16835		3.4
75	426968	U07616	Hs.17303	4 smphiphysin (Stiff-Mann syndrome with br	3.4
	430388 435061		Hs.240770 Hs.16394		3.4
	452291		Hs.28853		3.4 3.4
60	449714	AB033015	Hs.23941	KIAA1189 protein	3.4
80	443392		Hs.29342		3.4
	410082 445337		Hs.15831 Hs.12523		3.4 3.4
	408493		Hs.46039		3.4

	432731	R31178	Hs.287820	Ebronectin 1	3.4
	448758 432613	AB018311	Hs.21917	KIAA0768 protein	3.4
	432013	AW081698 AW207019	Hs.80712	KIAA0202 protein	3.4
5	425294	AF033827	Hs.148135 Hs.155553	serine/threonine kinase 33	3.4
_	410108	AA081659	Hs.318775	HNK-1 sulfotransferase OSBP-related protein 6	3.4
	406815	AAB33930	Hs.288036	IRNA isopentenylpyrophosphate transferas	3.4 3.4
	402855			a a c a a b c c c c c c c c c c c c c c	3.3
• •	422170	AJ791949	Hs.112432	anti-Mullerian hormone	3.3
10	445034	AW293376	Hs.143659	ESTs	3.3
	424378	W2B020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DKFZPS86J1624 protein	3.3
15	404819 436607	A11604702	Lin 044004	COT.	3.3
13	427315	AW661783	Hs.211061	ESTS	3.3
	452693	AA179949 179153	Hs.175563 Hs.48589	Homo saptens mRNA; cDNA DKFZp564N0763 (f	3.3
	454998	AW850180	H3.40003	zinc finger protein 228 gb:IL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo saplans (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapisns mRNA; cDNA DKFZp43400515 (f	3.3 3.3
	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.3
	421192	AA833718	Hs.204529	KIAA1806 protein	3.3
25	426695	AW118191	Hs.112729	ESTs	3.3
25	438885	A1886558	Hs.184987	ESTs	3.3
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103 453590	R42764	Hs.339654	ESTs, Weakly similar to 138022 hypotheti	3.3
	453616	AF150278 NM_003462	Hs.33578 Hs.33846	KIAA0820 protein	3.3
30	457285	AI038858	Hs.130522	dynein, exonemal, light intermediate poi	3.3
	436045	AB037723	Hs.5028	Kv channel-interacting protein 1 DKFZP56400423 protein	3.3
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.3 3.3
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3
~~	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.3
35	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3
	443898	AW804286	Hs.9950	Sec61 gamma	3.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3
	445953	AI612775	Hs.145710	ESTs	3.3
40	427940	AA417812	Hs.38775	EST ₅	3.3
70	414683 428484	S78298	Hs.76888	hypothetical protein MGC12702	3.3
	420649	AF104032 Al866964	Hs.184601 Hs.124704	solute carrier family 7 (cationic amino	3.3
	419498	AL036591	Hs.20887	ESTs, Moderately similar to S65657 alpha hypothetical protein FLJ10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3 3.3
45	436556	Al364997	Hs.7572	ESTs	3.3
	424369	R87622	Hs.26714	KIAA1831 protein	. 3.2
	457065	AI476318	Hs.192480	ESTs	3.2
	440210	AW874562	Hs.125298	ESTs	3.2
50	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
30	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	3.2
	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
	439924 411505	A1985897	Hs.125293	ESTs	3.2
	423175	AF155659 W27595	Hs.70565	molybdenum cofactor synthesis 2	3.2
55	415115	AA214228	Hs.18653 Hs.127751	hypothetical protein FLJ14627 hypothetical protein	3.2
	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
	410274	AA381807	Hs.61762	hypoxle-inducible protein 2	3.2
	437762	178028	Hs.154679	synaptolagmin I	3.2 3.2
~	438944	AA302517	Hs.92732	KIAA1444 protein	3.2
60	450313	AI038989	Hs.332633	Bardel-Biedl syndrome 2	3.2
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2
	410953	AW811768	Hs.334858	hypothetical protein MGC12250	3.2
	418527 420081	AA450388	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
65	420081 429498	AW510776 AA453800	Hs.94958	tubufin tyrosine ligase-like 1 ESTs	3.2
00	430099	AW194988	Hs.192793 Hs.20537	hypothetical protein FLJ13942	3.2
	434928	AW015595	Hs.4267		3.2
	435532	AW291488	Hs.117305	Horno saptens clones 24714 and 24715 mRNA Horno saptens, clone IMAGE:3682908, mRNA	3.2
~ ^	438306	AW188266	Hs.163645	ESTs	3.2 3.2
70	439274	AF086092	Hs.48372	ESTs	3.2
	440847	AA907511	Hs.130178	ESTs	32
	447750	AJ422234	Hs.143434	contactin 1	3.2
	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Hamo	3.2
75	430890	X54232	Hs.2699	glypicen 1	3.2
13	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450 430456	AB014526 AA314998	Hs.178121	K/AA0626 gene product	3.2
	430181	AF065314	Hs.241503	hypothetical protein	3.2
80	418512	AP-005514 AW498974	Hs.234785 Hs.89981	cyclic nucleolide gated channel alpha 3 diacylglycerol kinase, zeta (104kD)	3.2
	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (3.2
	450689	Al369275	Hs.243010	Homo saplens cDNA FLJ14445 fis, clone HE	3.2
	424899	AL119387	Hs.119062	ESTs	3.2 3.2
					~~

			I- 400045	n=.	3.2
				STs epcidin antimicroblei peptide	3.2
	451455 445078		Hs.4775 jt	inctophilin 3	3.2
_	447746		Hs.161359 E	STS	3.2
5	435458			Iomo sepiens clone 24841 mRNA sequence	3.2 3.2
	427729		Hs.300646 K Hs.89512 A	(IAA protein (similar to mouse paladin) NTPase, Ca⊷ transporting, plasma mambra	3.1
	417417 438810			typothetical protein DKFZp761N09121	3.1
	439570		Hs.269165	STs, Weakly similar to ALU1_HUMAN ALU S	3.1
10	432527	AW975028		STs	3.1 3.1
	416801			sal (Drosophila)-like 2	3.1
	421988 426509	AW450481 M31166		ESTs pentaxin-related gene, rapidly Induced b	3.1
	408786	AA773187		ESTs	3.1
15	433494	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	3.1
	412723	AA648459		hypothetical protein AF301222	3.1 3.1
	418329	AW247430	Hs.84152 Hs.109314	cystathlonine-bela-synthase hypothetical protein FLJ20980	3.1
	439456 428832	A1752409 AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
20	452780	BE171598	Hs.13522	ESTs, Weakly similar to I38022 hypotheti	3.1
	438192	A1859065		Homo sapiens AFG3L1 isoform 1 mRNA, part	3,1 3.1
	424939	AK000059	Hs.153881	Homo saplens NY-REN-62 antigen mRNA, par	3.1
	403053 404299	R58624	Hs.2186	eukaryotic translation elongation factor	3.1
25	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	A1468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1 3.1
	449101	AA205847	Hs.23016 Hs.166254	G protein-coupled receptor hypothetical protein DKFZp5681133	3.1
30	453240 440486	AI969564 BE243513	Hs.7212	hypothesical protein PP1044	3.1
20	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864	A1720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.1 3.1
35	438315	BE390513 AL117427	Hs.27935 Hs.172778	hypothetical protein MGC4837 Homo saplens mRNA; cDNA DKFZp566P013 (fr	3.1
33	426855 425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	3.1
	410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.1
40	425491	AA883316	Hs.255221	ESTS	3.1 3.1
40	456273 412140	AF154846 AA219691	Hs.1148 Hs.73625	zinc finger protein RAB8 Interacting, kinesin-like (rabkines	3.1
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.1
	432154	Al701523	Hs.112577	ESTs	3.1
4.5	453128	AW026516	Hs.31791	acylphosphalase 2, muscle type	3.1 3.1
45	438458	AW975186	11- 04044	gb:EST387294 MAGE resequences, MAGN Homo	3.0
	448616 429281	AF035621 AA830856	Hs.21611 Hs.29808	kinesin family member 3C Homo sepiens cDNA: FLJ21122 fis, clone C	· 3.0
	443906	AA348031	Hs.7913	ESTs	3.0
	417318	AW953937	Hs.12891	ESTs	3.0
50	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0 3.0
	444153		Hs.10414 Hs.47860	hypothetical protein FLJ10748 neurotrophic tyrosine kinase, receptor,	3.0
	408790 426327		Hs.44898	Homo sepiens clone TCCCTA00151 mRNA sequ	3.0
	451468		Hs.293663	ESTs, Moderately similar to 138022 hypot	3.0
55	422758		Hs.284180		3.0 3.0
	421633		Hs.106260		3.0
	428361 418932		5 Hs.183858 Hs.89484	cadherin 4, type 1, R-cadherin (relinal)	3.0
	416805		Hs.79981	Human clone 23560 mRNA sequence	3.0
60	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.0 3.0
	422709		Hs.153485	6 ESTs ESTs	3.0
	423135 424901		Hs.26411 Hs.18250		3.0
	42661		Hs.266251		3.0
65	42738	6 AW836261		7 ESTs	3.0
	42985				3.0 3.0
	43507 43509		Hs.35495 Hs.4749	ESTs Homo saptens mRNA; cDNA DKFZp761E13121 (3.0
	43621				3.0
70	43693	6 AL134451	Hs.19747	8 ESTs	3.0
	44585	5 BE247129	Hs.14556	9 ESTs	3.0 3.0
	45229				3.0
	43398 43022			9 phosphoserine aminotransferase ESTs, Highly similar to T00391 hypotheti	3.0
75	45102				3.0
. •	43523			cyclin-dependent kinase Inhibitor 2C (p1	3.0
	43956	56 AF086387	7	gb:Homo sepiens full length insert cDNA	3.0 3.0
	42578		Hs.15957 Hs.1414		3.0
80	4165 4168		Hs.4256	B ESTs	3.0
J	4103		Hs.3327	Homo sepiens cONA: FLJ22219 fis, clone H	3.0
	4114	11 AA34524		O ESTs, Weakly similar to KIAA1330 protein	3.0 3.0
	4240	66 Z 99348	Hs.1124	61 ESTs, Wealdy similar to 138022 hypotheti	3.0

	101010				3.0
	404048 429163	AA884766	g	b:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	454117	BE410100 1		daptor-related protein complex 1, sigma	3.0 3.0
5				(IAA1708 protein ESTs	3.0
J	434131 441255		Hs.171635 E	STs	2.9
	453900	AW003582	Hs.226414 1	STs, Weakly similar to ALUS_HUMAN ALU S	29 29
	453905			LIM domain kinase 1 net (chicken)-like 2	29
10	416602 431173		Hs.294068	ESTs	29
10	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	29 29
	436401			ESTs cadherin 13, H-cadherin (heart)	29
	422960 451558			ATP-binding cassette, sub-family A (ABC1	2.9
15	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	29 29
	433149	BE257872		hypothetical protein HES6	29 29
	434811 425897	AW971205 AA935315	Hs.114280 Hs.48965	ESTs Homo sapiens cDNA: FLJ21693 fis, clone C	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
20	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	29 29
	411124	AW196937	Hs.53929 Hs.89739	ESTs, Waskly similar to ALUB_HUMAN IIII cholinergic receptor, nicotinic, beta po	2.9
	419227 427651	BE537383 AW405731	Hs.18498	Homo saptens cDNA FLJ12277 fls., clone MA	2.9
~-	441707	R42637	Hs.21963	hypothetical protein DKFZp76180514	29 29
25	435741	A1240668	Hs.113099	ESTs ESTs, Highly similar to T46266 hypotheti	2.9
	437273 422939	AL137451 AW394055	Hs.120873 Hs.98427	ESTs, Wealthy similar to 138022 hypotheti	2.9
	439376	AA883521	Hs.222064	ESTs	29 29
20	439935	875105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
30	437267 453740	AW511443 AL120295	Hs.258110 Hs.311809	ESTs. Moderately similar to PC4259 femi	2.9
	400250	72.120200			29
	400992		11- 470007	hundhalted emisis E1 111155	2.9 2.9
35	408814 411849	N62499 AW984970	Hs.176227 Hs.18861	hypothetical protein FLJ11155 ESTs, Moderately similar to KIAA1276 pro	2.9
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	29
	423751	AW235633	Hs.46525	ESTS	2.9 2.9
	426910	AA470023 AF097994	Hs.190089 Hs.301528	ESTs, Moderately similar to ALU1_HUMAN A L-kynurentrie/alpha-aminoadipate aminotra	2.9
40	450203 459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	29
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9 2.9
	428500 421641	A1815395 A1638184	Hs.184641 Hs.106334	fatty acid desaturese 2 Homo sepiens clone 23836 mRNA sequence	2.9
	421141	AW117261	Hs.125914	EST8	29
45	407870		Hs.40719	hypothetical protein KIAA1164	2.9 2.9
	456723		Hs.4748 Hs.248122	adenylate cyclase activating polypeptide G protein-coupled receptor 24	2.9
	436456 421483				29
	412190	R16180	Hs.274461	ESTs	2.9 2.9
50	446131		Hs.290 Hs.127525	phospholipase A2, group V 5 ESTs	2.9
	441668 437387		Hs.28847	AD026 protein	29
	423420) AL571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	2.9 2.9
55	427958 429084		Hs.98280 Hs.19561	potassium intermediate/small conductance splicing factor 3b, subunit 3, 130kD	2.9
))	44706		Hs.21964		2.9
	43088	7 N66B01	Hs.26028	7 KIAA1841 protein	2.9 2.9
	44182 42412		Hs.7977 Hs.96917	KIAA0411 gene product ESTs	29
60	40873		Hs.23879	7 ESTs, Moderately similar to 138022 hypot	29
	44742	2 BE618703	Hs.98258	orthopedia (Drosphila) homolog	29 29
	43561 44699		Hs.4975 Hs.16758	potassium voltage-gated channel, KQT-lik Spir-1 protein	2.9
	43357			cadherin, EGF LAG seven-pass G-type rece	2.9
65	40844	7 AK002089	Hs.45080		2.9 2.8
	41958 41702		Hs.1447: 37 Hs.8090:		2.8
	4084			gb:xm67b05.x1 NCI_CGAP_CML1 Homo septens	28
-	4203	20 AB002361	Hs.9663	3 KIAA0363 protein	2.8 2.8
70					2.8
	4286 4244			80 enotase 2, (gamma, neuronal)	2.8
	4091	85 AW98160	1 Hs.2524	06 hypothetical protein FLJ 12298 similar to	2.8 2.8
75	4115		7 Hs.7066 Hs.2986		2.8
13	4268 4588			35 sin3-associated polypeptide, 30kD	2.6
	4200	71 AB02898	5 Hs.9480	6 ATP-binding cassette, sub-family A (ABC1	2.8 2.8
	4245		Hs.1507 Hs.3329		2.8
80) 444E) 4110			418 cell division cycle 2-like 1 (PITSLRE pr	2.8
-	416	111 AA03381	3 Hs.790	18 chromatin assembly factor 1, subunit A (2.8 2.8
	440				2.8
	408	554 AAB3638	,, 113.313	1/1 Illicited (sceptil correpasson to receive	

			LIA 2400		otic translation elongation factor	2.8
	403056 423449	R58624 AJ497900	Hs.2186 Hs.33067	ESTs	ODD BOLDONA GANGOVOLI IOV	2.8 2.8
	424188	AW954552	Hs.142634	zinc fir	nger protein	28
_	429006	AA443143	Hs.50929 Hs.293077	hypoth ESTs	etical protein FLJ13842	2.8
5	434981 437435	AW182577 AA249439	Hs.27027	hypoti	netical protein DKFZp762H1311	2.8 2.8
	442748	Al016713	Hs.135787	ESTs		28
	443312	N52025	Hs.46616	ESTa	, Weakly similar to 138022 hypotheti	2.8
10	450940 452738	A1744943 AL133800	Hs.143209 Hs.7086	hypot	hetical protein MGC12435	2.8
10	409182	AA064970	Hs.118145	ESTS		2.8 2.8
	439793	AA018825	Hs.7934	Krup; ESTs	pel-like factor 4 (gul)	2.8
	432683	AW995441 AK001991	Hs.10475 Hs.3781	eo i a	er to murine leucine-rich repeat pr	2.8
15	434269 429500	X78565	Hs.289114	hera	hrachion (lenascin C. cytolaclin)	2.8 2.8
	433290	R20077	Ha.302185	Hom	o sapians clone 23518 mRNA sequence ne zipper, putative tumor suppresso	2.8
	434276	AF123659 AL138079	Hs.93605 Hs.5012	brain	-specific membrane-anchored protein	2.8
	435977 430294	AL138079 AL538226	Hs.32976	auar	ilne nucleolide binding protein 4	2.8 2.8
20	425168	R96366			q37d04.s1 Soares fetal liver spleen	28
	428180	A1129767	Hs.182874 Hs.146090	ECT	nine nucleotide binding protein (G pr	2.8
	409348 409887	AI401535 AL137534	Hs.56876	Hor	no saniens mRNA: cDNA DKFZp434H1419 (1	28 28
	457211	AW972565	Hs.32399	E 41	(s, Wealdy similar to S51797 vasodilat rs, Wealdy similar to ALU1_HUMAN ALU S	28
25	430039	BE253012	Hs.153400 Hs.105461) ESI	othetical protein FLJ20357	2.8
	417642 419169	BE302665 AW851980			Ts, Weakly similar to \$72482 hypotheti	28 28
	434008	AA740878	Hs.11298	2 ES		2.8
20	446776	AW293417	Hs.15645 Hs.40369	ES	Te	2.8
30	408838 422565	A1669535 BE259035	Hs.11840	0 stn	ged (Orosophila)-like (sea urchin fas	2.8 2.8
	447397	BE247676	Hs.18442	F.	enzyme	2.8
	412530			3 hy	pothetical protein FLJ13346 mo sapiens cDNA FLJ13596 fis, clone PL	2.8
35	424330 446377			3 ES	STs .	2.8 2.8
55	458924	BE242158	Hs.24427	7 01	(FZP566O1646 protein	2.8
	447710		Hs.32824		STs	2.8
	404049 416913		4	gt	:RC1-DT0001-031299-011-a11 DT0001 Homo	28 28
40	42640	M78361	Hs.1697	43 H	omo sapiens cione 25121 neuronal ottaci	2.8
	41326		Hs.1347 Hs.6966	2 E	rpothetical protein FLJ20033 STs	2.7
	45899 42286		-		h:FST20390 Retina II Homo sapiens cDNA	· 2.7 2.7
	43052		2 Hs.2424	07 G	protein-coupled receptor, family C, gr	2.7
45	45202			55 F	(IÁA1173 protein Iomo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
	43202 45243			45 J	M4 protein	2.7 2.7
	43540	8 H07897	Hs.430	2 E	STs. Weakly similar to T29299 hypotheti	2.7
E 0	41879				ESTS ESTS	2.7
50	4388: 4234			R5R (CSR1 orolein	2.7 2.7
	4420	91 AW7704	93 Hs.182		guanine nucleotide binding protein (G pr	27
	4422			24	Homo sapiens cDNA: FLJ23285 fis, clone H gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.7
55	4124 5 4328			3005	solute carrier family 21 (organic anion	2.7 2.7
٠.	4164	04 AA1801	38 Hs.107		ESTs, Wealdy similar to YD38_YEAST HYPOT	2.7
	4413				COTe Weakly similar in B49647 G1P-0000	2.7
	4502 4263				Homo segiens CDNA FLJ114// TIS, Clone HE	27 27
6	O 428	722 U76456	3 Hs.19		tissue inhibitor of metalloproteinase 4 KIAA0591 protein	27
	449				Homo sepiens, clone IMAGE:3535476, mRNA,	27
	420 410	318 AA084		9259	FOTe Weakly similar to S23650 (8) TOVITU	2.7 2.7
_	414	603 R5839	4 Hs.25		ESTs, Wealdy similar to YEX0_YEAST HYPOT cytochrome b-245, beta polypeptide (chro	2.7
6		1096 H1857 1896 AW14			Homo spolens cDNA: FLJ22165 lts, clons H	27
		1856 AA347			ESTs, Wealthy similar to ZN43_HUMAN ZINC	2.7 2.7
		3304 AA339	622 Hs.19	38887	ESTs	2.7
-		1027 Al911 2545 N319		26444 4434	ESTs ESTs, Weakly strniter to 138022 hypotheti	2.7
,		2545 N3194 4201 AB02			KIAA0974 protein	2.7 2.7
		8560 BE61	3183 Hs.2	3213	ESTs	2.7
		6807 AA38		56682 59590	ESTs lymphocyte antigen 6 complex, locus H	2.7
-		:5825 A1925 10351 AF03	1508 FIS.1		RAD1 (S. pombe) homolog	2.7 2.7
•	42	5390 Al09	2634 Hs.1	156114	protein tyrosine phosphatase, non-recept	2.7
	42	27624 AA40		24895	ESTs gb:EST90805 Synovial sarcoma Horno saplen	2.7
			77823 38548 Hs.	117546	neuronalin	2.7 2.7
:		24560 AA1	58727 Hs.	150555	protein predicted by clone 23733	2.7 2.7
	4	32415 T16		289014 274414		2.7
		14865 AA1 15827 H17		2744 14 .23079	ESTs	2.7
	4					

	445568	H00918	Hs.268744		796 protein associated binding protein 1	27 27
	433315 428862	R96754 NM_000346	Hs.239706 Hs.2316		sex determining region Y)-box 9 (ca	2.7
	420002 447959	A1452784	Hs.270270	ESTs,	Wealdy similar to 2109260A B cell	2.7 2.7
5	426420	8E383808	Hs.322430		family, member 4	2.7
	436899	AA764852	Hs.291567	ESTs	4 (cell division cycle 14, S. cerevi	2.7
	444100	AA383343 AW043782	Hs.22116 Hs.293616	ESTS	4 formation about 144 or an arr	2.7
	426501 449092	U91641	Hs.22985		2,8-sialyltransferase	2.7 2.7
10	427311	AB020672	Hs.175411		0865 protein	27
	453313	8E005771	Hs.153746	hypol	helical protein FLJ22490	2.7
	404029	W26333	Hs.337438	EST	•	27
	416289 439108	AW163034	Hs.6467		płogyrin 3	2.6
15	418746	A1955289	Hs.300759		omal protein L36	2.6 2.6
	412046	Y07847	Hs.73088		related on chromsome 22	26
	435040	A1932350	Hs.152825 Hs.31622	EST	s actin associated protein 1	26
	453083 428167	U87223 AA770021	Hs.16332	EST	ß.	26
20	420028	AB014680	Hs.8786	cart	ohydrate (N-acetylglucosamine-6-O) s	26 26
	443715	AI583187	Hs.9700		n E1	2.6
	421247	BE391727	Hs.102910 Hs.151738		eral transcription factor (IH, polype rix metalloproteinase 9 (gelatinase B	2.6
	424687 415056	J05070 AB004662	Hs.77867	orto	nosine A1 recentor	2.6
25	451697	AW449774	Hs.295380	PO	M (POM121 rat homolog) and ZP3 fusion	2.6 2.6
	433701	AW445023	Hs.15155	ES		26
	457358	A1479755	Hs.129010		15 B2-associated binding protein 1	2.6
	430347	NM_002039 AB037807	Hs.23970 Hs.83293	hvr	othetical protein	2.6
30	418027 440491	R35252	Hs.24944	ES	Ts, Weakly similar to 2109260A B cell	2.6 2.6
50	425171	AW732240	Hs.16365			2.6
	459335	AW298545	Hs.25072	6 ES	i Ts, Weakly similar to B34323 GTP-blindi	2.6
	425402	AI215881 AB037815	Hs.24970 Hs.32156		AA 1394 protein	2.6
35	453169 433647	AA603367	Hs.2222		BTs	26 26
55	450414	A1907735	Hs.2144		AA1716 protein	2.6
	446233		Hs.2520 Hs.6607		STs STs	2.6
	415446 445873		Hs.2519	46 D	xy(A)-binding protein, cytoplasmic 1-l	2.6
40	413012		Hs.7513	7 K	AA0193 gene product .	2.6 2.6
	428671	BE297851	Hs.1894		nc finger protein 179	26
	427158		Hs.1662	31 E	STs omo saplens clone TUA8 Cri-du-chat regi	2.6
	408984 45951		Hs.4947 Hs.2468		ST	2.6
45	40269					26 26
	40803				STs	2.6
	42289				STS STS	2.6
	42313 43879		Hs.109		enethonin 1	2.6
50	43987		Hs.467	36 i	hypothetical protein FLJ23476	2.6 2.6
	44019	2 AA8722B		596	ESTS	26
	41970			/4 307	hypothetical protein hypothetical protein DKFZp434l2117	2.6
	4494: 4368:			560	cainexin	2.6
55	4484				ESTS	2.6 2.6
	4013	24			SMC2 (structural maintenance of chromoso	26
	4141				hymohold enhancer-binding factor 1	2.6
	4339 4280		Hs.21		ESTs, Moderately similar to Transforming	2.6 2.6
60	4291		Hs.66	087	ESTs	26
•	4230	773 BE2529			MAD (mothers against decapentaplegic, Dr phospholnositol 3-phosphate-binding prot	2.6
	4489				ESTs, Moderately similar to S65657 alpha	2.6
	_ 4440 _ 4120		7 Hs.18		adenviate kinase 5	2.6 2.6
6	5 441		12 Hs.79	61	Homo saplens clone 25012 mRNA sequence	26
_	425		Hs.1		peanut (Drosophila)-like 2	26
	432			7022 23296	ESTs, Weakly similar to T34549 probable ESTs, Weakly similar to T38022 hypotheti	2.6
		234 AW084 1478 AF0831			neuro-oncological ventral antigen 2	2.6
7		1982 AA714	335 Hs.2	71883	ESTs	26 26
•	416	858 AW961	605 Hs.2	1145	hypothetical protein RG083M05.2	26
		3257 Al3340		1614 8785	HSPC065 protein Ksp37 protein	2.6
		8748 AW593 4984 H1547		32898	fatty acid desaturase 1	2.6
7		3404 T3298		02720	ESTs	\ 26 26
•	43	4779 AF153	815 Hs.	0151	potassium inwardly-rectifying channel, s	2.6
	42	0582 BE047		9093	Homo sapiens chromosome 19, cosmid R2837 protein tyrosine phosphatase, receptor t	2.6
		2856 AF034 6440 AJ471		30881 196008	Homo saniens cDNA FLJ11723 tis, clone HE	2.6
5		16440 AI471 18527 AI969	••-	15325	RAB7, member RAS oncogene family-like 1	2.6
•		3216 AF21	7412 Hs.	47320	neuroligin 3	2.6 2.6
	43	35380 AA67		192221 194687		2.6
	42	28966 AF05	9274 118.	124001	170	

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Pkey CAT Number Accession AW195262 R27858 AW811262 412225 1284108_1 AW902042 N77591

					-Maril contain Et 190272	2.6
	439653	AW021103	Hs.6631 Hs.146101	hypoth ESTs.	etical protein FLJ20373 Weakly similar to T45070 protein k	26
	419304 422991	AJ271326 H10940	Hs.48965	Homo	sapiens cDNA: FLJ21693 fis, clone C	2.6 2.6
	448548	R13209	Hs.21413	solute	carrier family 12, (potassium-chi	2.6
5	435370	A1964074	Hs.225838	EST8	P434B168 protein	2.5
	408875	NM_015434	Hs.48604 Hs.172597	col (D	msophila)-like 3	2.5
	457005 430154	AJ007421 AW583058	Hs.234726	serine	(or cysteine) proteinase inhibito	2.5 2.5
	438549	BE386801	Hs.21858	trinuc	leofide repeat containing 3	2.5
10	427951	AI826125	Hs.43546	ESTs	to both associated protein 18	2.5
	411800	N39342	Hs.103042	Micro	tubula-associated protein 18 i, Moderately similar to ALU7_HUMAN A	2.5
	457683	AI821877 AB002336	Hs.140002 Hs.26395	ervito	rocyte membrane protein band 4.1-li	2.5
	451422 430713	AA351647	Hs.2642	euka	nyotic translation elongation factor	25 25
15	428826	AL048842	Hs.194019	altra	-lin	2.5
	428963	AW382682	Hs.258208	Hom	o sapiens, clone MGC:15606, mRNA, com e carrier family 11 (proton-coupled	2.5
	428141	D50402	Hs.182611 Hs.119357	EST		2.5
	429550	AW293055 AA223599	Hs.6351	dea	vage and polyadenylation specific fa	2.5 2.5
20	438662 435760	AF231922	Hs.213004		mosome 21 open reading frama 62	2.5 2.5
20	427513	AI476318	Hs.192480			2.5
	430061	AB037817	Hs.230188	KIA Don	A1396 protein no sapiens clone 24672 mRNA sequenc a	2.5
	435923	BE301930 BE326521	Hs.5010 Hs.159450	1 EC1	Ta	2.5
25	417123 439699	AF086534	Hs.18756	FS"	rs. Moderately similar to ALU1_HUMAN A	2.5 2.5
2.5	412980	AJ815750	Hs.20977	hyp	othetical protein MGC3129 similar to	2.5
	427209	H06509	Hs.92423		A1566 protein	2.5
	424327	AA431707	Hs.31209 Hs.21605	ES ES		25
30	436340 450650	R42246 T65617	Hs.10125	7 hv	withetical protein MGC3295	2.5 2.5
30	439444		Hs.54578		Ts, Weakly similar to I38022 hypotheti	2.5 2.5
	400777				formed epidermal autoregulatory factor	2.5
	439478	AF049460	Hs.6574	de,	mma-aminobutyric acid (GABA) A recepto	2.5
35	450407		O Hs.24969 Hs.24944	y ya	nuclein, alpha interacting protein (sy	2.5
33	450385 432558		Hs.1772		STS	2.5 2.5
	400860					2.5
	410361				ranylate binding protein 1, interferon- STs	2.5
40	41606				ddised low density lipoprotein (lectin	2.5
40	41499 45282	- : - 		6 tr	anscription factor-like 5 (basic helix	2.5 2.5
	41779			71 E	STs	2.5
	41807	9 R40058	Hs.6911		STs	2.5
15	40849		Hs.2377 Hs.188	-	STs hosphodiesterase 4B, cAMP-specific (dun	2.5
45	44210 43737			1 530	iomo saniens mRNA; cDNA DKFZp54/DUZ3 (if	2.5 2.5
	42980		Hs.223	025 F	RAB31, member RAS oncogene family	2.5
	42495	59 NM_0057			activated p21cdc42Hs kinase hypothetical protein MGC5618	2.5
£0	4274				NAG-5 protein	2.5
50	4089 4152		Hs.834	6	FSTs	2.5 2.5
	4157		Hs.179	C67	nucleosome assembly protein 1-like 1	2.5
	4178	73 BE2666		659	Homo sapiens, Similar to RIKEN cDNA A430 Homo sapiens cDNA FLJ11364 fis, clone HE	2.5
	4183				transcription factor 17	2.5
55	4210 4232				ESTe Weekly similar to ubiquitous TPK M	2.5
	4235				ESTs, Wealdy similar to DYLX_HUMAN CYTOP	2.5 2.5
	4279	61 AW293	165 Hs.14		ESTs, Weakly similar to I38022 hypotheti	2.5
~	428				CRRI31 protein	2.5
60) 428 428			4600	ch-m67d11 r1 Soares total felus_Nb2HF8_	2.5
		943 AW086		636	COTe Wookly similar to KIAA1392 protein	2.5 2.5
	432	427 AL037	530 Hs.66		Homo sapiens cDNA FLJ11602 fis, clone HE	2.5
_	_ 435	347 AW014		16963	ESTs ESTs, Weakly similar to A46010 X-linked	2.5
6:		7949 U7851			ESTS	2.5
		3208 AL041 0286 U 2958			cholinemic receptor, muscarinic 3	2.5 2.5
		1523 AW51	4283 Hs.3	01771	ESTe Weakly similar to ALUF_HUMAN !!!!	2.5
	44	1805 AA28		01914	neuronal specific transcription factor D ESTs, Weakly similar to TC17_HUMAN TRANS	2,5
7		2337 Al371		29257 131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.5
		2789 AW90 5556 AI910		12887	actin-related protein 3-beta	2.5 2.5
		19086 Al628		208037	ECT.	2.5 2.5
_	45	9583 Al907			gb:IL-BT152-080399-004 BT152 Homo sapien	
7	75	401 F 0P:				
		ABLE 88: key:	Unique Fo	s probe	set identifier number	
		key: AT number:	Gene clus	ter num	ber	
_	A	ccession:	Genbank:	eccessi	on numbers .	
8	30	_				

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AA665089 AA135130 AA484059 AA102419 AW877765
H46739 H51513 H19779
                 412436
                 416120
416871
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1626761_1
                                                              H89716 N90792 N24283
AW934714 BE181007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
AA318223 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821
AA319435 N56456 AA319377 AW961532 T48452 AA694424
AA831498 AID17191 AA491211 AA761823 AA714555 AA768099 AA688286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319842
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                                      163001_1
  5
                                     222336_1
                  422864
                                      2231B4_1
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                                      223410_1
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                                                               AW853758 H56414
AA828125 AA834883 AA330555
R98366 AL33929 AA351636 H78818 AA477084 Z28957 H80194
AF121179 BE162736 AA358827
                   423756
425168
                                      231725 1
                                       247552_1
10
                                      252729_1
266650_1
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AA377823 AW954494 AI022688

AA418703 AA418711 BE071915 BE071920 BE071912

AA431765 AA432015

AA436760 AW227453 BE327496 N47347 N56967

D80842 AA443145 AL119015 AW904500

AA884766 AW974271 AA592975 AA447312

AW975387 AA598607 AA742735
                   426413
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296453_1
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428858
 15
                    429007
                                       298301 1
                                        300543_1
                    429163
                                        368950_1
41555_1
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AK001069 AA633055

AA742843 AA808575 AW976668

AW975186 AA807807 D29548

AA828995 AA834879 AI926361

AF086387 W77884 W72711

AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400

AI568422 D80113 T59074
                     436190
                                        431713_1
457837_1
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                                        467651_1
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491966_1
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  25
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                                         611496 1
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450625
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84032_1
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AI902519 AI902518 AI902516
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AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
   30
                      454996
                                          1248640 1
                      455350
                                          1283853_1
                      TABLE 8C:
                                                        Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                      Pkey:
Ref:
    35
                                                         Indicates DNA strand from which exons were predicted. 
Indicates nucleotide positions of predicted exons.
                       Strand:
                       N_position:
                                                                                            Nt position
     40
                                                                     Strand
                                              8131663
                                                                     Plus
                        400777
                                                                                            118372-118619
                                              8131663
9757499
                        400780
                                                                     Minus
                                                                                            91888-92018,98131-98294,99474-99570
151830-152104,152649-152744
                                                                     Minus
                        400859
                                              9757499
8096828
                        400860
                                                                      Minus
                                                                                            140390-140822
     45
                         400992
                                                                      Plus
                                                                                            234057-234174
110326-110491
                         401324
                                               9863791
                         402408
                                               9798239
                                                                      Minus
                                               9909420
                                                                                             20393-20767
                         402604
                                               9909420
8569863
                                                                                             47680-47973
                         402605
                                                                      Minus
                                                                                             82366-82515
59763-59909
      50
                                                                       Minus
                          402693
                          402855
                                                                       Minus
                                                7671252
                          404029
                                                                       Plus
                                                3688074
3688074
                                                                                             54421-56R08
                                                                       Minus
                                                                                              75765-78156
                          404049
404283
                                                                       Minus
                                                 2276311
                                                                                              99460-99564
       55
                                                                                              3826-4025
                          404299
                                                5738652
                                                                       Minus
                                                                                               103456-103664
                           404541
                                                 8318559
                                                                        Plus
                                                                                               138651-139153
                          404584
404593
                                                 9857511
                                                                        Phis
                                                 9944086
9856648
                                                                                               74922-75788
173763-174294
                                                                        Minus
                                                                                              16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 51728-51836
        60
                           404721
404819
                                                                        Minus
                                                 4678240
                                                  7249119
                                                                        Minus
                            405238
                                                                                               91191-91254,91510-91589
2830-2967
                                                                        Plus
                            405771
                                                  7018349
                                                   4007557
                                                                         Plus
                           405819
                                                                                                137114-139033
        65
                            406311
                                                  9211559
                                                                         Minus
                           TABLE 9A:ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 9A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the ARymeth/Eace Hu03 GeneChip array such that the ratio of "everage" glioblastoma to "everage" normal adult CNS tissues was greater than or equal to 2.0. The "everage" glioblastoma level was set to the 75th percentile amongst various glioblastoma level was set to the 75th percentile amongst various glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Place: Inhous Ens nonbeset identifier number
         70
                                                               Unique Eas probeset identifier number
                             Pkey:
ExAccn:
                                                               Exemplar Accession number, Genbank accession number
           75
                             UnigenelD:
                                                               Unigene number
                             Unigene Tille:
                                                                Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue
                                                                           UnigenelO
           80
                                                 ExAccn
N78223
                                                                                                 Unigene Title
                                                                                                 transcription factor
carbonic anhydrase XII
                                                                            Hs.108106
                              452461
                                                                                                                                                                                                                   15.2
                                                   AF037335
                                                                            He 6338
                                                                            Hs.36820
                                                                                                  Bloom syndrome
                               453941
                                                  U39817
```

				- 44	townst IDO4	12.4
		BE614387	Hs.333893		target JPO1 metalloproteinase 7 (matrilysin,	12.0
	428330	L22524 AJ199268	Hs.2256 Hs.19322		sapiens, Similar to RIKEN CONA 2010	11.7
	447342 422163	AF027208	Hs.112360		nin (mouse)-like 1	11.4
5	439451	AF086270	Hs.278554	hetero	chromatin-like protein 1	11.2 10.2
_	424800	AL035588	Hs.153203	MyoD	family inhibitor	10.0
	416111	AA033813	Hs.79018		natin assembly factor 1, subunit A (ine and glycine-rich protein 2	9.9
	444190	A1878918	Hs.10526 Hs.73625		interacting, kinesin-like (rabkines	9.9
10	412140	AA219691 AW235786	Hs.195359	hypo	hetical protein MGC10954	9.8
10	449340 409731	AA125985	Hs.56145	thym	osin, beta, Identified in neuroblast	9.4
	439978	BE139460	Hs.124673	Hom	saniens cDNA FLJ11477 fis, clone HE	8.9
	411411	AA345241	Hs.55950		, Wealdy similar to KIAA1330 protein	8.9 8.2
	456516	BE172704	Hs.222746		1610 protein	7.9
15	420092	AA814043	Hs.88045	EST	B Harifand andrie Cl. 110600	7.9
	422631	BE218919	Hs.118793	nypo	thetical protein FLJ10688 (sex determining region Y)-box 11	7.9
	453392	U23752 Al969251	Hs.32964 Hs.115325	RAP	7, member RAS oncogene family-like 1	7.9
	438527 427581	NM_014788	Hs.179703		A0129 gene product	7.8
20	418661	NM_001949	Hs.1189	E2F	transcription factor 3	7.8
20	440684	Al253123	Hs.127356	ES1	s, Highly similar to S21424 nestin (H	7.8 7.7
	429643	AA455889	Hs.167279		E-finger-containing Rab5 effector pro	7.5
	409638	AW450420	Hs.21335	EST	S	7.5
26	444665	BE613126	Hs.47783 Hs.127792		ggressive lymphoma gene a (Drosophila)-like 3	7.5
25	456759	BE259150 Al335773	Hs.270123			7.4
	412777 436607	AW661783	Hs.21106	l ES	Ts.	7.3
	432058	AW665996	Hs.13072	es (Ts, Wealdy similar to ALU1_HUMAN ALU S	7.3 7.3
	417061	A1675944	Hs.18869		mo sepiens cONA FLJ12033 ffs, clone HE	7.3 7.2
30	428976	AL037824	Hs.19469		homolog gene family, member t	7.1
	433244	AB040943	Hs.27128	5 KV	A 1510 protein Ts, Wesidy similar to T00079 hypotheti	7.1
	436726	AA324975	Hs.12899	a Ec	on67b05.x1 NCL_CGAP_CML1 Homo sapiens	7.1
	408432 434164	AW195262 AW207019	Hs.14813	5 se	rine/threonine kinase 33	7.0
35	445873	AA250970	Hs.25194	6 po	ly(A)-binding protein, cytoplasmic 1-l	7.0
	439726	AW449893	Hs.29370)7 E	3Ts, Weakly similar to 138598 zinc ting	7.0 6.8
	432656				HC class II transactivator	6.8
	431117	AF003522	Hs.25050		dia (Orosophila)-like 1	6.8
40	453387		Hs.25280 Hs.18310		STs STs	6.6
40	418821 437034		TR. 1031	o, c	p:ny91c01.s1 NCI_CGAP_GC81 Homo sapiens	6.6
	411252		Hs.6932	вŇ	ID-2 protein	6.5
	424687		Hs.1517	38 n	natrix metalloproteinase 9 (gelatinase B	6.4 6.3
	452953		Hs.2717	41 E	STs. Weakly similar to A45010 X-linked	6.3
45	433532			_ 9	b:EST387475 MAGE resequences, MAGN Homo	6.3
	420311				luman DNA sequence from clone RP4-530I15	6.2
	418097		Hs.2186	90 6	STS b:nj32b03.s1 NCI_CGAP_AA1 Homo saplens	6.2
	40730- 43525				ytokine-like protein C17	6.1
50	44944		Hs.574	-: -	ESTs	6.1
50	40379					6.0 6.0
	42551	7 AF12117			gb:AF121179 Homo sapiens liver (Chang L-	6.0
	42067				butyrylcholinesterase	5.9
	43554				ESTs AF15q14 protein	5.8
55	41821			NOO	gb:Homo sapiens full length insert cDNA	5.B
	43908 40803				hypothetical protein FLJ10300	5.7
	4122				gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
	4361		53 Hs.133		hypothetical protein MGC15729	5.7
60			Hs.300		trinucleotide repeat containing 12 ESTs, Wealdy similar to 138022 hypotheti	5.7
	4291				SRY (sex determining region Y)-box 4	5.6
	4181		1 HS.03	404	OLL (200 notalisated to See 1). por 1	5.6
	4055 4424		89 Hs.38	178	hypothetical protein FLJ23468	5.6
6:	5 4425				ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
٠.	4130	410257			chitinase 3-tike 1 (cartilage glycoprote	5.5 5.5
	4205		748 Hs.59		ESTs	5.5
	4080				dihydrofolate reductase	5.4
7	443			34074 17112	ESTs, Moderately similar to ALU6_HUMAN A Homo sapiens cDNA: FLJ22322 fis, clone H	5.4
7				39020	Homo saplens cDNA FLJ14098 fis, clone MA	5.3
		115 AA446 900 AW003		26414	ESTs. Weakly similar to ALUS_HUMAN ALU S	5.3
		168 AW379			gb:RC1-HT0256-081199-011-f01 HT0256 Hamo	5.3
	432	789 D2636	1 Hs.3		KIAA0042 gene product	5.3 5.2
7	5 437	036 AI5715		33022	ESTS	5.2
		247 BE391		02910	general transcription factor IIH, polype ESTs, Weakly similar to ALUF_HUMAN IIII	5.2
		1523 AW514		01771 5960	v-myc avian myelocytomatosis viral relat	5.1
		1106 BE382 7211 AW97		2399	ESTs, Weakly similar to 851797 vasodilat	5.1
9		4157 AW16		12481	ESTs. Weakly similar to \$66668 hydrogen	5.1
•		3343 AA324	1643 Hs.2	246106	ESTs	5.1 8.1
		5292 NM_0	05824 Hs.	155545	37 kDa leucine-rich repeat (LRR) protein	5.1 5.1
		6679 AA07	3786		gb:zm66b07.r1 Stratagene neuroepithelium	5.1

		4100ECC0 1	11. 40.4770 (POT	5.1
				EST Hone HQ0310 PRO0310p1	5.0
				ESTs	5.0
			Hs.279854	mannosidase, alpha, class 2B, member 1	4.9
5	420730			polymerese (DNA directed), della 1, cata	4.9
•	441217			ESTs	4.9
	453385			ESTS	4.8
	418203		Hs.83758	CDC28 protein kinase 2	4.7
_	450813		Hs.203376	ESTs	4.7
10	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.7
_	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7 4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	4.6
1.5	405771		11. 400400	PAT-	4.6
15	457065	AJ476318	Hs.192480	ESTS	4.6
	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	400859	1103703	No. 110114	ESTs	4.6
	435267	N23797	Hs.110114	EST8	4.5
20	443454	A1057494	Hs.133421 Hs.118983	hypothetical protein FLJ 12150	4.5
20	452811	AA937079 AW511443	Hs.258110	ESTs	4.5
	437267 435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.5
	454269	A1961060	Hs.129908	KIAA0591 protein	4.5
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
25	422765	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	4.5
23	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423758	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo saplens	4.5
	417308	H60720	Hs.B1892	KIAA0101 gene product	4.5
	422170	AJ791949	Hs.112432	anti-Mullerian hormone	4.4
30	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.4
•	406568	AF088886	Hs.11590	cathepsin F	4.4
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	4.4
	402516				4.4
	432865	AJ753709	Hs.152484	ESTs, Wealdy similar to 138022 hypotheti	4.4
35	413625	AW451103	Hs.71371	ESTs	4.4
	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4 4.4
	416933	BE561850	Hs.80506	amati nuclear ribonucleoprotein polypept	4.4
40	438192	AI859065	Hs.337620	Homo sepiens AFG3L1 isoform 1 mRNA, part	4.3
40	457374	AA493662		gbmh05d12.s1 NCI_CGAP_Thy1 Homo saplens	4.3
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3
	444386	BE065183	00070	gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202	AW085781	Hs.26270	hypothetical protein FU11588 ESTs	4.3
45	441020	W79283	Hs.35962	minichromosome maintenance deficient (S.	4.3
43	414733	BE514535	Hs.77171	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	407902	AL117474	Hs.41181	Horro sebicing ranged experience for	4.3
	405701 451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homotog 5 (Drosophila HP1 alph	4.2
50	433323	AA805132	Hs.30701	ESTs	4.2
50	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.27210		4.1
	441269		Hs.17878		4.1
55	418727	AA227609	Hs.94834	ESTs	41
	433006	BE242758	Hs.19022		4.1
	436480	AJ271643	Hs.87469		4.1
	430786		Hs.31293		4.1 4.1
	445372		Hs.14492		4.0
60	410555		Hs.64311		4.0
	457465				4.0
	422094				4.0
	442029				4.0
65	459321				4.0
05	421308 420567				4.0
	44700				4.0
	44829		Hs.3348		3.9
	43969				3.9
70	44070		Hs.162	insulin-like growth factor binding prote	3.9
, 0	45309				3.9
	45702				3.9
	40464				3.9
_	45037		7 Hs.8850	a disintegrin and metalloproteinase doma	3.9
75	43013				3.9
	43771			79 ESTs	3.9
	43849		2 Hs.3012	99 ESTs	3.9
	42991	9 AA46069		hypothetical protein FLJ23024	3.9
	41360			gb:yg73g11.r1 Soares Infant brein 1NIB H	3.9
80				140 ESTS, Weakly similar to ALU1_HUMAN ALU S	3.9
	44879				3.9
	4493				3.8 3.8
	4522	03 X57522	Hs.158	164 transporter 1, ATP-binding cassette, sub	3.0

3.8

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	42576	9	U72513	Hs.159	1486 H	uman l	RPL13-2 pseudogena mRNA, completa	3.8 3.8
	4042	95		11- 026	261 6	elmen	te binding protein 1, interferon-	3.8
	4103 4287		BE391804 NM_016625	Hs.626 Hs.19	1201 h	waaiha	fical arabin	3.8 3.8
5	4091		AL136877	Hs.50	758 🖇		structural maintenance of chromoso	3.8
•	4301		AA468591	Hs.16		ESTs	dherin beta 16	3.8
	4474		AW262580	Hs.14	1014	допос	CHOIN SOL 10	3.8 3.7
	4058 4377		AW137817	Hs.24	4353	ESTS		3.7
10	418	383	BE387036	Hs.12	211	ecid ph	osphatase 5, tartrate resistant Moderately similar to A56194 throm	3.7
	444		AW747996		50999 58282	KIAAO	040 gene product	3.7 3.7
	425 425	502	NM_014656 R98895		25823	ESTs		3.7
		741	NM_007019		3002	ubiqui	in carrier protein E2-C	3.7
15		424	1404500	Hs.2	7	olyclo	e dehydrogenase (decarboxylating;	3.7
		469 1072	M64590 H70854		83059	Hamo	contone PRO10HZ (THINA, COMPLETE COS	3.7 3.7
		1872	U82010	Hs.7	7513	COXI	0 (yeast) homolog, cytoctrome c oxid	3.7
~~	42	6071	AW138057		163835 39584	ESTS	nomal secondated 1	3.7
20		9078 8037	M93119 N47474		39230	antac	cium intermediate/small conductance	3.7 3.7
		6547	H62914	Hs.	288946	EST	, Weakly similar to PC4259 terms	3.6
		6899	AA764852		291567	EST:	ST388086 MAGE resequences, MAGN Horno	3.6
25		18722 10652	AW975977 AJ216751	, Hs.	143977	EST	S	3.6 3.6
23		28450	NM_0147	91 Hs.	184339	KIA	0175 gene product s, Weakly similar to 138022 hypotheti	3.6
	4	52103	R42764	Hs	339854	CCT	•	3.6
		09048	H59990 AF088060		.37699	ab:1	lomo sapiens full length insert cDNA	3.6 3.6
30) 2	39546 43544	AI076315	i He	.16359	EQT	'e	3.6
50	4	18478	U38945	H	.1174		in-dependent kinase inhibitor 2A (me	3.6
		35889	A1249107 AA76752		s.269901 s.22030	pair	ed box gene 5 (B-cell lineage specif	3.6 3.6
		120301 138078		7 H	s.131693	FS'	Te	3.6
3.5	5.	408420	NM_006		s,447 6 6	reti	nilis pigmentosa 2 (X-linked recessi yx13d08.s1 Soares melanocyte 2NbHM Ho	3.5
		416871		014 14	s.13922	-	itention factor C (activator 1) 2 (40	3.5 3.5
		424085 446291			s.14623	int	arferon, gamma-inducible protein 30	3.5 3.5
	_	43228	AK0012	39 F	ls.27426		pothetical protein FLJ10377 Ts, Highly similar to unnamed protein	3.5
4	U	43612			łs.35406		-CV/VTTUB4U1091199-023-603 L10010 UQUO	3.5 3.5
		41125 41923			4s.18459	e u	encione chia: FL 173241 hs. Clone C	3.5 3.5
		43506	5 BE0843	391			:RC4-BT0310-110300-015-b08 BT0310 Homo omo sapiens, clone IMAGE:3682908, mRNA	3.5
	~	43553			Hs.1173(Hs.4418!		CTe	3.5
4	5	44710 41053		-	Hs.6417		TOnco Na Imprending Ivsesemsi (VSCU	3.5 3.5
		42215	6 N3452	4		g	b:yy56d10.s1 Soares_multiple_sclerosis_ ynein, exonemal, light intermediate pol	3.5
		4536			Hs.3384 Hs.2838	58 F	omo sapiens mRNA full length insert cDN	3.5
-	50	43974 4538			Hs.3623	2 L	3AAA186 gene product	3.5 3.5
-	, ,	4249	54 NM_0	00546	Ha.1846		umor protein p53 (Li-Fraumeni syndroma)	3.5
		4207			Hs.1594	ICA 1	AP3 protein ESTs, Weakly similar to ALUC_HUMAN IIII	3.4
		4267 4206			Hs.124	704 I	ESTs, Moderately similar to S65657 alpha	3.4 3.4
	55	4488	31 AL080	0123	Hs.221		einc finger protein 23 (KOX 16) forkhead box M1	3.4
		4443		0274	Hs.239			3.4
		4020 442		59584	Hs.323	53	mitogen-activated protein kinase kinase	3.4 3.4
		414	300 Al304	4870	Hs.188		ESTs hypothetical protein MGC5370	3.4
	60		670 H583	173 19808	Hs.332	330	gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4 3.4
		414 452		5513	Hs.23	3420	ESTs	3.4
			416 AW4	09985	Hs.76		hypothetical protein MGC2721	3.4
	65			865834 75035	Hs.13	3100	EST8 gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4
	65		3257 BEO 3857 ALO	80235	Hs.35	861	nic-mc06E4621 pmlain	3.4 3.4
			7404 NM	_007350	Hs.82		pleckstrin homology-like domain, family neutrophil cytosolic factor 1 (47kD, chr	3.4
				13934	Hs.15 Hs.21		ESTs	3.4
	70			5224 757055		4060	EQTe	3.4 3.4
	, 0			009640	Hs.2	3368	ESTs, Moderately similar to S65657 alpha Homo saplens cDNA: FLI22785 fis, clons K	3.4
				45325	Hs.2	71923	gb:CM2-BT0593-210300-123-d09 BT0693 Homo	3.3
				088746 5569	Hs.1	B845	ESTS	3.3 3.3
	75			3193		3948	endothelial cell growth factor 1 (platel gb:lL3-ST0141-131099-017-A02 ST0141 Homo	3.3
	. •	4	54631 AV	VB11324	11- 5	ne4n	1AV binding omjela	3.3
				1000734 2002310		0640 101463	Human Chromosome 18 BAC clone CIT9875K-A	3.3 3.3
				N248508	Hs.	79727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
	80	4	49676 AV	N380579	Hs.	209657	ESTs hypothetical protein FLJ10719, KIAA1794	3.
				K001581 L120611	MS.	334828	gb:DKFZp761H119_r1 761 (synonym: hamy2)	3.
				948829	Hs.	213788		3.

175

3.3

	435380		Hs.192221	EST8	e monophosphate synthetase (orotal	3.3
	426746 453362	J03626 H14988	Hs.2057 Hs.107375	ESTs		3.3
	456473	AI202788	Hs.25682	Homo	saplens mRNA for KIAA1863 protein,	3.3 3.3
5	416426	AA180256	Hs.210473		sapiens cDNA FLJ14872 fis, clone PL	3.3
	445777	AI580371	Hs.145384 Hs.132571	ESTs	septens mRNA; cDNA DKFZp564P016 (fr	3.3
	423757 431941	AL049337 AK000106	Hs.272227	Home	sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299	74400.00			•	3.3 3.3
10	404108				n26c07.r1 Soares Infant brain 1NIB H	3.3
	425189	H16622	Hs.78531	go:yr	o sapiens, Similar to RIKEN cDNA 5730	3.3
	449318 450193	AW236021 Al916071	Hs.15607	Hom	o saplens Fanconi anemia complementat	3.2
	427725	U56839	Hs.180533	mile	nen-activated protein kinase kinase	3.2 3.2
15	424051	AL110203	Hs.138411	Hom	o sapiens mRNA; cDNA DKFZp588J1922 (f esteryl ester transfer protein, plas	3.2
	418968	NM_000078 M33782	Hs.89538 Hs.23391	Horr	to saplens, Similar to transcription f	3.2
	449248 439416	W58294	Hs.56254	EST		3.2
	401598	AA172108	Hs.110950		C protein	3.2 3.2
20	408380	AF123050	Hs.44532		iquitin	3.2
	450325	A1935962 AA625947	Hs.26289 Hs.25750	ES1	ia.	3.2
	428730 457536	AA305233	Hs.278712	euk	aryotic translation initiation factor	3.2 3.2
	426836	N41720	Hs.172684	Ves	icle-associated membrane protein 8 (e	3.2 3.2
25	442710	AI015631	Hs.23210	ES	l'a lin-dependent kinase inhibitor 2C (p1	3.2
	435232 430970	NM_001262 AI018210	Hs.4854 Hs.144083			3.2
	416192	NM_005036	Hs.998	bet	oxisome proliferative activated recep	3.2 3.2
	446876	H09380	Hs.300964	ES	TS	3.2
30	451459	AI797515	Hs.270560) ES	Ts. Moderately similar to ALU7_HUMAN A mo saplens, clone IMAGE:4299322, mRNA,	3.2
	407603 413840	AW955705 AI301558	Hs.62604 Hs.14638	ı Ri	IA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.20179	2 ES	Πa	3.2 3,2
	432593	AW301003	Hs.51483		Ts, Weakly similar to hypothetical pro	3.2
35	458788	A1457098	Hs.28084 Hs.27879		STs STs	3.2
•	455909 419311	BE156417 AA689591	110.21013	_ at	rnv66a12.s1 NCI_CGAP_GCB1 Homo saplens	3.2
	439710			at	r:Homo sapiens full length insert cDNA	3.2 3.1
40	434559	AF147315	11- 40-900		o:Homo saplens full length insert cDNA como saplens cDNA FLJ13047 fis, clone NT	3.1
40	455800		Hs.16707 Hs.14631		NA binding molif protein, X chromosome	3.1
	436703 414799		Hs.7732	B in	sulin-like growth factor binding prote	3.1
	437860		Hs.2798	98 H	omo saplens cDNA; FLJ23165 tis, ciona L	3.1 3.1
40	434182		Hs.1185		-protein gamma-12 subunit DC20 (cell division cycle 20, S. carevi	3.1
45	417900 434769		Hs.8290 Hs.1342		lomo saplens cDNA FLJ12676 fis, clone NT	3.1
	41482		Hs.7743	2 .	oldernal growth factor receptor (avian	3.1 3.1
	42641	3 AA377823		9	b:EST90805 Synovial sarcoma Homo sapien STs, Weakly similar to 2109260A B cell	3.1
50	44795		Hs.2702	2/0 1	STS. Weakly Shimai to 21032000 5 co.	3.1
50	40458 42176		Hs.1481	35 (serine/threonine idnase 33	3.1 3.1
	41998	6 Al345455	Hs.7891		GA-binding protein transcription factor,	3.1
	41694			78 (niban protein enhancer of zesta (Drosophila) homolog 2	3.1
55	41476 44961			075	ESTs	3.1
"	43474		8 Hs.295	368	FSTe	3.1 3.1
	43427	74 AAB2853			ESTs, Moderately similar to ALU1_HUMAN A serum amyloid A1	3.1
	42789				hynothetical protein FLJ20357	3.1
60	4176 4524				ESTs, Wealdy similar to C55663 diligodend	3.1 3.1
00	4461	31 NM_000	929 Hs.290		nhospholinase A2, group V	3.1
	4400			648	ESTs, Weakly similar to 138022 hypotheti gb:EST94100 Activated T-cells XII Homo s	3.1
	4265 4221		Hs.11	2341	protesse inhibitor 3, skin-derived (SKAL	3.1
65	4062					3.1 3.1
-	4470	39 AV6617	98 Hs.28	2915	EST8	3.1
	4048		1		gb:Homo sapiens (clone 104) retinoblasto	3.1
	4069 4190			280	ESTs	3.0
70	350	894 AI07666	57 Hs.18		ESTS	3.0 3.0
	432				hypothetical protein FLJ20397 chromosome 20 open reading frame 1	3.0
		426 AF0981 202 AW962		52049	ESTs Weskly similar to 138022 hypotheti	3.0
	407	047 X65965	5		gb:H.sapiens SOD-2 gene for manganese su	3.0 3.0
7:	5 418	241 M2668			LIM domain only 1 (rhombolin 1)	3.0
		1599 Z97837		5476 45342	differentially expressed in FDCP (mouse hypothetical protein FLJ14642	3.0
		2950 BE018 3670 AA431		34832	EŠTs	3.0
	446	975 BE248	448 Hs.1	6695	ublquitin-activating enzyme E1-like	3.0 3.0
8		7756 AA767		97098	ESTs deoxythymidylale kinase (thymidylale kin	3.0
		6084 L1699 2374 AL135		'9006 101865	to the second delibration of the second deli	3.0
		3885 H9180		5284	ESTs	3.0
	• • •				•	76

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	434008	AA740878	Hs.112982	ESTs	0114 - 1714 PIGET-6 1714073 (fr	3.0 3.0
	452568	AAB05634	Hs.300870 Hs.182330	Homo 58 ESTs	plans mRNA; cDNA DKFZp547M072 (fr	3.0
	414239 421013	A1288330 M62397	Hs.1345	mutated	in coloractal cancers	3.0 3.0
5	424635	AA420687	Hs.115455		piens cDNA FL114259 fis, clone PL	3.0
	410276	A1554545 N29862	Hs.68301 Hs.44104	ESTs ESTs		3.0 3.0
	433865 406028	142002	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			3.0
4.5	401626		Hs.21691	ESTs	•	3.0
10	415949 418583	H10562 AA604379	Hs.86211	hypothe	tlical protein	3.0 3.0
	417933	X02308	Hs.82962		tate synthetase apiens cDNA: FLI22487 fis, clone H	3.0
	434577	R37316	Hs.17976 Hs.16994	9 Homos 3 Homos	septens cDNA FLJ13569 fls, clone PL	3.0 2.9
15	430437 427940	A1768801 AA417812	Hs.38775	EETA		2.9
10	456060	C14904	Hs.45184	n COTe	sapiens cDNA FLJ12284 fis, clone MA	29
	421988 448775	AW450481 AB025237	Hs.16133 Hs.388	nudbs (nucleoside diphosphate linked moi	29 29
	438598	AI805943	Hs.3260	37 hypoth	efical protein MGC5178	2.9
20	429612	AF062649	Hs.2525 Hs.4090		ry tumor-transforming 1	2.9 2.9
	451189 401558	AA016019	15.4030			2.9
	426207	BE390657	Hs.3002	6 HSPC	182 protein	29
25	404721					2.9 2.9
23	401384 417288		Hs.1088	12 hypol	helical protein FL122004 asome (prosome, macropain) subunit,	2.9
	427648	A1376722	Hs.1800 Hs.183	nes cets	•	29 29
	435928 431740		Hs.183	MAN EST	Moderately similar to AF116721 67	2.9
30	42824	H55709	Hs.225		amia inhibitory factor (cholinergic	29
	43997			662 EST 553 EST	s s, Weakly similar to unnamed protein	29 29
	43311 42375			25 EST	's	29
	40674	8 AW3391	06 Hs.217		extn A2	2.9
35	42215 40558		Hs.120)521 LU	•	2.9 2.9
	44091	1 AA9095		3562 E81	l's le morphogenetic protein 2	2.9
	4124				Ts	29 29
40	4450- 4101	14 AW5905	540 Hs.27		T	2.9
-10	4192	17 AA5045	71		8860e12.rl NCI_CGAP_GCB1 Homo sapiens	2.9
	4158 4481				XM-like membrane protein precursor	2.9 2.9
	4533	31 A)2406	65 Hs.8	one CC	iTs plein phosphatase 4 (formerly X), cata	2.9
45				444	andmilia eulfata nontangivean besyapiv	29 29
	4383 4543		811	gb	:7803C12 Chromosome / Fetal Brain Color	2.9
	421	491 H9999			STs DC7 (cell division cycle 7, S. cerevisi	2.8
5(452	291 AF015 446 F0889		corr C	CT ₀	2.8 2.8
٦,		518 W763	26	gi	bzd60d04_r1 Soares_fetal_heart_NbHH19W on Hippel-Lindau syndrome	2.8
		7221 L1540 2493 AW47		174007 v 250173 h	ypothetical protein FLJ13158	2.8 2.8
	419	2493 AW47 3451 Al907	117 Hs.	00534 e	vntexto bindina protein 2	28
5		8789 BE53	•	ACA47 E	ypothetical protein MGC15548 ESTs	2.8 2.8
		4126 AA33 8695 AV66		282284	ESTs, Wealdy similar to 138022 hypotheti	2.8 2.8
	41	8973 AAZ	3058 Hs	207044	ESTs	2.8
6				.307944 .101047	transcription factor 3 (E2A immunoglobul	2.8 2.8
•		3647 AA6	03367 Hs	.222294	ESTs protein tyrosine phosphatase, receptor-1	2.8
		15817 U88		s.78887 s.300717	sodium channel, voltage-gated, type III,	2.8 2.8
			8850 H	s.130746	ESTS Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
•		32022 AL1	62042 H	s.272348 s.149585	Homo sapiens mikina; curka ukrzprotetztz (tengsin	28
		00517 AF2 133023 AW	.72000	s.87409	#	2.8 2.8
		148734 BE	814070 H	ls.326416	Homo sapiens mRNA; cONA DKFZp564H1916 (f ribosomal protein S2	2.8
				ls.182426 ls.194637	BANP homolog, SMAR1 homolog	2.8 2.8
				ls.125221	ESTs	28
		403961		Hs.22509	ESTs	2.8
			807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, ctone KA	28 28
	75	440483 A	200836	Hs.150386	ESTS gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
			<i>N</i> 947710 66037	Hs.38173	ESTA	2.8 2.8
		411632 A	W854829		gb:QVZ-CT0261-201099-011-f01 CT0261 Homo ESTs, Wealdy similar to ALU5_HUMAN ALU S	2.8
	80	438221 A	1798853 A578027	Hs_122224	obm/20h01.s1 NCI_CGAP_HSC1 Homo sapishs	28 28
	6 U	455510 A	A422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	2.8
		447769 A	W873704	Hs.320831 Hs.243886		2.8
		427701 <i>F</i>	A411101	12.24000	17	7
					1 /	

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					e-I cell membrane-associated gly	2.8
	433800	A1034361 H97552	Hs.135150 Hs.269060	ESTs	8-I CSN (USTION STIC-STATION &)	2.8 2.8
	439662 425694	U51333	Hs.159237	havalda	ase 3 (white cell)	28
_	414747	U30872	Hs.77204 Hs.135150	CENTROIT	nere protein F (350/400kD, mitosin ne-i cell membrane-associated gly	2.8
5	414598 447752	AJ094221 M73700	Hs.105938	tactotra	nsferin	28 28
	408761	AA057264	Hs.238936	ESTs, \	Weakly similar to (defline not ava	27
	453350	A)917771	Hs.61790 Hs.279789	histone	etical protein FLJ23338 deacetytase 3	27
10	456629 439538	AW891965 AA837323	Hs.164047	COTA		2.7 2.7
10	458814	A1498957	Hs.170851	L	Wealdy similar to Z195_HUMAN ZINC	27
	456029	BE255990 BE072881	Hs.218329	ab:RC	etical protein 2-870548-200300-012-e09 BT0548 Homo	27
	451129 456412	AW749617	Hs.280776	tankyn	ase, TRF1-interacting ankyrin-rela	2.7 2.7
15	453536	AA137000	Hs.62578	ESTs	netical protein FLJ21816	2.7
	438378	AW970529 U44060	Hs.86434 Hs.14427	Homo	saptens cONA: FLJ21800 fis, clone H	2.7 2.7
	425745 448322	N23033	Hs.155814	ESTs		27
	451592	AIB05416	Hs.213897 Hs.12827	ESTs		2.7
20	429466 429747	M85835 M87507	Hs.2490		1 considerelated cysteine pr	2.7 2.7
	455514	AW983871		ah-Ri	C1_HN0003-220300-021-bU/ HNUVUS HUNU	2.7
	414732	AW410976	Hs.77152 Hs.79572	-othe	thromosome maintenance deficient (S. epsin D (tysosomal asparty) protease	. 2.7
25	444207 427421	AI565004 AA402414		coate	orner protein complex, subunit beta	2.7 2.7
23	449655	At021987	Hs.59970	EST	5	27
	422648		Hs.11889 Hs.18463	A hune	anoma associated gene sihelical protein FLJ20005	27
	428494 406895		Hs.1725	مأمم ۸۰	matalidae troci hinding Digikiii (1)8	2.7 2.7
30	453255	AA278167			pyrintanian osaplens, clone IMAGE:3605822, mRNA	2.7
	427348			20 501	00650 protein Ts	2.7
	435370 407862		7 Hs.5072	4 Hor	no sapiens cDNA FLJ10934 ffs, clone OV	27 27
	411874	4 AA09510			Ts vA1806 protein	2.7
35	421193 43589		8 Hs.2049 Hs.1899	44 60	Ta .	2.7 2.7
	41460		Hs.251	9 ES	Ts, Weakly similar to YEXO_YEAST HYPOT Ts, Moderately similar to ALU4_HUMAN A	2.7
	45346				TS	2.7
40	43655 42752			565 mi	nichromosome maintenance deficient (S.	2.7 2.7
70	40388	31			oalipopratein C-I	2.7
	43177		78 Hs.268	5/1 84	onipoprotest Cr	2.7 2.7
	40498 4482		34 Hs.208	30 kb	nesin-like 2	2.7
45				244 m	litotic spindle coiled-coil related prot lycogen synthase 1 (muscle)	2.7
	4119 4047		NA LIS.111			2.7 2.7
	4470	72 D61594		279 ty	rrosylprotein sulfotransferase 1 b:yu89a11.s1 Soares fetal liver splean	2.7
51	4221			nac b	washalical postein FLJ21841	2.7
50) 4396 4369				ib:nv54h12r1 NCI_CGAP_Ew1 Homo sapiens	2.7 2.7
	412	833 AW960			ibosomal protein S19 ESTs	2.7
	457	245 A17454 861 A16965		14579 l 1427 l	Homo sapiens cDNA; FLJ21800 fis, clone H	2.7 2.7
5:	5 453	263 R9177		I	EST8 gb:601159362F2 NIH_MGC_53 Homo saplens c	27
		385 BE380		36452	gp:501 159362F2 MIN_WGG_33 TIGHT SEPTEMBER	2.7
		764 AA824 285 AI971		0422	CCTs Washin similar to 138022 hypotheti	2.7 2.7
_	424	853 BE54	9737 Hs.1		Human EST clone 122887 mariner transposo mitogen-activated protein kinase-activat	2.7
6		0037 BE40 9892 N736		27789 0309	ESTs	2.7 2.7
		4201 AB02		4131	KIAA0974 protein	2.7
		2279 AA28		31260 247551	hypothetical protein FLJ13164 metadin 1	2.7
-	· ·	7954 J030 0371 U807		£47.551	1100 Carrier 1	2.7 2.7
•	45	2449 AWD	68858 Hs.	20943	ESTS	2.7
				291015 81170	ESTs plm-1 oncogene	2.7
	44			19192	cyclin-dependent kinase 2	2.7 2.7
•	70 4	03680			gb:CM4-ST0189-051099-021-05 ST0189 Homo	2.7
	4		313110)7410 Hs	.69280	Homo saplens, clone IMAGE:3636299, mRNA,	2.6 2.6
			1594 Hs	.29002	KIAA1706 protein	26
	75 4)37766 Hs	.146085	KIAA1345 prolein	26
		105808 119700 AFC	384935 Hs	.92357	galactokinase 1	2.6 2.6
		35972 W9	5088 H	3.114198	ESTs	2.6 2.6
	4	153568 S70		s.557 s.9701	adrenergic, sipha-10-, receptor growth arrest and DNA-damage-inducible,	2.6
				s.86437	CCTs Mighty similar to AF219140 1 9880	2.6 2.6
		428209 AA	424197 H	s.98947	ESTs, Wealdy similar to \$33496 bypsin (2.6
				s.272155 s.64859	ESTS ESTS	2.6
		-1440 DAGGOOL			178	

					2.6
			Hs.177576 rr Hs.156346 te	iannosyl (atpha-1,3-)-glycoprotein beta- ipoisomarasa (DNA) II alpha (170kD)	26
			Hs.111219 E	STs, Moderately similar to ALU1_HUMAN A	2.6
-	401324			are the the latest a 120022 beautiful	26 26
5	425234 443210	AW152225 AI692649		STs, Weakly shrillar to 138022 hypotheti ypothetical protein MGC13168	2.6
	457244	AA581385	Hs.162473 E	STs, Wealthy similar to 138022 hypotheti	2.6
	417144	AA382104	Hs.81337	ectin, galactoside-binding, soluble, 9	2.6 2.6
10	433933	Al754389 AA226869	Hs.133494 I Hs.16520 I	torno sapiens cione TCCCIA00164 mRNA sequ rypothetical protein DKFZp762L0311	2.6
10	437437 434206	AW136973		ESTs, Wealthy similar to S89890 milliogen I	26
	400992			1 DOLUMENT NAMED OLI 402 UNONIE Vorro	26 26
	455530	AW984744 AA765788		gb:RC1-HN0015-040400-011-d03 HN0015 Homo ESTs	2.6
15	436139 448330	AL036449	Hs.207163	ESTs	2.6
	412942	AL120344	Hs.75074	milogen-activated protein kinase-activat	2.6 2.6
	432753	NM_014075	Hs.336938 Hs.186755	Homo saplens PRO0593 mRNA, complete cds ESTs	26
	433430 436693	AI863735 AW973223	Hs.303197	B-cell CLL/lymphoma 7C	2.6
20	429482	AF076974	Hs.203952	transformation/transcription domain-asso	2.6 2.6
	432715	AA247152	Hs.200483 Hs.279898	ESTs, Wealdy similar to KIAA1074 protein Homo sapiens cDNA: FLJ23165 fis, clone L	26
	414217 434165	A1309298 AA971328	Hs.95361	myosin VIIA (Usher syndrome 18 (autosoma	2.6
	414835	AA156720	Hs.185342	ESTs	2.6 2.6
25	424489	T48851 AA281959	Hs.149250 Hs.5210	D-siglec precursor, glia maturation factor, gamma	2.6
	436495 403797	A-201838	TIBLETO	granical reserve	2.6
	434573	AW372340	Hs.159717	ESTs	2.6 2.6
30	418841 415785	NM_002332 R82419	Hs.89137 Hs.23603	low density itpoprotein-related protein ESTs, Moderately similar to ALUS_HUMAN A	2.6
30	450608	AA010365	Hs.193229	ESTs	2.6 2.6
	425304	AA463844	Hs.31339	fibroblast growth factor 11 3-phosphoadenosine 5-phosphosulfate sy	26 26
	432268 410507	BE311856 AA355288	Hs.274230 Hs.40834	transitional epithelia response protein	2.6
35	427343	A1880044	Hs.176977	protein kinase C binding protein 2	2.6 2.6
	420917	AW135716	Hs.117330	ESTs transcription elongation factor B (SIII)	2.6
	414399 446089	L47345 A1860021	Hs.155202 Hs.270651	ESTs, Moderately similar to A47582 B-cel	2.6
	440829	AF136407	Hs.7446	chromosome 6 open reading frame 5	26 26
40	408475	AA315514	Hs.47986 Hs.127698	hypothetical protein MGC10940 ESTs, Moderately similar to 2109260A B c	26
	450946 421462	AA374569 AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	2.6 2.6
45	422887	A1751848 NM_00518	Hs.49215 1 Hs.82129	ESTs carbonic anhydrase III, muscle specific	26
45	417435 437389		Hs.271586	hypothetical protein DKFZp762M115	2.5
	408981	AW500797		Gem-Interacting protein	2.5 2.5
	432180 418079		Hs.272822 Hs.6911	RuvB (E coll homolog)-like 1 ESTs	2.5
50	437820		Hs.323838	ESTs. Weakly similar to alternatively sp	2.5 2.5
	439585				2.5
	425681 435177		Hs.42936	ESTS	2.5
	437323	AA371145			2.5 2.5
55	422114 448478		Hs.111801 Hs.203456		2.5
	42662			ESTs	2.5
	44876	4 Al568607	Hs.18211		2.5 2.5
60	45,838 40372		Hs.24621 Hs.13434		2.5
00	44488		Hs.14855	9 ESTs	2.5 2.5
	45617		Hs.27193		2.5
	42484 40627		Hs.15347 19 Hs.83920	peptidylglycine alpha-amidating monocxyg	2.5
65	41805	4 NM_0023	18 Hs.83354	lysyl oxidase-like 2	2.5 2.5
	44593			hypothetical protein FLJ22329 gb:tl.3-CT0214-150200-074-E06 CT0214 Homo	2.5
	45496 4423			59 ESTa	2.5
70	4565	83 AF 17989			2.5 2.5
70	4342 4168		Hs.4464 Hs.8040	g growth arrest and DNA-damage-inducible,	2.5
	4245		71 Hs.2389	54 ESTs, Weakly similar to KIAA1204 protein	2.5 2.5
	4060	38 Y14443	Hs.8821		2.5
75	4134 4230		1515.2048 BO Hs.2048		2.5
/-	4108		9 Hs.9365	9 protein disulfide isomerase related prot	25 25
	4398	341 AF0389	61 Hs.6710		2.5 2.5
	4538 _ 4450			559 ESTs	2.5
80) . 449	520 BE4077	97 Hs.237	checkpoint with forkhead and ring finger	2.5 2.5
	406			342 ribosomal protein L13 gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	412 423	370 AW946 642 AW452			2.5
				170)

	420257	AVA/075780	Hs.165607	ESTs		2.5
		AW975789 U31116	Hs.77501	SEFCO	glycan, beta (43kD dystrophin-assoc	25
	416097	BE387371	Hs.118964	hypot	hetical protein FLJ20085	2.5 2.5
~	428619	AK002140	Hs.187378	hypot	helical prolein FLJ11278 Ilagen-prolina, 2-oxoglutarata 4-di	2.5
5	413976 445223	BE295452 AW291553	Hs.75655 Hs.254983	ESTS		25
	423926	X03833	Hs.1722	interle	eukin 1, alpha	2.5 2.5
	410165	BE560228	Hs.71869	abob,	osls-associated speck-like protein	2.5 2.5
10	406474	414900444	Hs.157975	EST		2.5
10	433908 439755	AW298141 AW748482	Hs.77873		omalog 3	2.5
	437528	N59646	Hs.169745	CRUM	bs (Drosophila) homolog 1	25 25
	420734	AW972872	Hs.293736	EST	S o process	25 25
1.5	415346	Z43108	U- 100070		SC13E071 normalized infant brain cDN	2.5
15	419337	AW291112 R09478	Hs.209978 Hs.18041	EST		2.5
	444606 430061	AB037817	Hs.230188	KIA	1396 protein	2.5
	413407	AI356293	Hs.75339		itol polyphosphate phosphatase-like	2.5 2.5
20	411965	BE467339	Hs.280115	EST	s phase-promoting complex subunit 7	25
20	409278	AA3466B3	Hs.52763	ana	DUSS-bround compan agent.	2.5
	403142 401714					2.5
	425081	X74794	Hs.154443		ichromosome maintenance deficient (S.	2.5 2.5
~~	416505	H66470	Hs.16004	ES		2.5
25	431518	AA743462 BE613468	Hs.165337 Hs.107515	ES'	rs, Weakly similar to T00329 hypotheti	2.5
	448623 428301	AW628666	Hs.98440	ĒS	Ts, Weakly similar to 138022 hypotheti	2.5
	404366	***********				2.5 2.5
	449733	R74546	Hs.29438	Ho	mo sapiens cDNA FLJ12094 fis, clone HE IL-8T152-080399-004 BT152 Homo sapien	2.5
30	459583	A1907873		gb:	RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	402856 420751	AW939659 J03019	Hs.99913	gu. ad	renergic, bela-1-, receptor	2.4
	436805	AA731533	Hs.270751	t ES	Te .	2.4
	420285	AA258124	Hs.29387	B ES	Ts, Moderately similar to ZN91_HUMAN Z	2.4 2.4
35	453496	AA442103	Hs.33084		tute carrier family 2 (facilitated glu	24
•	453853	AL040600 AW103986	Hs.18808	s ei	STs cxd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	2.4
	407909 454630			gt	:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4
	451026		Hs.15749	12 C	r-d4 (mouse) homolog	2.4 2.4
40	420779	L12398	Hs.99922		opamine receptor D4	24
	438322		Hs.22134	19 E	STs b:QV0-HT0367-150200-114-h04 HT0367 Hamo	2.4
	455908 419625		Hs.91640) n	uclear factor of kappa light polypeptid	24
	440773			41 H	omo sapiens, Similar to RIKEN CDNA 2700	2.4 2.4
45	450823		Hs.2201	1 0	omplement-c1q turnor necrosis factor-rel	24
	447247				tomo sapiens cDNA FLJ13090 fis, clone NT eutrophil cytosolic factor 4 (40kD)	24
	429109		Hs.1983 Hs.2093		STs	2.4
	451802 41941		Hs.3942	9 1	STs	2.4
50	40709		Hs.2240	5 1	eukocyte immunoglobulin-like receptor,	2.4 2.4
	42356				nypothetical protein FLJ 13633	2.4
	42750		Hs.1317 Hs.2699		ESTs KIAA1278 prolein	2.4
	45177 43684			28	ESTs	2.4
55	43158		21 Hs.2662		Homo saplens cDNA FLJ14115 fis, clone MA	2.4 2.4
	44061				hypothetical protein FLJ 12879 cardiotrophin-like cytokine; neurotrophi	24
	42372				GDP-mannose pyrophosphorylase 9	2.4
	45212 41950				ATP_hinding cassette, sub-family C (CFTR	24
60	4534				gb:600944574F1 NIH_MGC_17 Homo saprens c	2.4 2.4
	. 4197	92 AA25089			ESTs ESTs, Weakly similar to T09052 hypotheti	2.4
	4527		Hs.106	1042	gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
	4104 4386			51	cleavage and polyadenylation specific fa	2.4
65	4024	08				2.4 2.4
-	4439	50 NM_001	425 Hs.999		epithelial membrane protein 3	24
	4146		38 Hs.760	586	glutathione peroxidase 1	2.4
	4030		5.4		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo saptens	24
70	4320 0 4316			7749	unc93 (C.elegans) homolog A	24
• `	4550	023 AW850	907		gb:IL3-CT0220-310100-055-H11 CT0220 Homo	24 24
	426				nucleoparin-like protein 1	2.4
	446				ESTs plasminogen activator, urokinase	24
7	5 414	774 X02419 252 AA346			ESTs	2.4
•		918 AA209		3754	hypothetical protein FLJ12606	2.4 2.4
	427	550 BE242		79608	nuclear RNA helicase, DECD variant of DE	2.4 2.4
		020	202 11-44	1402	Cbo/p300-interacting transactivator, wit	24
0		7846 AA425 7222 A15254			hypothetical protein MGC2383	24
0		7222 A15254 3639 BE269			proteasome (prosome, macropain) subunit,	24
		2706 AW44		57150	ESTs, Moderately similar to SUR1_HUMAN S	24 24
	401	1676			•	27
					190	

	428882	AA436915	Hs.131748	EST:	i, Moderatety similar to ALU7_HUMAN A	2.4
	436277			EST	; droitin sulfate proteoglycan 3 (neur	2.4 2.4
	426271 406353	AF026547	Hs.169047	GIO!	moral source proceedings in a friend	24
5	409193	AA131483		gb:z	008e05.r1 Stratagene neuroepithelium	2.4 2.4
	431431		Hs.252953 Hs.30800		an DNA sequence from clone RP3-403A15 s, Wealdy similar to S65657 alpha-1C-	24
	407889 453335	R34556 AW857376	Hs.169238		syltransferase 3 (galactoside 3(4)-L	2.4
	450621	AW297288	Hs.55918	hype	othetical protein FLI11354	2.4
10	419652	AL157485	Hs.91973	hype EST	othedical protein	2.4 2.4
	421151 437848	BE174431 AA773866	Hs.63386 Hs.244569		a phagus cancer-related gene-2	2.4
	420581	AA847602	Hs.106510	EST	s, Moderately similar to ALU2_HUMAN A	24
16	405288		11- 40000C		. ·	24 24
15	453527 429875	R49570 Al091815	Hs.180236	ES.	s qa58b08.s1 Soares_NhHMPu_S1 Homo sapi	24
	436360	A1962798	Hs.136754	ES		2.4
	418592	X99226	Hs.284153	Fer	coni anemia, complementation group A	2.4 2.4
20	419991 449539	AJ000098 W80363	Hs.94210 Hs.58446	eye	s absent (Orosophila) homolog 1 Te	2.4
20	419870	AW403911	Hs.266175		sphoprotein associated with GEMs	24
	404584				- -	24 24
	454276	AW294996	Hs.255374 Hs.132370	ES	Ts DPH axidese 1	24
25	423746 415558	AW361817 AAB85143	Hs.125719	ES		2.4
23	428141	D50402	Hs.182611	so	ute carrier family 11 (proton-coupled	2.4
	406953	1.36847	Un 44917		:Human (clone p17/90) rearranged iduro NA0877 protein	2.4 2.4
	444471 451031	AB020684 Al360187	Hs.11217 Hs.4254		Ts	24
30	455302	AW997641		ob	:RC6-BN0052-170200-011-D08 BN0052 Homo	24
	449063	Al627352	Hs.236547	H	mo saplens, clone IMAGE:2905978, mRNA.	24 24
	401048 434420	AA688278	Hs.194864	hv	pothetical protein FLJ22578	2.4
	425848	BE242709	Hs.159637		tyl-tRNA synthetase 2	2.4
35	449086	AI628357	Hs.208037		STs	24 24
	415238 448337	R37780 AW208453	Hs.21422 Hs.3782		5Ts 5Ts	24
	416991	N36389	Hs.141296	K	AA0226 gene product	2.3
40	412600	L28824	Hs.74101		deen tyrosine kinase omo sepiens, clone IMAGE:3357127, mRNA.	2.3 2.3
40	418385 440769	AW590613 BE581793	Hs.301040 Hs.21446		IAA1716 protein	2.3
	450437	X13956	Hs.24998		ypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629		ypothetical protein MGC3121	2.3 2.3
45	406739 418506	AI566709 AA084248	Hs.182426 Hs.85339		bosomal protein 52 Sprotein-coupled receptor 39	2.3
72	410286	Al739159	Hs.61898		KFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	E	STs	2.3 2.3
	405605 416913	AW934714			b:RC1-DT0001-031299-011-e11 DT0001 Homo	2.3
50	426509	M31166	Hs.2050	i	entaxin-related gene, rapidly induced b	23
	445828	F05802	Hs.81907		STS	2.3 2.3
	457195 420372		Hs.196647 Hs.29386		(IAA0527 protein Homo saplens, clone IMAGE:3535476, mRNA,	2.3
	423198		Hs.1634		cell division cycle 25A	2.3
55	457730	AW753813	11 40004		gb:RC1-CT0268-060100-013-e01 CT0268 Horno	2.3 2.3
	412014 447131		Hs.43761 5 Hs.17456		ESTs, Weskly similar to A46010 X-linked retinoic acid receptor responder (tazaro	2.3
	446288				ESTs	2.3
۲۵	436954		Hs.13042	5	ESTs	2.3 2.3
60	411658 404240)		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
	456094				gb:yw57e09.r1 Soares_placenta_6to9weeks_	2.3
	41695		Hs.19078	35	ESTs, Moderately similar to S65657 alpha	2.3 2.3
65	40673 45845		Hs.1350	95	gb:qy15h09.x1 NCL_CGAP_Bm23 Homo saplen ESTs	23
05	45233		Hs.1919		KIAA1733 protein	2.3
	40852	3 AW833259		87	ESTs	23 23
	45547 43632		2 Hs.1409	e2	gb:PM0-MT0011-240300-001-c09 MT0011 Homo ESTs, Weakly simitar to I38022 hypotheti	2.3
70	45000		Hs.1088		hypothetical protein FLJ21709	2.3
. •	41817	1 H23896	Hs.1257	90	leucine-rich repeat-containing 2	2.3 2.3
	41913		Hs.2217 3 Hs.2938		ESTs spinster-like protein	23
	44593 42208				ESTs, Weakly similar to SFR4_HUMAN SPLIC	23
75	44991	11 AI262106	Hs.1265	53	ESTs	2.3
	41707		Hs.8113		interleukin 1 receptor entagonist eukaryotic translation initiation factor	2.3 2.3
	41174 4356		3 Hs.718' Hs.497!		potassium voltage-gated channel, KQT-lik	2.3
	4234	91 AA19176	5 Hs.129	673	eukaryotic translation initiation factor	2.3
80					ESTs ESTs, Wealdy similar to I38022 hypotheti	2.3 2.3
	4114 4386				ESTS. WEBRY SHEET IN INCOME IN POSITION	2.3
	4326		Hs.308		mitogen-activated protein kinase 7	2.3

	452198		Hs.61210	ESTs, Wealthy similar to 138022 hypotheti	2.3 2.3
		AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3
	404054		Hs.225706	ESTs, Weakly similar to 138022 hypotheti	2.3
5	100100			ESTs	2.3
,	440210 446727		Hs.16032	KIAA0523 protein	2.3
	453775		Hs.35120	replication factor C (activator 1) 4 (37	23
	438379	N23018	Hs.171391	C-terminal binding protein 2	23 23
	449919		Hs.200141	ESTs	23
10	415293		Hs.106541	ESTs methionine adenosyltransferase I, alpha	23
	441126		Hs.323715 Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
	408203 434941	AA053137 AW073202	Hs.334825	Homo sepiens cDNA FLJ14752 fis, clone NT	2.3
	450748	AI733093	Hs.130016	ESTS	23
15	404185				23
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3 2.3
	451370	AI791929	Hs.300782	ESTs	2.3
	400034	4141074464	U. 252073	ESTs	2.3
20	407723 431320	AW071161 AW969474	Hs.252873 Hs.183070	ESTS	2.3
20	431320	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707	AW003879	Hs.126522	Homo saplens, clone MGC: 16722, mRNA, com	2.3
	419225	U70073		gb:HSU70073 Human Homo sapiens cDNA clon	2.3 2.3
	444556	A1277924	Hs.145199	ESTs	2.3
25	405741				23
	400917	AA736777	Hs.293770	ESTs	2.3
	432567 437949	U78519	Hs.41654	ESTs, Wealdy similar to A46010 X-linked	2.3
	450514	AC005785	Hs.25059	A kinase (PRKA) anchor protein 8	23
30	418400	BE243026	Hs.301989	K1AA0246 protein	2.3 2.3
	444019	BE173977	Hs.10098	putative nucleolar RNA helicase	23
	406326		15- 47400	ESTs, Weakly similar to FLJ00004 protein	2.3
	412077	N51107 W19744	Hs.47199 Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.3
35	427647 414528	AA148950	Hs.188836	ESTs	2.3
55	414854	BE546797	Hs.51483	ESTs. Weakly similar to hypothetical pro	2.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	. 23 23
	439467	AW292275	Hs.158365	ESTs	2.3
40	402627		00000	cat eye syndrome chromosome region, cand	23
40	451711	AK000461 AW975531	Hs.26890 Hs.154443		2.3
	424308 423869	BE409301	Hs.134012		2.3
	405915	0040300	110.10101		23
	431503	NM_012129	Hs.258570	i claudin 12	23
45	423306	W88562	Hs.10819	B ESTs	2.3 2.3
	443232	AF161521	Hs.9081	phenylalanyl-IRNA synthetase beta-subuni	2.3
	433064	D79991	Hs.30002	SH3-containing protein SH3GL82; KIAA1848 3 ESTs	2.3
	434437 436191	AI912566 BE407866	Hs.18781 Hs.17025		2.3
50	420006		Hs.94300		2.3
50	447942		Hs.33478		2.3
	403166				2.3 2.3
	422119		Hs.11188	2 KIAA0590 gene product	2.3
55	403751		Hs.16994	6 GATA-binding protein 3	2.3
))	426451 427413		Hs.17778		2.3
	409091			23 ESTs	2.3
	440491		Hs.2494		2.3 2.3
	42772		Hs.1804	79 hypothetical protein FLJ20116	23
60	405747		Hs.3116	O1 EST	2.3
	43821		1 115.3110	ui E91	23
	40465 42352		Hs.1297	38 potassium voltage-gated channel, Shaw-re	22
	42679		Hs.1723		2.2
65	44442	4 AI654684			2.2 2.2
	43403				2.2
	42765				2.2
	43522		Hs.104 6 Hs.1541	HGF activator 162 HIV-1 rev binding protein 2	22
70	43827		Hs.151		2.2
, (42468 4 29 98				2.2
	4420		Hs.128	417 hypothetical protein FLJ14009	22
	4151	98 AW0094	80 Hs.943	natural killer cell transcript 4	2.2 2.2
~	4205				2.2
75					2.2
	4437				2.2
	4232 4465				2.2
	4122				2.2
86	9 4210	MD AA7150	26 Ha.135	280 ESTs	2.2
-	4262	12 571824		1988 neural cell adhesion molecule 1	2.2 2.2
	4555			gb:PM3-BN0142-200300-001-c04 BN0142 Homo 0255 major histocompatibility complex, class	2.2
	4068	351 AA6097	84 Hs.18	1533 HISTOR RESIDENT PRODUCES AND	

					22
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.2 2.2
	419575	U43431	Hs.91175	topoisomerase (DNA) III alpha	2.2
	418672	L44284 AA210718	Hs.159743 Hs.104157	ESTs ESTs, Wealty similar to KIAA0694 protein	2.2
5	456261 415737	AA167626	Hs.118743	ESTs	5.5
,	447554	AJ391598	Hs.36119	ESTs, Wealthy similar to ALU1_HUMAN ALU S	2.2 2.2
	405159				2.2
	442177	AW661820	Hs.211413	ESTS	22
• • •	446139	H77395	Hs.39749 Hs.172843	ESTs ESTs	2.2
10	458339	AW976853	NS.172040	2013	2.2
	401876 439566	AF086387		gb:Homo sapiens full length insert cDNA	2.2
	425079	H09963	Hs.2257	vitronactin (serum spreading factor, som	2.2 2.2
	441837	AA361743	Hs.179881	core-binding factor, beta subunit	2.2
15	430644	AB015419	Hs.247710	preproprotactin-releasing peptide	2.2
	431474	AL133990 NM_002285	Hs_190642 Hs_38070	ESTs lymphoid nuclear protein related to AF4	22
	407739 424244	AV647184	Hs.143601	hypothetical omtein hCl A-Iso	2.2
	438057	AW294544	Hs.125785	ESTs, Wealdy similar to CORB MOUSE CORNI	2.2 2.2
20	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.2
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2.2
	404170	1100074		gb:Human retinoic acid receptor gamma 2	2.2
	406902	M32074 AA770599	Hs.144055		22
25	437902 401012	M/11/0333	143.14.1000	2010	2.2
22	446502	Al302654	Hs.208024		2.2 2.2
	442554	AW467376	Hs.129640	ESTs	2.2
	443021	AA368546	Hs.8904	lg superfamily protein	2.2
20	421141	AW117261	Hs.125914 Hs.8984	ESTS Homo sapiens chromosome 14 BAC 98L12	2.2
30	443070 446566	BE388662 H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.17286	2 ESTs	2.2 2.2
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cu	2.2
	431468	AW248431	Hs.25652		2.2
35	416185	AW975861			2.2
	437319 402064	BE410958	Hs.56406	(total opposite data to the control opposite	2.2
	413335		Hs.48442	ESTs .	2.2 2.2
	408212		Hs.43728	hypothetical protein	2.2
40	406169			totadoutio 12 mandos pieho 2	2.2
	451099		Hs.2595		2.2
	407335		Hs.1587 Hs.2389		2.2
	409715 431921		Hs.5887		2.2
45	44382		Hs.9877	hypothetical protein	2.2 2.2
	43245	8 A1968598		8 malignant cell expression-enhanced gene/	2.2
	41972		Hs.1274		2.2
	42317			TO THE PERSON OF	2.2
50	45108 41521			11 Homo sapiens cDNA FLJ11421 fis, clone HE	2.2
-	44224			4 Homo sapiens cDNA: FLJ23285 fis, clone H	2.2 2.2
	441B3	O AA38310			2.2
	40666		Hs.172 50 Hs.928		2.2
55	44337 43255		90 ms.920 Hs.177		2.2
,,,	40814		Hs.810	57 hypothetical protein MGC2718	2.2 2.2
	4198				2.2
	4394				2.2
60	4384				2.2
OU	4501 4091				2.2
	4288			1904 hypothetical protein FLJ 12671	2.2
	4294		03 Hs.20	1039 aristaless-like homeobox 3	2.2 2.2
,	_ 4330				2.2
65					2.2
	4082 4274			8728 methyl-CpG binding dornain protein 3	2.2
	408			3345 ESTs. Weakly similar to 138022 hypotheti	2.2
_	445		845 Hs.27	glycine dehydrogenase (decarboxylating:	2.2 2.2
70	0 431	446 AW 2 94		5369 Homo sapiens cDNA FLJ 10265 fis, clone HE	2.2
		660 AA909		2282 sotute carrier family 30 (zinc transport nuclear transcription factor, X-box bind	2.2
		099 NM_00 857 AA866		27797 Homo sapiens CDNA FLJ11381 fis, clone HE	2.2
	415	857 AA866 245 N5965		7252 ESTs	2.2
7	5 44	657 R1497		gb:y142f10.s1 Soares fetal liver spleen	2.2 2.2
•		521 AW50	1216 Hs.1	08945 KIAA0515 protein	2.2
		1819 BE177		66148 hypothetical protein FLJ 13231 82642 ESTs	2.2
		5530 AV658 5797 AI291		82642 ESTs 2800 ESTs	2.2
Я		5797 AI291 4812 X7275		7367 monokine induced by gamma interferon	2.2
		3028 AB00		1442 RecQ protein-like 4	2.2
	41	2133 U834	50 Hs.7	3614 solute carrier family 31 (copper transpo	2.2 2.2
	40	7881 AW07	'2003 Hs.4	0958 heparan suttate (glucosamine) 3-O-sutfot	2.6

				a contracts	2.2
	437033	AW248364	Hs.5409 Hs.24937	RNA polymerase i subunit transformer-2 alpha (htra-2 alpha)	2.2
	422732	AA577455 AI417358	Hs.73677	ESTs	2.2
	416388 452849	AF044924	Hs.30792	hook2 protein	2.2 2.2
5	446615	BE513202	Hs.15589	PPAR binding protein	2.2
-	428361	NM_015905	Hs.183858 Hs.182382	transcriptional intermediary factor 1 ESTs	2.2
	446279 422938	AA490770 NM_001809	Hs.1594	centromere protein A (17kD)	22 22
	403969	(4m_00 1000			2.2
10	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept turnor necrosis factor receptor superfami	22
	429736	AF125304	Hs.212680 Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
	447091 422017	AW089548 NM_003877	Hs.110776	STAT induced STAT Inhibitor-2	2.2 2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	22
15	438726	AB033103	Hs.6385	KAA1277 protein ESTs	2.2
	453315	8E544203 AL039379	Hs.24831 Hs.209602	ESTs, Wealdy similar to ubiquitous TPR m	2.2
	423244 433610	AA806822	Hs.112547	ESTs	2.2 2.2
	429451	BE409861	Hs.20283	heme oxygenase (decycling) 1 gb:yh67f08.r1 Soares placenta Nb2HP Homo	22
20	417980	R32235			2.2
	406347	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	2.2 2.2
	414406 401827	BC23/304		•	22
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr ESTs, Moderately similar to A47582 B-cel	2.2
25	452294	AI871925	Hs.11789	ES18, MODERACHY SUITED TO PATE SOL	2.2
	404084 456786	AK002084	Hs. 13285	hypothetical protein FLJ11222	2.2 2.2
	435031	A1632091	Hs.11687	ESTS	21
	442609			setenoprotein N hypothetical protein from EUROIMAGE 1703	2.1
30	439732				2.1
	421506 439253			? EŠTs	21 21
	409669		1 Hs.2202	5 hypothetical protein MGC13098	2.1
	429574	BE268321	Hs.2089	2 hypothetical protein MGC861 12 hypothetical protein DKFZp5470065	2.1
35	437470			nvezpsasitsza orotein	21
	408941 44768				21 21
	45958		Hs.2070		2.1
40	43913				2.1
40	42818 44202			E ECTe	21 21
	43098			ob EST384925 MAGE resequences, MAGL Homo	2.1
	44360	9 AV65023	1 Hs.282		21
4.5	41716				2.1
45	44453 43839			·	2.1 2.1
	4420			191 ESTs	2.1
	4562	78 BE3003	69 Hs.289		2.1
50	4169			nn hadrovernethelbilana svnihasa	2.1
50) 4178 4452			no CCTe Weath similar to ALU1 HUMAN ALU S	2.1 2.1
	4527		616	gb:RCS-LT0054-140200-013-D01 L10054 none	21
	4349	26 BE543			2.1
55	4215				21. 21
٥.	4249 437		453 Hs.16	2339 ESTs	21
	435	958 H9818			21
	421				21
6	n 410	431 BE261 503 AI570		TEAC ECTe	21 21
0		127 Al478	416 Hs.2	2003 CCTe Wealdy similar to ALU1_HUMAN ALU 3	2.1
		897 BE06		9233 ESTs, Moderately similar to 178885 serin 54 ESTs	2.1
		1112 H178	00 Hs.7		2.1
6		5577 7162 AWOC	5505 Hs.5	64 thyroid harmone receptor coactivating pr	2.1 2.1
•		1460 AI797	550 Hs.2	19652 ESTs	21
		7402 H545		3490 hypothetical protein FLJ20452 3852 ESTs	2.1
		5828 AA70 6398 AI68:		costa miseless was MMTV integration site fami	2.1
7				anna Hama ennione chromosome 19. COSMID PGDV	2.1 2.1
•		2020 AA7	22012 Hs.	55757 ESTs, Wealdy similar to AT2A_HUMAN POTEN gb:HSC2QE041 normalized infant brain cDN	2.1
	41	5586 Z454		ANDRE ESTA	21
				68272 FSTs. Wealdy similar to CA13 MOUSE COLLA	2.1 2.1
•			72330 Hs	283022 triggering receptor expressed on myelolo	21
	4	31741 AA5	14783 Hs	191701 ESTs	21
				209203 ESTs 146726 ESTs	2.1
			47060 Hs 306007 Hs	59461 DKFZP434C245 protein	21 21
		100822			2.1
		12760 AW		41324 ESTs 65238 95 kDa retinoblastoma protein binding pr	2.1
				65238 95 kDa retinoblastoma protein butuary pa 315689 Homo sapiens cDNA: FLJ22373 fis, clone H	2.1
	•			104	

	424242	AA337476	Hs.293984		etical protein MGC13102	21 21
	452560	BE077084 AI924228	Hs.336432 Hs.115185	ESTS	Moderately similar to PC4259 ferri	2.1
	456437 458922	BE501B31	Hs.282053	ESTa		2.1 2.1
5	439231	AW581935	Hs.141480	Homo	sapiens mRNA; cDNA DKFZp434N079 (fr phosmin/nucleoptasmin 3	2.1
	419488 411829	AA316241 AW865749	Hs.90691	ab:QV	3-SN0021-100500-185-c03 SN0021 Homo	2.1
	457192	AL135682	Hs.22452	Homo	canions mRNA for KIAA1737 Drotten.	21 21
10	422128	AW881145	U- 24006	gb:Q\ ESTs	D-OT0033-010400-182-e07 OT0033 Homo	21
10	452571 423699	W31518 H41850	Hs.34665 Hs.131846	PCAF	associated factor 65 alpha	21
	406610	[]41050	. 4 4 . 4 . 4			21 21
	453638	AW814996		gb:Mi	R1-ST0206-170400-024-h09 ST0206 Homo ST72900 Ovary II Homo sapiens cDNA 5	2.1
15	418856 437623	AA362858 D63880	Hs.5719	gu.c.	nosome condensation-related SMC-asso	2.1
13	410908	AA121686	Hs.10592	EST	;	2.1 2.1
	420221	N25991	Hs.43725	EST		2.1
	424739 425398	AA346108 ALD49689	Hs.221610 Hs.156369	hypo	thetical protein similar to tenascin	2.1
20	424901	Z11933	Hs.182505	POU	domain, class 3, transcription tacto	21 21
	411096	U80034	Hs.68583	milo chilo	chondrial intermediate peptidase ISC3JF101 normalized infant brein cDN	2.1
	415635 418181	F13168 U37012	Hs.83727	clea	vage and polyadenylation specific ta	2.1
	407103	AA424881	Hs.256301	- Burn	vhetical contain MGC13170	2.1 2.1
25	454389	AW752571		gb:l	L3-CT0213-170100-055-F02 CT0213 Homo	2.1
	400021 439228	N51700		gb:	y72d01.s1 Soares_multiple_sclerosis_	2.1 2.1
	456505	AA504595	Hs.11141			21
20	405258	AI184564	Hs.10165	4 ES	Ta.	21
30	444645 430246	A1269069	Hs.10926	8 hyp	othetical protein FLJ12552	2.1 2.1
	458687	AW02481	Hs.17008	8 GL	UT4 enhancer factor	21
	403857					2.1
35	400258 422221	AA306649	Hs.16937	'0 FY	N oncogene related to SRC, FGR, YES	2.1 2.1
	441054	AA913591		30 ES	iTs e-span transmembrane protein M83	2.1
	452700 454606		Hs.28894 2	et ur	:MR4-ST0124-181299-020-b06 ST0124 Homo	2.1
	448954	AB01456	Hs.2261	8 101	AANEEA orolein	<u>2</u> .1 2.1
40	443148			94 E	STs, Wealthy similar to ALUS_HUMAN ALU S siquinol-cytochrome c reductase core pr	2.1
	453486 437695			42 E	STs	2.1 2.1
	425449	X52056	Hs.1574	41 6	bleen focus forming virus (SFFV) provir	2.1
15	447270			26 F	eneral transcription factor IIIC, polyp STs, Wealdy similar to TSGA RAT TESTIS	2.1
45	43587 43638			94 6	ST•	21 21
	43583	7 AI68921			omo sapiens cDNA FLJ11431 fis, clone HE	21
	45828 42379				STs STs	2.1
50	40804				lesmoplakin (DPI, DPII)	2.1 2.1
	40272		01 Hs.274	24 I	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.1
	45199 41754			040 1	hypothetical protein FLJ22439	2.1 2.1
	4148	57 AW402	89 Hs.920	1 1	nodulator recognition factor I chromosome 21 open reading frame 62	2.1
55	43570 42800			1137	hynothetical protein	2.1
	4478)4 Hs.164	1285	ESTs, Weakly similar to AFG1_YEAST AFG1	21 21
	4190				hemopoletic cell kinase forkhead box G1B	2.1
60	4310 4210				tumor necrosis factor, alpha-induced pro	2.1
00	4164	35 Al4313	01 Hs.17	9703	KIAA0129 gene product	2.1 2.1
	4370			2531	ESTs, Weakly similar to SS9501 interfero gb;yd40e03.r1 Soares fetal liver spleen	21
	4593 4022					2.1 2.1
6:	5 412	280 AW20			hypothetical protein DKFZp434E1723	2.1
	4266 438			874 34987	pregnancy-associated plasma protein A ESTs	2.1
	436 426				gb:EST374787 MAGE resequences, MAGG Homo	21 21
7	404	561		050	bromodomain adjacent to zinc finger doma	2.1
7		932 AA45 175 W290		9066 9066	hypothetical protein DKFZp667O2416	21
		867 AA33	1886		ob:EST35757 Embryo, 8 week I Homo sapien	2.1 2.1
	458	604 W379		007 88969	Sarcolemmal-associated protein HSCARG protein	2.1
7		1650 T084 1729	na.c		,	21
•	433	3675 AW9		5319	ribonucleotide reductase M2 polypeptide	21 21
		8741 W376 7037 BE08		84492 80976	ESTs antigen identified by monoclonal antibod	21
	41	7037 BE08 5079 R431	79 Hs.2	22895	hypothetical protein FLJ23548	2.1 2.1
8	80 43	9262 AA83	2333 Hs.:	333045	ESTs	2.1
		3108 6718 AW0	15227 Hs.:	289053	hypothetical protein FLJ14733	2.1
				187660	putative RabS GDP/GTP exchange factor ho	2.1

				. may 15 th Ohiomeseans 7 Eated Davis aDNA	2.1
	409745	AA077391 BE620712	Hs.33026	gb:7B14E12 Chromosome 7 Fetal Brein cDNA hypothetical protein PP2447	2.1
	453485 418177	N44967	Hs.5663	ESTs	21
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	21 21
5	454434	AAD83558	Hs.261286	ESTs	21
	406085 424441	X14850	Hs.147097	H2A histone family, member X	21
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	2.1 2.1
	424576	BE154142 AL045228	Hs.96833 Hs.130831	ESTs Homo sapiens mRNA; cDNA DKFZp434L137 (fr	2.1
10	423660 403509	AF231919	Hs.18759	KIAA0539 gene product	21
	441940	AW298115	Hs.128152	ESTs	21 21
	439190	AW978693	Hs.293811 Hs.111471	ESTs ESTs	2.1
15	417791 423701	AW965339 AA329856	Hs.143022	ESTs	2.1
13	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.1 2.1
	459642	/BE243103 - N631024	Hs.24948	gb:TCAAP2E0949 Pediatric acute myalogeno synuclein, alpha interacting protein (sy	2.1
	450385 425159	NM_004341	Hs.154868	carbamovi-phosphate synthetase 2, aspart	2.1
20	425591	, AW294734	Hs.279727	Home satiens cDNA FLJ14035 fts, clone HE	2.1 2.1
	445101	T75202	Hs.12314 Hs.21400	Homo sapiens mRNA; cDNA DKFZp586C1019 (I ESTs	2.1
	412811 426369	H06382 AF134157	Hs.169487	Kreisler (mouse) mai-related leucine zip	21
	435924	AW029203	Hs.191952	ESTS	21 21
25	418388	R72332	Hs.29258 Hs.28514	Homo sapiens cDNA FLJ11364 fis, clone HE testes development-related NYD-SP21	2.1
	452235 452313	AL039743 Y00486	Hs.28914	edenine phosphoribosyltransferase	2.1
	450704	H85157	Hs.40696	ESTS	2.1 2.1
20	427539	AA405205	Hs.97960	ESTs, Wealthy similar to T51145 ring-box	2.1
30	402028 405362				2.1
	414718	' H95348	Hs.107987	ESTS	2.1 2.1
	433424	R68252 AJ200759	Hs.163566 Hs.44737	ESTs ESTs	2.0
35	444875 449523			chemokine (C-C motif) receptor 5	2.0 2.0
55	456072	H54381		gb:yq89a03.s1 Soares tetal liver spleen	2.0
	436331		Hs.12018 Hs.21192	ESTs Homo sapiens clone 25155 mRNA sequence	2.0
	448418 447250		Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0 2.0
40	448192	R43915	Hs.4958	ESTs phospholnositol 3-phosphate-binding prot	2.0
	448966			T-cell immune regulator 1	2.0
	40860: 410790		_	gb:IL2-UM0079-090300-050-A08 UM0079 Homo	2.0 2.0
	43687	2 X15624	9744	gb:Human H1 RNA S Homo sepiens mRNA; cDNA DKFZp434K1815 (f	20
45	43223		Hs.2741: Hs.9094	ESTs	2.0
	43658	8 AA75923	3 Hs.1265	6 ESTS	2.0 2.0
	45248			Homo sepiens cDNA FLJ13329 fis, clone OV Homo sepiens cDNA: FLJ23449 fis, clone H	2.0
50	43042 () 43203			73 Interleukin 20	2.0
٠,	41446	0 L00727	Hs.898	dystrophia myotonica-protein kinase	2.0 2.0
	43350				2.0
	42790 44310			07 ESTs	2.0 2.0
5	5 4345	04 AIB8734	1 Hs.121		2.0
	4543				2.0
	4435 4497			iO cyclin B1	2.0 2.0
_	4526	82 AA4561			2.0
0	O 4123 4293				2.0
	4358			19 Jun dimerization protein p21SNFT	2.0 2.0
	4007	774 R58624			2.0
4	4535 55 4193				20
•	440	529 T26460	Hs.22	50 ESTs	2.0 2.0
	443	206 AB0114			2.0
		360 AA448 660 Al6588		IS13 EST6	2.0
•		030 Al3655		100 Homo saptens mRNA for FLJ00016 protein.	2.0 2.0
	411	048 AK001		hypothetical protein DKFZp434G0522 gb:Homo sapiens clone csneg8-1 immunoglo	2.0
		5624 AF052 5666 T9996			2.0
	440	5143 BE245	342 Hs.30	6079 sec61 homolog	2.0 2.0
,	75 431	7698 R6183	7 Hs.79		2.0
		6607 AA387 9246 AW41			2.0
		2564 AI148	006 Hs.2	2120 ESTs	2.0 2.0
	. 43	2682 AI376		9588 ESTs 12193 mutS (E. coli) homolog 5	2.0
		2140 BE29 8215 BE61		3812 syntaxin 10	2.0
		7129 AI381	1800 Hs.3	00684 calcitonin gene-related peptide-receptor	2.0 2.0
		2772 AW5	03680 Hs.5		
				186	

	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA 2.0
	411380	AW841619		gb:RC1-CN0017-120200-012-609 CN0017 Homo
	430603	AA148164	Hs.247280	HHV ASSACISIED VECUX
_	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge 2.0
5	401125	AW411491	Hs.2186	eukaryotic translation elongation factor
	412939 448740	BE250632	Hs.8026	eaction 2
	454390	AB020713	Hs.56966	KIAA0906 protein 2.0
	415012	NM_004383	Hs.77793	C-SCC (VIOSITIE) KATASC
10	410407	X66839	Hs.63287	carbonic anhydrase IX 2.0
	403478		Hs.97871	Homo sapiens, clone IMAGE:3845253, mRNA, 2.0
	456485	A1393037 A1538226	Hs.32976	munica auricatida hintina protein 4
	430294 411669	8E612676	Hs.303116	stromal cell-derived factor 2-like 1 2.0
15	451944	AW445218	Hs.210876	
1.7	436395	AJ227900		go:nomo sapiens paras miros, to ecc. 100
	456457	AA252905	Hs.194477	E3 ubiquilin ligase SMURF2 2.0 KIAA0130 gene product 2.0
	449123	D50920	Hs.23106 Hs.333388	Harm enriche chore IMAGE:3957135, MRNA,
20	409214 437619	AW405967 AW351491	Hs.334853	hundhelical centain Ft 123544
20	453348	BE272318	Hs.8595	hypothetical protein FLJ12438 2.0
	424382	AA351898	Hs.23539	PSIE
	447079	AA280057	Hs.105280	ES1s, Weakly samuar to discourse in the same and
25	449501	AI652924	Hs.231942 Hs.121555	: music IF
25	422893	X98411 Y17114	Hs.73393	aves sheart (Dimenshila) homolog 4
	412125 434845	BE267057	Hs.32532	t hypothetical protein R32184 1
	410422	AL042014	Hs.33469	B Homo sapiens, clone MGC 15203, mr.NA, com
	430255	AK000703	Hs.32382	2 Homo saprens micros for the contract of the
30	451656	BE327088	Hs.21275	2 ESIS 20
	442068	BE312873 AW197626	Hs.31493 Hs.27190	1 FSTs. Moderately similar to S08686 finge
	446846 442690		Hs.16004	7 ESTe Weekly similar to 928095 line-1 of 4.0
	454277			E FSTe Waskly similar to 2157_HUMAN ZINC
35	426910		Hs.19008	99 ESTs, Moderately similar to ALU1_HUMAN A 2.0 2.0
-	402798			2.0
	404554			
	TABLÉ	QR-		
40	Pkey:	U.	Inique Eos pro	beset Identifier number
	CAT m		Sene cluster ni	
	Access	sion: (Genbank acces	sion numbers
		CATAL	ber Accessi	00
45	Pkey 40790	CAT Nutr 9 1025254	1 AW103	on 386 BE156395 BE156391 BE156190 BE156184 BE156388 BE156394
40	40843		1 AW195	262 R27868 AWB11262
	40919		1 AA1314	83 AA065156 AA076448 891 A1347618 A1361453 A1088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
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6 0	41044			134 BE063456 AW748795 BE150839 357 AW803423 AW812233 R06814
50	41079			039 AW834040 AW834047 AW845410 BE003128 AW852479
	41125 41135			
	4116			
_	4116	58 1252987		1829 AW854805 AW854841 AW854825 AW654622 AW654655 AW855610 AW855601 AW855605 5598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605
55	4118			5749 BE179419 BE179492 2042 N77591
	4122			6614 AW946622 AW946663 AW946667 AW946615 AW946619
	4123 4123			7046 AMMATERO AMBATERT AWA7713
	4132		3 1 BE07	5035 BE074999 BE075006 BE075005 BE075034 BE073006 BEV73037
60	4136		5.1 RS170	87 BE152515 Z44834 H23397
•	4144			7904 BE294312
	414			9808 98 F06295 R13085
	415			10 F07928 R53367
65	415	586 15401		81 F12393 174437
٠.		635 15408	53_1 F131	68 R21289 T77628
		871 16267	61_1 H987	16 N90792 N24283 34714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
		913 16300	1_1 AW9	34714 BE 161007 BE 162500 AW 145902 AW 145004 BE 16440 BE
7	417	980 17129	54_1 K32	235 R32247 R32219 113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353 AW088477
70	<i>)</i> 418	333 173_2	A188	113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE033126 AW932118 BE40317404 AA831618 A1124782 AA889402 7846 AW502624 W81697 W81695 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 A1124782 AA889402
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AW975977 AA729469 AA747132
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AW809752 AW810271 AW809944 AW810319 AW810215 AW810368 AW810167
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                         TABLE 9C:
                                                       Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunharn, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunharn, et al. (1999) Nature 402:489-495.
                         Pkey:
                         Ref:
                                                        Indicates DNA strand from which exxins were predicted. Indicates nucleotide positions of predicted exons.
        60
                          Strand:
                          Nt_position:
                                                                                        Nt position
                                                                                        185223-188402,186878-187275
91888-92018,98131-98294,99474-99570
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400859
                                            7465000
                                                                   Plus
                                                                   Minus
Minus
                                            9757499
         65
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140390-140822
                                            7283186
8096828
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                           400992
                                                                                         736-1137
                                            7230838
7232177
                                                                    Minus
                           401012
                                                                                         736-1137
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401384
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Plus
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		9798099	Minus	95342-195511
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		9931216	Plus	20393-20767 12138-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-
5	-TOEOZ.			26895,29279-29469
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	402798	3355547	Plus	23596-23867
	402856	9801288	Minus	90119-90411
	403048	4210991	Plus	44275-44592,49656-49955
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	403142	9444521	Plus	89286-90131 67762-67940,68695-68856,70394-70507
	403166	9838127	Minus	
	403478	9958258	Plus Minus	116458-116564 157184-157415
1.5	403680	7331517	Minus	158794-160929
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	403/97	7708910	Minus	2574-3408
	403881	7710245	Minus	107250-107685,108924-109213
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	404054	3548785	Ptus	66713-69175
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	404170	9930793	Plus	168836-169248
	404185	4572584	Minus	129171-129327 116132-116407,116653-116922
	404240	5002624	Minus Minus	75747-75947
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	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69039-70100
	404584	9857511	Plus	138651-139163
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	404756	7706327	Plus	82849-83627
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	404984	6939882	Plus	87221-87505 79659-79804
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	405747		Minus	153933-154060
	40577		Plus	91191-91254,91510-91589 109758-111166
<i>E E</i>	40580		Plus Plus	62383-62583
55	40588		Minus	43717-43859
	40591 40602		Minus	177469-177829
	40602		Plus	18665-18843
	40616			12620-14251
60	40626			2570-2731
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	40634		Plus	90900-91091
	40647	74 9795567	Plus	52758-53211
	40657	77 7711730		11377-11509
65	4066	10 8312226	i Plus	13096-13334

TABLE 10A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 10A fists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS fissues. These were selected from 59580 probesets on the
Altymetriz/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" agreater than or equal to 3. The "average" normal CNS issues. These were selected from 59580 probesets on the
75th percentile amongst various normal CNS issues. The "average" globlastomal sevel was set to the 85th percentile amongst various tumor samples. In order to remove
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific background levets of non-specific hybridization, the 10th percentile values amongst various non-malignant tissues was subtracted from both the numerator and the
gene-specific 70

75

80	Pkey	ExAcon	UnigenelO	Unigene Title	R1
	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	136.7
	417275	X63578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7

			Hs.65248	منممه	cytoplasmic, intermediate polype	22.6
	410657 419954	AF063228 D14720	Hs.93883	envolin	notein zero (Charcol-Maño-1000)	21.2 18.5
	459247	N46243	Hs.110373	CCT-	Minhly similar to 14252b Secreted	15.5
_	416133	NM_001683	Hs.89512	ATPas	e, Ce⊷ transporting, plasma membra tein convertase subtilisin/kexin t	15.2
5	415018	AW138239 AW206437	Hs.78977 Hs.4290	ESTA		14.8
	417167 433940	H06129	Hs.7459	cyclic	AMP-regulated phosphoprotein, 21	13.4 13.1
	413324	V00571	Hs.75294	andin.	snoria missalm anoman	12.6
••	439830	AA846666	Hs.151489	ESTS ESTS	Weatly similar to XE7_HUMAN PROTEI	12.6
10	408068 412636	AW148652 NM_004415	Hs.167398 Hs.74316		optakin (OPI, OPII)	. 12.5
	412030	AB011106	Hs.196012		0534 protein	12.2 12.2
	412638	AA910199	Hs.203838	EST	SALL ALL STATE OF DAIRING CONT DES	12.1
	423690	AA329648	Hs.23804	ESIS	, Wealdy similar to PN0099 son3 prot diacytglycerol synthase (phosphatida	11.9
15	456844 418318	A1264155 U47732	Hs.152981 Hs.84072	trans	membrane 4 superfamily member 3	10.9
	442593	R39804	Hs.31961	EST		10.8 10.4
	446353	AI290919	Hs.153661			10.3
20	420290	AW977318	Hs.194480	EST	8 01118231F1 NIH_MGC_17 Homo sapiens c	10.3
20	414220	BE298094 AI568801	Hs.71721	EST		10.2
	414290 426365	AA376667	Hs.10283		binding motif protein BB	10.0 10.0
	414937	R38698	Hs.12382	ES1	S	9.5
	419643	F06066	Hs.91791	chr	mosome 11 open reading frame 25 c10d08.s1 Stratagene tung (937210) H	9.5
25	407173	T64349 R55745	Hs.16733			9.5
	412454 439366	AF100143	Hs.6540	fibr	oblast growth factor 13	9.4 9.3
	415315	F12240	Hs.25065		thymosin, alpha (gene sequence 28)	9.2
	441790	AW294909	Hs.13220			9.1
30	448117	H49129	Hs.17298			9.0
	400661 433558	AA833757	Hs.20170	9 ES	Ts. Weakly similar to T24435 hypotheti	9.0 9.0
	412453		Hs.1673	30 ES	Ts .	8.9
	408920	AL120071			ronectin leucine rich transmembrane p	8.7
35	409031			70 PI	Ts O010 protein	8.3
	428106 446544			E	STs, Wealdy similar to Unknown (H.sapis	8.2 8.2
	423479		26 Hs.1292	08 de	ath-associated protein kinase 2	8.2
	439480		Hs.1253		STs, Weakly similar to \$33990 finger or tent transforming growth factor beta b	8.0
40	41803		Hs.8333 Hs.9720	13 61	nati inducible cytokine subfamily A (Cy	8.0
	45649 41020	·		11E C	ternanti disease 3 (autosomai dominanti)	8.0 8.0
	41460		38 Hs.765	50 H	omo sapiens mRNA; cDNA DKFZp564B1264 (f	7.9
	40842				naJ (Hsp40) homolog, subfamily B, membe STs	7.9
45	43707			22 C	ypothetical protein FLJ22344	7.9
	40843 43815				ansforming growth factor, beta recepto	7.9 7.8
	44020	9 H05049	Hs.222		eurexin 3	7.8
	4081				STs, Weakly similar to T00331 hypotheti nuclear receptor subfamily 4, group A, m	7.8
50	41741 4105			112	-homosome 9 open reading frame 5	7.8
	4296			1388	Homo sapiens BAC clone CTB-50N22 from 7q	7.7 7.7
	4058	00			hypothetical protein FLJ20761	7.7
55	4217			/8/4 682	hypothetical protein FKSG32	7.7
55	4263 4234				contactin 1	7.7 7.6
	4451		10 Hs.14	6304	ESTs	7.6 7.6
	4162	294 D8698			KIAA0227 protein contactin 1	7.6
60	4240				ESTs	7.5
O(J 4374 4054		, ,,,,,,			7.5 7.4
	421	224 AW40		25812	ESTs	7.4
	442			1810	CDA11 protein gb:IL5-HT0731-110500-087-c08 HT0731 Homo	7.2
6:	5 459	476 BE185 673 AA744		36345	ESTs	7.1
U.		673 AA744 836	1550	500 10		7.1 7.1
		958 AB020		2653	KIAA0844 protein	7.1
	430	152 AB00		34642	aquaporin 3 ESTs	7.1
7		9474 AW98	15019 HS.1	55849		7.1
,		1780 6052 AA35	8760		gb:EST67699 Fetal lung II Homo sapiens c	7.0 7.0
		3605 AF04	7826 Hs.1	29887	cadherin 19, type 2	7.0
	43	3098 AW19		151143	ESTs guanine nucleotide binding protein (G pr	6.9
-		9511 AI436		296261 227583	Homo sapiens chromosome X map Xp11.23 L-	6.8
′				184216	DKFZP564C152 protein	6.8
		9273 BE27	1180 Hs.	293490	ESTs, Weathy similar to 138022 hypotheti	6.8 6.8
	44	3155 R54		23772	ESTs ESTs	6.8
		50561 R490		25909 .288215		6.8
•				128204	ESTs	6.8 6.7
		48426 BEO	18315 Hs	280776	tankyrase, TRF1-interacting ankyrin-rela	6.6
	4	23589 AA3	28082 Hs	.209569	ESTs	

	*1000	N379882 +		STs b:HSC3HH101 normalized infant brain cDN	6.5 6.4
			Hs.181353 U	IDP-Gal:betaGlcNAc beta 1,3-galactusyfir	6.4
				STs	6.4
5	450642			opine IV	6.4 6.4
				olycythemia rubra vera 1; cell surface QAA0231 protein	6.4
				ESTs	6.4
	447482			QAA1233 protein	6.4
0	400332	S66407	Hs.248032 F	FLT4	6.3
_	440703			Homo sepiens mRNA; cDNA DKFZp434G227 (fr	6.3 6.3
	448129			ESTs	6.3
	454076			ESTs gb:EST69040 Fetal lung II Homo sapiens c	6.3
5	425526 421913	AA359933 AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
,	434273	AA913143	Hs.26303	ESTs	6.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2 6.2
	451301	AI769514		EST	6.2
	430754	AW862610		ESTs ESTs	6.2
20	438356	AA805530 BE304678	Hs.48527 Hs.119598	ribosomal protein L3	6.2
	422743 453355	AW295374	Hs.31412	Homo sapiens cDNA FLI11422 fis, clone HE	6.2
	425388	AW081394	Hs.97103	ESTs	6.2
	452502	AI904296	-	gb:PM-BT046-220199-285_1 BT046 Homo sapi	6.1
25	402548			507-	6.1 6.1
	457534	AI761307	Hs.232226	ESTs Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	408165	AL137573	Hs.43143	FIGURE SUPPLIES HAVEN LANGE CHOOSE TWO IS	6.1
	404958 432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs	6.1
	422262	AL022315	Hs.113987	lectin, galactoside-blnding, soluble, 2	6.0 6.0
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588	Un 227571	gb:601311808F1 NIH_MGC_44 Homo sepiens c regulator of G-protein signaffing 4	5.9
35	430004 401521	U27768	Hs.227571	Indiana a character of transfer	5.9
"	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.
	417761	R13727	Hs.21435	ESTs	5. 5.
40	424806	AA382523	Hs.105689	MSTP031 protein	5. 5.
40	441695	T12411	Hs.183745 Hs.272558	hypothetical protein FLJ13456 endomucin-1	5
	457483 417175	AB034694 R44558	Hs.94002	ESTs	5
	437483	AL390174	10.54002	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5
	436427	AI344378	Hs.143399	ESTs	5
45	411939	AJ365585	Hs.146246	ESTs	5 5
	459053	A1807052	Hs.210361	EST8 gb:MR1-ST0206-130400-023-d06 ST0206 Hamo	5
	411052	AW814950 Z98949	Hs.326843		5
	431063 450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5
50	408478	NM_000806		gamma-aminobutyric acid (GABA) A recepto	5
	442676	A1733585	Hs.130897		
	446443	AV659082	Hs.134228	ESTs .	į
	400865	**********	Hs.290855	ESTs	
55	459080 407952	AW192083 AI215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	
رر	431984		Hs.272284	Human DNA sequence from clone GS1-256022	
	425705		Hs.159265	5 kruppel-related zinc finger protein hcK	
	442238				;
20	422994				
60	457148		Hs.184627 Hs.10338		
	428356 415927		Hs.78919		
	402092				
	440526	AI832243	Hs.21147		
65	444409		Hs.49265		
	41787		Hs.86320 Hs.33354		
	45823 43070		Hs.25065		
	45618		Hs.44940		
70	42742	4 AA402453	Hs.11301	11 ESTs	
•	43735	4 AA749215		88 ESTs	
	45561			gb:CM1-BT0614-160300-149-f02 BT0614 Homo 60 neurofilament, heavy potypeptide (200kD)	
	42929 42786				
75	40855		Hs.4636		
, ,	44420			94 ESTs	
	42283	31 R02504	Hs.3329		
	40318			The sale, and binding pentage & adjacenda	
0.0	4180				
80) _. 4303: 4315:		Hs.2396 Hs.2729		
	4319				
	4374				
				191	

	438285	AA782845	Hs.22790	ESTs		5.2 5.2
	439901	N73885	Hs.124169	ESTs		5.2
	438507	AA809052	Hs.211275 Hs.197621	ESTs ESTs		5.2
5	449222	AW293984 AK001507	Hs.306084	Homo sa	piens clone FLB6914 PRO1821 mRNA,	5.2 5.2
)	402834 419042	T81429	Hs.221065	ESTs		5.2
	438777	AA731199	Hs.293130	ESTS		5.1
	445071	A1280245	Hs.149504 Hs.256096	ESTs ESTs		5.1
10	408016	AW136827 AA934589	Hs.49696	CCT.		5.1 5.1
10	412047 436953	AW959074	Hs.23648	Homo s	apiens cDNA FLJ13097 fis. clone NT	5.1
	436773	AW078629	Hs.82110		d SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319 Hs.20953	ESTs ESTs		5.1
1.5	453830	AA534295 AA022888	Hs. 176065	ESTS		5.1 5.1
15	459580 417616	R07728	Hs.268668	ESTs		5.1
	423457	F08208	Hs.283844	similar	to rat tricerboxylate carrier-li validylinositol binding clathrin as	5.0
	441535	AL135735	Hs.7885 Hs.79348	encord of	or of Guaratein signalistig /	5.0 5.0
30	416490	AF090116 N62889	Hs.107242	. Hama	socions cDNA FLJ12965 fis, clone N1	5.0 / 5.0
20	417284 447135	T58148	140.00	ah-shC	Manne et Stratagene lung (93/210) m	5.0
	448605	AL109678	Hs.21597		sapiens mRNA full length insert cDN	4.9
	442240	A1791883	Hs.292719 Hs.15399	EST8	ne kinase, mitochondrial 1 (ubiqui	4.9
26	459399	BE407712 AA864870	Hs.18130		ve gene product	4.9 4.9
25	427972 432944		Hs.38512	FOT-	•	4.9
	440198			gb:60	1345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	A1097452	Hs.13509 Hs.28904	4 14	n envious cDNA FLJ12048 ffs, clone ME	4.9
20	416040		Hs.14487	1 Home	o sapiens cDNA FLJ13752 ffs, clone PL	4.8 4.8
30	444922 436670		Hs.2015	S EST		4.8
	448072		Hs.2490			4.8
	40893	6 AL138043				4.8
25	41262		8 Hs.1719 Hs.1241	02 EST	·	4.8 4.8
35	41494 42925		Hs.9184	6 hype	othetical protein DKFZp761C121	4.8
	45356	7 AI742835		8 hypo	othetical protein FLJ11175 no sapiens mRNA; cDNA DKFZp564O1262 (f	4.6
	40790				no sepiens cONA FLI14446 fis, clone HE	4.7
40	44102) ms.1734			4.7 4.7
40	40513 45527		89	gb:	QV3-BN0046-150400-151-g09 BN0046 Homo	4.7
	4462	18 AV6571	59		AV657159 GLC Homo sapiens cDNA clone lanoma-derived laucine zipper, extra-n	4.7
	4433		3 Hs.133	244 me	SUOUS-08:1460 (Specific Subject and a	4.7
45	4021		07 Hs.793	81 cra	ancalcin	4.7 4.7
45	4165 4382			543 Ho	rno sapiens cONA FLJ10919 hs, clone OV	4.7
	4204	80 AL1373	61 Hs.981		pothetical protein	4.6
	4008	00 Y10262			es absent (Drosophila) homolog 3 STs	4.6
E (*	435		150 HS.27			4.6 4.6
50) 404 ¹ 430		1 Hs.24		protein-coupled receptor 22	4.6
		571 AW020)775 Hs.56		STs	4.6
	445	924 AJ2646			STs	4.6
-	- 444	585 AW170		4336 L	Lumber ONA companies from clone RP1-238U15	4.6 4.6
5:	O 421	044 AF061 274 AI458		28677 P	tuman DNA sequence from clone RP1-50024	4.6
		475 W563	39 Hs.10		ESTs Homo sepiens cDNA FLJ14115 fis, clone MA	4.5
		4311 BE54			ESTs	4.5
		4272 A1651 5235 A1564		20207	EQT#	4.5 4.5
0		5235 A1564 4327 BE40			ESTs, Weakly similar to T24435 hypotheti	4.5
		4630 BE41	0857		gb:601301177F1 NIH_MGC_21 Homo sapiens c gb:yu56e10.r1 Soares fetal liver spleen	4.5
		4456 H743	14			4.5
_	. 40)1024 14699 AI811	ccoa Nei	76930	synuclein, alpha (non A4 component of am	4.5 4,5
C				33067	ESTs	4.5
		05138			gb:PM2-HT0225-031299-003-f11 HT0225 Homo	4.5
	4	13544 BE1	47225	00463	CCTo Weakly similar to 138022 hypother	4.5
	70 4			28462 .112482	Homo sepiens unknown mRNA sequence	4.4
				150269	ESTs	4.4 4.4
		29876 ABC	28977 Hs	,225974	KIAA 1054 protein	4.4
	4	145481 AW		.148836	ESTs ISL1 transcription factor, LIM/homeodoma	4.4
	75		_002202 Hs	.505	IOPI Statesham	4.4
		404769 444331 AW	/193342 H	.24144	ESTs	4.4 4.4
		429726 AW	/628326 Hs	3.27151	ESTs .	4.4
		449093 AB	*****	s.22998	neuresin 1 hypothetical protein FLJ20623	4.4
	٥٥			s.27337 s.179662	austosomo occombiy omigin 1-lixa 1	4.4
	80		19294 H 13053	J. , . JOUE	ob:vh31a05.r1 Soares placenta Nozitir fromo	4.4 4.4
		419656 AE	3002314 H	s.92025	KIAA0318 gene product	4.4
		425864 U	56420 H	ls.159903	offactory receptor, tarrily 5, substantily	
					107	

192

	435078	AW518888	Hs.40937	7 ESTs		4.4
	413493	BE144444		nh-MR	0-HT0168-141199-002-09 HT0168 Homo	4.3 4.3
	432712	AB016247 R25754	Hs.28803 Hs.3011		C5-desaturase (fungal ERG3, delta	4.3
5	459650 404828	P23/34	113.3011			4.3 4.3
•	423782	AI472209	Hs.3231			4.3
	426867 426802	AA460967 AA385182	Hs.2266 Hs.4669	n ECT.		4.3 4.3
	457353	X65633	Hs.2481		iocortin 2 receptor (adrenocorticotr 23-HT0622-130400-012-a07 HT0622 Homo	4.3
10	412112	BE180342	Hs.3061	100 001	IE avalaia	4.3
	401522 419055	N47812 A1365384	Hs.115	71 Home	o sapiens cDNA FLJ11570 fis. clone HE	4.3 4.3
	410171	H07892	Hs.124	31 FSTs		4.3
1.5	419564	U08989	Hs.911 Hs.325	02E H	e carrier family 1 (neuronal/epithe o sapiens cDNA FLI20848 fts, clone AD	4.3
15	458789 455040	AL157468 AW852286		ah-O	MALCT0225-100400-187-008 CTUZZO NORIO	4.3 4.3
	438533	A1440266	Hs.170	673 EST	s. Weakly similar to T24832 hypotheti s. Weakly similar to ALU1 HUMAN ALU S	4.2
	459005	AA447679 U76421	Hs.144 Hs.853		using desminsed RNA-SDBCIDC, D1 [II	4.2
20	418489 433389	AF038171	14.00	ab:t-	lomo sapiens clone 23671 mRNA sequenc	4.2 4.2
20	454356	AW390363		522 hype	othetical protein from Xq28 s. Wealdy similar to 1901303A Leu zip	4.2
	442339	BE299668 AA285362		(DYI ESI Ab:A	1TH277 HTCDL1 Homo sapiens cDNA 5/3	4.2
	421249 443998	AI620661	Hs.29	6276 ES1	rs e e e e e e e e e e e e e e e e e e e	4.2 4.2
25	452197	AW02359				4.2
	451117 404 50 1	AAD15752 AW24725		E44 ~~	tanoida nhosohondasa	4.2 4.2
	410378		Hs.41	1693 Dn	aJ (Hsp40) homolog, subfamily B, membe	4.2
20	422528	AB01118		18087 KU 27992 ES	A0610 protein	4.1
30	440323 425767			27992 E3 59483 Chi	romosome 1 open reading frame 7	4.1 4.1
	434460		8 Hs.3	852 K)	AAO368 protein	4.1
	410362			40070 EG	oprotein convertase subfilisin/kexin t	4.1
35	413121 409401			634 H	omo sapiens cDNA: FLJ22547 fis. clone H	4.1 4.1
22	45023	5 AA00751	2 Hs.1		STs. Weakly similar to B34087 hypotheti	4.1
	44975			10977 E	515, Wealthy String to Both 1970 Homo sapien	4,1
	42181 40849			136182 E	STs	4.1 4.1
40	43026	1 AA3051			ypothetical protein HT023 JAA1622 protein	4.1
	43410 45183			40070 E	OTA .	4.1 4.1
	41177		01	9	b:QV4-HT0538-040500-193-f05 HT0536 Homo	4.1
4.5	4376			153026 8	SWAP-70 protein pb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0
45	4302 4002		153	,	mirror services and Transfer an	4.0 4.0
	4298			.225841 1	DKFZP434D193 protein	4.0
	4531				aspartoacylase (aminoacylase 2, Canavan ESTs	4.0
50	4180 4053		3 113		2010	4.0 4.0
50	4279	31 AW20			ESTS	4.0
	4287			s,143691 s,59821	ESTs ESTs	4.0
	4494 4531			5.21068	hundhalical periols	4.0 4.0
55	456	407 AW96		- 0004	gb:EST380690 MAGE resequences, MAGJ Homo huntingfin-associated protein interactin	4.0
		869 NM_0 784 T6515		s.8004 s.102399	ESTs, Moderately similar to S65657 appna	4.0 4.0
		195 AA35	2026 H	s.94319	VPS10 domain receptor protein	4.0
-	429	628 H096 1087 F120		ls.13268 ls.332579	ESTs ESTs	4.0
6		1087 F120 1840 AW5	02122	13.332373	gb:UI-HF-BROp-afr-c-08-0-UI-1 NIH_MGC_5	4.0 4.0
		2854 AA43	17061 t	ts.14060	proxineticin 1 precursor ESTs, Weakly similar to A45010 X-linked	4.0
				ts.190173 ts.97872	EĈTo	4.0
6	5 41	4990 C177	758	Hs.221652	Homo sapiens cDNA FLJ14323 fis, clone PL	3.9 3.9
•	41	2678 AA1	15575	Hs.114914	ESTs	3.9
		5629 0200 A105	6871	Hs.15276	ESTs	3.9
	45	10299 A105 13098 Z25		Hs.86379	FSTe	3.9 3.9
7	70 43	15752 AF2	30801	Hs.303172	gb:Homo sapiens growth hormone receptor Homo sapiens mRNA; cDNA DKFZp547G133 (f	3.9
		11005 Z41 14516 AI3	305 07802	Hs.135560	ESTs. Weakly similar to T43458 hypotheti	3.9 3.9
		12257 AW	503831	Hs.323370	Human EST clone 25267 mariner transposon	3.9
	4:	22563 BE	299342	Hs.19348 Hs.123017	hypothetical protein FLJ13119 Human unproductively rearranged ig mu-ch	3.9
		43850 AV	1388 1014723	Hs.334612	ESTs	3.9 3.9
	4	12677 AW	/029608	Hs.17384	ESTS CONTRACTOR OF GTERM	
			117352	Hs.120828		3.9
;		105377 114376 BE	393856	Hs.66915	ESTs, Wealty similar to 16.7Kd protein (3.9 3.9
	4	153341 Al	758912	Hs.29634 Hs.30192		3.9
			V241821 10164	Hs.80298		3.9
						_

		400117	Un 1257/2	FCT.	3.9
	427264 422746			ESTs glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acut	3.9
	414666	NM_004466		glypican 5	3.8
5	418217	A1910647	Hs.13442	ESTs	3.8 3.8
	419118		Hs.139204	ESTs	3.8
	445017 405867	A1205493	Hs.176860	ESTs	3.8
	422750	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
10	453863	X02544	Hs.572	orosomucoid 1	3.8
	457821	H47166	Hs.124322	ESTs, Weakly similar to A47582 B-cell gr	3.8 3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600 456083	AL047034 U46922	Hs.119747 Hs.77252	ESTs fragile histidine triad gene	3.8
15	413341	H78472	Hs.191325	ESTs. Wealdy similar to T18967 hypotheti	3.8
	449057	AB037784	Hs.22941	KIAA1363 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8 3.8
	414764	AW013887	Hs.72047	ESTs	3.7
20	404391 433629	R13140	Hs.13359	ESTs	3.7
20	424738	Al963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7 3.7
25	440530	AA888546	Hs.174187	ESTS ESTS	3.7
25	433930 409662	AA620338 AW452320	Hs.273781 Hs.279726	ESTs	3.7
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	A1248205	Hs.153244	EŠTs	3.7
20	408593	R19566	Hs.197617	ESTs	3.7 3.7
30	417091	AA193283	Hs.291990	ESTs ESTs	3.7
	4485 56 423135	AW885606 N67655	Hs.5064 Hs.26411	ESTS	3.7
	400135	1107000	1.0.20411		3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Hamo	3.7
35	457221	AW383197	Hs.218260	ESTs	3.7 3.7
	451660	AIB07927 BE247275	Hs.249601 Hs.151787	ESTs U5 snRNP-specific protein, 116 kD	3.7
	401600 446818	Al342668	Hs.279765		3.7
	447795	AW295151	Hs.163612		3.7
40	427562	R56424	Hs.26534	ESTs	3.6 3.6
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622 gb:QV4-HT0316-091199-028-405 HT0316 Homo	3.6
	454339 439274	AW381980 AF086092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880		3.6
45	422897	AA679784	Hs.4290	ESTs	3.6
	429656	X05608	Hs.211584		3.6 3.6
	421908		Hs.285814 Hs.41717		3.6
	407978 426452		Hs.121647		3.6
50	400685				3.6
	417154	A1674701	Hs.21388		3.6 3.6
	447178		Hs. 16089		3.6
	423893 449231		Hs.13484 Hs.29857		3.6
55	411607			gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
	405977	,			3.6 3.6
	441470		Hs.30198		3.6
	423568 441235		6 Hs.12981 Hs.13557		3.6
60	450236			· · · · · · · · · · · · · · · · · · ·	3.6
•	425384			9 Homo sapiens clone 24533 mRNA sequence	3.6
	42677				3.6 3.6
	41483		Hs.77439 5 Hs.11789		3.6
65	416879 400879		нэ.1170.		3.6
••	42515		3 Hs.2704		3.6
	43222	2 Al204995		gb:an03c03.x1 Stratagene schizo brain S1	3.5 3.5
	41504			gb:HSC3JD031 normalized infant brain cDN	3.5
70	40153 44649		Hs.1534	60 ESTs	3.5
, ,	43132			ESTs, Wealdy similar to 2109260A B cell	3.5
	44589	B AF07062	3 Hs.1342	3 Homo sapiens clone 24458 mRNA sequence	3.5
	45590			gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5 3.5
75	41642			6 eukaryotic transtation initiation factor gb:CM0-BT0365-061299-122-g09 BT0365 Homo	3.5
,,	45569 40567		•	Berguit & Lance an inter Ban a Lance . Miles	3.5
	41820	07 C14585	Hs.3477		3.5
	4253	83 D83407	Hs.156		3.5 3.5
80	4170				3.5
OU	J 4083 4177		78 Hs.444 Hs.191		3.5
	4456			297 ESTs	3.5
	4087				3.5

						2.5
	413164	BE068494		gb:Mi	R1-BT0371-050500-009-812 BT0371 Homo 1273249F1 NIH_MGC_20 Homo sapiens c	3.5 3.5
	414593 453220	8E386764 AB033089	Hs.32452	gb:ou Homo	sapiens mRNA for KIAA1263 protein.	3.5
	415621	A1648602	Hs.55468	ESTS		3.5 3.5
5	454437	AI248173	Hs.191460 Hs.149383	hypol EST:	hetical protein MGC12938	3.5
	446066 423374	AI343931 AB037770	Hs.127656	KIAA	1349 protein	3.5
	419347	C15944	Hs.90005	supe	riorcervical ganglia, neural specifi	3.5 3.5
10	418515	NM_006218 W45679	Hs.85701 Hs.169854		phoinositide-3-kinase, catalytic, al thetical protein SP192	3.5
10	451776 432305	M62402	Hs.274313	insul	in-like growth factor binding prote	3.5 3.5
	456995	T89832	Hs.170278	EST	8	3.5 3.5
	403323 425022	M95724	Hs.154207	cent	romere protein C 1	3.5
15	439394	AA149250	Hs.56105	EST	•	3.4 3.4
	433803	AIB23593	Hs.27688	EST	s s, Wezidy similar to KIAA1324 protein	3.4
	450715 411474	A1266484 AW848427	Hs.31570	gb:l	L3-CT0214-150200-075-H10 CT0214 Homo	3.4
	415076	NM_000857	Hs.77890	QUA	oviate cyclase 1, soluble, beta 3	3.4 3.4
20	423826 459495	U20325 BE544158	Hs.1707	coc	eine- and amphetamine-regulated trans 501076707F1 NIH_MGC_12 Home sapiens c	3.4
	427173	BE255017	Hs.97540	ĔS	Ts	3.4 3.4
	408112	AW451982	Hs.248613	ES		3.4
25	446092 416868	N33522 A1656856	Hs.145894 Hs.292597	ES		3.4
23	458234	BE551408	Hs.127196	ES	Ts	3.4 3.4
	419555	AA244416		ďρ	nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens :601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	414314 400425	BE312991 AY004252	Hs.287385	PF	l domain containing 12	3.4 3.4
30	414366	BE549143			:601076456F1 NIH_MGC_12 Homo sapiens c	3.4
	434053 449997	AW445136 AI683052	Hs.134946 Hs.201577		STs AA1829 protein	3.4
	433461	AI636047	Hs.19762) E	STs	3.4 3.4
25	428006	AA41B743	Hs.98306 Hs.15189		IAA1862 protein arcoglycan, delta (35kD dystrophin-asso	3.4
35	424695 443294		Hs.13305		STs	3.4 3.4
	428212	AW444451			STs	3.4
	457673 446390		Hs.27203 Hs.14992	a n	ypothetical protein PRO2822 ypothetical protein FLJ11151	3.3
40	428536		Hs.2288	٧	isinin-like 1	3.3 3.3
	426597		Hs.14560 Hs.30268		:STs rypothetical protein	3.3
	410366 458258				STs	3.3
	40173	3			small inducible cytokine subfamily A (Cy	3.3 3.3
45	40903 42578		Hs.5000 Hs.1595	28 I	Homo sapiens done 24400 mRNA sequence	3.3
	43332		9 Hs.2364	4 (ESTs, Wealdy similar to S65824 reverse t	3.3 3.3
	41454				aldehyde dehydrogenase 1 family, member ESTs	3.3
50	43499 45635			4	homeo bax D3	3.3 3.3
	42652	7 NM_0010	37 Hs.1702	38	sodium channel, voltage-gated, type I, b cell division cycle 25C	3.3
	45426 40030		9 Hs.656 Hs.1915		totate hydrolase (prostate-specific memb	3.3
	43407	77 AF11665	9 Hs.3211	51	Homo sapiens PRO1412 mRNA, complete cds	3.3 3.3
55					ESTs Down syndrome critical region gene 4	3.3
	44920 41793		Hs.170)44	FSTs	3.3 3.3
	4233	10 AA32522			Homo sapiens cDNA FLJ14218 fis, clone NT fatty sold binding protein 1, liver	3.3
60	4366) 4534		Hs.524 7 Hs.617		hypothetical protein FLJ14451	3.3
•	4201	64 AW3390	37 Hs.249	80	ESTs	3.3 3.3
	4478				ESTs proenkephalin	3.3
	4198 4445				ESTA	3.3 3.2
6:					Homo sapiens mRNA; cDNA DKFZp564D1462 (f ESTs	3.2
	4152 4181				ESTs	3.2
	4300	355 NM_00	219 Hs.23		phosphoinositide-3-kinase, catalytic, be	3.2 3.2
70	A210			4415	gb:EST378726 MAGE resequences, MAGI Homo Homo saplens cDNA FLJ10229 fis, clone HE	3.2
/	U 432 408		814 Hs.28	9005	Homo saciens cDNA: FLJ21532 fis, clone C	3.2 3.2
	400	409 AF153			Homo sapiens winged helix/forkhead trans hypothetical protein FLJ10971	3.2 3.2
	446 425				ESTs, Weakly similar to similar to ankyr	3.2
7	5 403	092				3.2 3.2
	452	971 AI8738		789	ESTs gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
		186 BE141 1485	~~·		9	3.2
•	401	1949	w76		gb:EST384766 MAGE resequences, MAGL Homo	3.2 3.2
8		7452 AW97: 4100 Al693:		26043	chromosome 21 open reading frame 51	3.2
	441	8440 AA173	467 Hs.6	2402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2 3.2
	42	1200 AA284	1811 Hs.2	64433	ESTS	3.2

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		000437	Hs.234392	alatalat.	activating factor acetythydrola	3.2
	430142 433197	NM_000437 AB040889	Hs.281022	MAAGA	SS erotoin	3.2 3.2
	443509	AV645470		gb:AV6	45470 GLC Homo sapiens cDNA clone	3.2 3.2
_	440827	A1733110	Hs.128128	ESTs	.4-N-acetylglucosaminyltransferas	3.2
5		NM_016161 AW370362	Hs.278960	~~~	LB10255181099-012-007 B10233 NONO	3.2 3.2
	409257 459235	BE246010	Hs.271468	Homo	sapiens mRNA for FLI00038 protein,	3.2 3.2
	416789	AA223439	Hs.79933	cyclin	sapiens mRNA; cDNA DKFZp761D09121 (3.2
4.0	429809	AL162010	Hs.223603 Hs.6187	CCT.		3.2
10	420156 455577	AW449258 BE006341	15.0107	gb:RC	2-BN0127-240300-011-b05 BN0127 Homo	3.2 3.2
	400617	AF151064	Hs.36069	المصية	untioni profein	3.2
	437129	AL049327	Hs.302057		sapiens mRNA; cDNA OKFZp564E016 (fr	3.2
	451820	AW058357	Hs.337353 Hs.278672	ESTs	srane component, chromosome 11, surfa	3.2
15	457535 419956	AA609685 AL137939	Hs.40096	FSTs.		3.1 3.1
	456235	AA203637			58b12.r1 Soares_fetal_liver_spleen_	31
	423930	AA332697	Hs.42721	ESTs		3.1
20	403796	AA114016	Hs.75746	aidet	yde dehydrogenase 1 family, member	3.1
20	414085 445886	AJ793176	Hs.14559			3.1 3.1
	414401	AJ760159	Hs.12483	EST:	s s. Weatdy similar to 178885 serine/th	3.1
	441573	BE563966	Hs.6529			3.1
25	450725	R71389 AJ282933	Hs.17595 Hs.23294	hypo	thetical protein FLJ14393	3.1 3.1
25	458805 417868	AI078534	Hs.12259	2 EST	S	3.1
	458391	AI792628	Hs.13327			3.1
	423346		Hs.12741	ob:E	aptojanin 1 RC1-CT0302-140300-016-104 CT0302 Homo	3,1
30	454486 408341			7 ES1	ís.	3.1 3.1
30	410669				eroxide dismutase 2, mitochondrial	3.1
	404907	•			Ts, Moderately similar to alternativel	3.1
	434910			C2 C2	Tė	3.1
35	436990 441921			20		3.1 3.1
33	45467)7	gb:	RC3-ST0186-070100-016-004 STU 180 HUNU	3.1
	42947	0 AI878901	Hs.2038		anine nucleotide binding protein (G protein 11	3.1
	40434				nor octoin translationally-controlls	3.1 3.1
40	40821 41731			ab	:zr32f09.r1 Soares_NhHMPU_S1 Homo sapi	3.1
. 40	42732	2 AK0020	17 Hs.176	2 2 7 hy	pothetical protein FLJ 11155 pothetical protein FLJ 13920	3.1
	41100			-43 E	ÎTe	3.1
	42533 4267			921 56	ema domain, immunoglobulin domain (lg),	3,1 3.1
45				75 K	IAA 1576 protein	3.1
7.5	4296	08 U49250		862 T	-box, brain, 1 broblast growth factor 9 (glia-activat	3.1
	4423				STs	3.1
	4284 4116			346 n	eurofilament 3 (150kD medium)	3.1 3.1
50	4479		577 Hs.94		STs	3.1
	4139			245 t 292 d	STs paired-like homeodomain transcription fa	3.1
	4196				STs	3.1 3.1
	4251 4271		931 Hs.12	ence 1	ESTs	3.1
5:	5 429	060 AW13		4995	hypothetical protein DKFZp43400320 olfactory receptor, family 1, subfamily	3.1
		708 U7830 1084 A1487			COTA MANUL Similar IO LOWIZZ NYBOURU	3.1 3.1
		506 AW84	7346		~~-DCA_CT0264_240999-021-e01 CTU2V2 HOTTO	3.0
_	414	1529 AA34!	5824 Hs.7	6688	carboxytesterase 1 (monocyte/macrophage	3.0
6		2963 M791		3234 2401	ESTs CD69 antigen (p60, early T-cell activati	3.0
		7696 BE24 8175 BE29		25160	humothetical protein FL 113102	3.0 3.0
		4686 BE40	9757 Hs.2	3189	ESTs, Moderately similar to TBB2_HUMAN T	3.0
	45	8360 AI027		32253	ESTs ESTs	3.0
Ć				247377 224768	ESTs	3.0 3.0
				145362	immortalization-upregulated protein	3.0
		2018 AAS	24447 Hs.	152377	ESTs hypothetical protein FLJ 13397	3.0
	70 4	07988 N47	760 Hs.	285107	hypothetica protest t & 1995.	3.0
		05911 18808 Al82	1836 Hs	10359	ESTs	3.0 3.0
			72048 Hs	192534	£CTe	3.0
	4	52893 H18		.22869	ESTs, Moderately similar to KIAA1395 pro KIAA0853 protein	3.0
				.136102 .15780	ATP-binding cassette: sub-family A (ABC)	3.0
		112000 AW 105793	J. J.J. 110		-	3.0 3.0
		110711 AB		.65746	KIAA0318 protein gb:QV4-0T0067-010300-121-d01 OT0067 Homo	3.0
			/884776 /978309 H	s.1 362 35		3.0
				s.192719	COTA	3.0 3.0
			v974956		gb:EST387061 MAGE resequences, MAGN Homo	3.0

TABLE 108:

4.

PCT/US02/29560 WO 03/025138

Unique Eos probeset identifier number CAT number: Gene cluster number Genbank accession numbers Accession: 5 CAT Number Pkey 409257 1112994_1 1156071_1 AW370362 AW809101 AW502122 AW502125 AW501663 AW501720 409840 411052 AW814950 R98513 H69459 BE176242 H54583 AW844776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258 AW848776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258 AW848427 AW848990 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162 AW853498 AW853442 AW853590 AW853433 AW853592 1230374_1 411279 1237516 1 1247047_2 10 411474 411607 1251251_1 BE170301 AW861539 AW904851 BE154336 BE154090 BE154275 BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 A11772 1257386 1 412112 1277883_1 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 AW893614 AW893615 HB5789 HB3501 BE180230 BE1068706 BE106825 BE1068408 BE1068408 BE1068295 BE1068498 BE1068705 BE1068208 BE1068408 BE1068408 BE1068295 BE1068408 BE1068528 BE1068408 BE1068408 BE1068408 BE1068508 BE1068408 BE1068508 BE1068408 BE1068508 15 413164 1351422 1 20 25 413493 1373555_1 F13044 T77009 BE145525 BE145493 BE147225 BE147205 BE147234 413510 1374377_1 413544 414220 1375671_1 1426940_1 BE298094 BE267860 BE312991 BE272945 1435028_1 1438636_1 414314 BE549143 BE390613 BE277344 30 414366 H74314 BE299593 BE386764 BE387560 414456 414593 1447655_1 1464909_1 BE410857 BE390605 F13142 Z42926 F06135 F06147 H08517 D51360 T75341 415047 1517450_1 166644_1 1706092 1 35 AA195602 W01148 N40632 R23053 R79884 R76271 417313 417888 R23033 R79884 K76271 AA244416 AA244401 AA285362 AW752386 AW847156 AA285373 AW879575 AW879558 AW966652 AW966653 AA294989 AA385977 BE048255 AA313383 AA298419 185884_1 419555 200649_1 204833_1 421249 421640 40 207654_1 221034_1 421813 BE048255 AA313083 AA298419 BE409561 BE162756 AW732798 AA359933 AA358889 AW955306 AW962995 AW837746 AW837755 AW837697 AA469153 A1718503 AA469225 A204995 AW827539 AW969908 AW440776 AA528756 AF038171 Z43209 F07347 422760 252776_1 314437_1 425526 430212 432222 343347_1 45 433389 36497 1 AW974956 AA781075 AA654944 AF230801 AF230800 AA401795 AA398260 434961 396357_1 41050_1 43756_1 435752 437483 AL390174 AW898817 440198 443509 48824_-2 BE560093 AV645470 TB4636 T82805 AA358760 AA158850 AW062737 AW062738 AV656291 50 57199_1 446052 446218 65988_1 66686_1 AV657159 BE145509 BE145512 BE145505 BE145507 447135 70963_1 912206_1 T58148 AW516579 AW059603 BE243534 BE243752 AI880228 L44326 452346 AI904296 BE007223 R30587 BE394588 AW024754 BE183166 BE183167 55 919733_1 452502 454065 998401 1 BEJ34988 AWIZ4794 BE143100 BE15J107 BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 454186 1049791_1 BE141749 AW177598 AW381980 BE152244 BE152235 BE152238 BE152232 60 454339 454486 1122972_1 1215703_1 AW857077 AW861268 AW847383 AW795787 AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787 454506 454673 1219857_1 AW812807 AW812815 AW812802 AW852286 AW851934 AW852096 AW852274 AW996689 AW996380 AW996453 BE085550 AW868687 BE085595 1228669_1 1250028_1 1262318_1 455040 65 455225 455577 1333898_1 BE006341 BE006307 BE006311 BE078070 BE061030 BE077927 455617 BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946 BE155527 BE155503 BE155188 BE155126 455697 1351148_1 455901 456235 1381569_1 AA203637 AA832266 H67452 AW868614 AA243209 AA281411 70 168686_1 456407 457452 184986 AW972675 AA541366 AA523039 BE155356 BE153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492 339381_1 919196_1 459150 75 TABLE 10C: Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons. Pkey: Ref: Strand: 80 Nt_position: Pkey 400661 Strand Nt position

84912-85187

8118474

Plus

	400685	8118768	Minus	72969-73050,73713-73800
	400865	1945037	Minus	44482-45526
	400878	9864757	Plus	31493-32842
	401024	8117489	Plus	60551-60802
5	401315	9212516	Minus	198960-199619
•	401485	7341723	Ptus	68009-68209,68841-69077
	401521	7705251	Ptus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
	401738	2982169	Minus	41547-41757
10	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
	402176	7543687	Minus	10-750
15	402546	7637348	Ptus	24673-25170
	403092	8954241	Plus	174720-175016,175104-175408,175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
	403796	8099896	Minus	75073-77664
20	404391	3135305	Minus	26030-26173,27852-27997
	404769	B099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
	404907	7331453	Minus	102880-103828
25	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
30	405377	5649375	Plus	216656-216848
	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
35	405867	6758731	Minus	74553-75173
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 11A fists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on
the Affymetrix/Eos Hu03 Gene-Chip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was
set to the 75th percentile amongst various normal CNS tissues. The "average" norm-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th
percentile amongst various CNS tissues. The "average" norm-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to
remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and
the denominator before the ratios were evaluated.
Play:

Unique Eos probeset Identifier number
ExAccn:
Exemptar Accession number, Genbank accession number
Unique end produced from number 40 45

50

UnigenelD: Unigene Title: R1: R2: Unigene number
Unigene gene title
Ratio of 75th percentile normal central nervous system tissue to 85th percentile turnor
Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Pkey	ExAcco	UnigenetD	Unigene Titte	R1	R2
	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22 .6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
•	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	1B.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
65	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6	16.5
~~	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
70	446353	AI290919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10283	RNA binding motif protein 88	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9,5	10.9
	412454	R55745	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTS	9.1	12.8
	433558	AA833757	Hs.201769		9.0	14.7
	412453	R20205	Hs.167330		9.0	13.7
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
	409031	AA376836	Hs.76728	ESTA	8.7	8.6
	446544	AI531932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapla	8.2	20.0
	439480	AL038511	Hs.125316		8.2	8.3

					9.0	8.9
			Hs.101915 S	targandt disease 3 (autosomal dominant) InaJ (Hsp40) homolog, subfamily B, membe	8.0 7.9	9.6
	408428 437073			STs	7.9	11.3
	408434	AW195317	Hs.107716	ypothetical protein FLJ22344	7.9 7.8	16.4 34.3
5	440209	H05049	Hs.22269	eurexin 3 STs, Weakly similar to T00331 hypotheti	7.8	9.0
	408119 429611	W26213 AI889077	Hs.101672 Hs.211388	tomo sapiens BAC clone CTB-60N22 from 7q	7.7	5.0
	423440	R25234	Hs.143434	contactin 1	7.7 7.6	9.9 9.1
	445148	AI214510		ESTs	7.6 7.6	7.6
10	416294 424087	D86980 N69333		KIAA(1227 protein contactin 1	7.6	10.3
	437479	R61866		ESTs	7.5	9.3 2.8
	430573	AA744550		ESTs	7.1 7.1	10.4
15	448958	AB020651 AW968619	Hs.22653 Hs.155849	KIAA0844 protein ESTs	7.1	3.0
13	419474 423605	AF047826	Hs.129887	cadherin 19, type 2	7.0	6.9
	433098	AW190593	Hs.151143	ESTs	7.0 6.9	9.2 3.1
	449511	AI436187	Hs.296261 Hs.184216	guanine nucleoide binding protein (G pr DKFZP564C152 protein	6.8	5.0
20	428414 443155	AL049980 R54485	Hs.23772	ESTs	6.8	3.5
20	450561	R49674	Hs.25909	ESTs	6.8 6.8	8.1 2.0
	433068	NM_006456	Hs.288215	sialytransferase	6.6	10.5
	423589 415681	AA328082 AI379882	Hs.209569 Hs.72630	ESTs ESTs	6.5	9.0
25	413510	F13044	10.72022	qb:HSC3HH101 normalized infant brain cDN	6.4	7.1 9.5
	427992	Y15014	Hs. 191353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4 6.4	5.7
	450642	R39773 D86984	Hs.7130 Hs.199243	copine IV KIAA0231 protein	6.4	8.2
	429322 447482	AB033059	Hs.18705	KIAA1233 protein	6.4	2.3
30	446129	AW244073	Hs.145946	ESTs	6.3 6.3	8.3 2.1
	421913	AI934365	Hs.109439 Hs.26303	osteoglycin (osteoinductive factor, mirne ESTs	6.2	10.3
	434273 408480	AA913143 AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2	3.5
	451301	AI769514	Hs.209890	EST	6.2 6.2	12.4 8.1
35	438356	AA805530	Hs.48527	ESTS	6.2	8.6
	426388 452502	AW081394 AI904296	Hs.97103	ESTs gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1	2.8
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1	6.3 6.3
40	442979	AW440782	Hs.174743	ESTs	6.1 6.0	3.8
40	408713 430004	NM_001248 U27768	Hs.47042 Hs.227571	ectonucleoside triphosphate diphosphohyd regulator of G-protein signalling 4	5.9	21.4
	425087	R62424	Hs.126059	ESTs	5.9	8.1
	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9 5.8	3.1 12.5
45	417175	R44558	Hs.94002	ESTs gb:Homo sæjens mRNA; cDNA DKFZp547J184	5.8	2.2
45	437483 436427	AL390174 Al344378	Hs.143399	ESTs	5.8	13.8
	450382		Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7 5.7	4.4 12.5
	408478			gamma-aminobutyric acid (GABA) A recepto ESTs	5.7	6.8
50	442676 446443		Hs.130897 Hs.134220		5.7	6.4
50	459080	AW192083	Hs.29085	ESTs	5.6 5.6	15.6 8.2
	431984			Human DNA sequence from clone GS1-256O22 ESTs	5.6	6.2
	428356 417877		Hs.86320	ESTs	5.4	4.9
55	429290			neurofilament, heavy polypeptide (200kO)	5.3 5.3	13.1 6.6
	40855		Hs.46362 Hs.27221	5-hydroxytryptamine (serotonin) receptor cadherin 7, type 2	5.2	6.0
	43193 43828			ESTs -	5.2	7.3
	43990	1 N73885	Ha.12416	9 ESTs	5.2 5.2	2.7 8.1
60	44922		4 Hs.19762		5.2 5.1	2.5
	40801 43695				5.1	3.0
	43677				5.1	7.3 12.9
	40926				5.1 5.1	3.4
65	45383			ESTs phosphatidylinosital binding clathrin as	5.0	4.8
	44153 41649			regulator of G-protein signalling 7	5.0	20.1
	4172	84 N62889	Hs.1072	12 Homo sapiens cDNA FLJ12965 fis, clone NT	5.0 5.0	3.9 6.1
70	4486				4.9	6.7
70	4422 4279				4.9	5.2
	4160	40 AW8191	58 Hs.2890	44 Homo sapiens cONA FLJ12048 fls. clone HE	4.9 4.8	2.8 3.7
	4449				4.8	6.6
75	4089 4149				4.8	3.1
, ,	4292	54 H10133	Hs.918	6 hypothetical protein DKFZp761C121	4.8	2.3 9.1
	4079	106 AA3696			4.8 4.7	2.2
	4165 4204				4.7	2.8
80) 404		J. 110.501		4.6	22
	430	95 U66581			4.6 4.6	7.4 5.4
	438 444				4.6	6.0
	444	JUJ ATT.10	180000	100		

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							2.2
	414272	, 44,	Hs.46988	ESTS	ein, alpha (non A4 component of am	4.5 4.5	30.9
	414699 423449	AI815523 AI497900	Hs.76930 Hs.33067	ESTs	Eur's Bloug (upu vos comboneur or a	4.5	20.8
_	433521	T66087	Hs.112482	Homo	sapiens unknown mRNA sequence	4.4 4.4	2.0 19.2
5	429876	AB028977	Hs.225974 Hs.27151	KIAA1 ESTs	054 protein	4.4	10.2
	429726 449093	AW628326 AB035356	Hs.22998	Réure	xin 1	4.4	9.4 15.1
	415716	N59294	Hs.179662		osome assembly protein 1-like 1	4.4 4.4	8.2
10	419656	AB002314 U56420	Hs.92025 Hs.159903		0316 gene product ory receptor, family 5, subfamily	4.4	2.4
10	425864 435078	AW518888	Hs.40937	EST	, ·	4.4	5.7 5.9
	432712	AB016247	Hs.288031		-C5-deseturase (fungal ERG3, delta	4.3 4.3	6.0
	426867	AA460967 BE180342	Hs.22668	EST:	C3-HT0622-130400-012-a07 HT0622 Homo	4.3	3.2
15	412112 410171	H07892	Hs.12431	EST:	1	4.3 4.2	5.3 5.0
	442339	BE299668	Hs.227591	EST	s, Wealdy similar to 1901303A Leu zip TH277 HTCDL1 Homo sapiens cDNA 5/3	4.2	3.5
	421249 422528	AA285362 AB011182	Hs.118087		A0610 protein	4.2	3.9
	434460	AA478486	Hs.3852	KIA	A0368 protein	4.1 4.1	8.3 7.0
20	410362	H04811	Hs.93164	prop	rotein convertase subtilisin/kerin t s. Wealdy similar to 834087 hypotheti	4.1	3.9
	449754 408496	H00820 Al683802	Hs.30977 Hs.136182			4.1	4.7
	434101	AA625205	Hs.259599	KIA	A 1622 gratein	4.1 4.0	6.3 2.5
25	430212	AA469153	Hs.32042	200	nc67f04.s1 NCI_CGAP_Pr1 Homo sepiens artoacylase (aminoacylase 2, Canavan	4.0	7.4
25	453165 456407	S74727 AW968614	113.32042	c b:8	EST380690 MAGE resequences, MAGJ Homo	4.0	5.1 32.3
	441869	NM_003947	Hs.8004	hun	itingtin-associated protein interactin	4.0 4.0	4.5
	429628	H09604 F12079	Hs.13268 Hs.332579	ES'		4.0	6.9
30	410087 419910	AA662913	Hs.190173	3 ES	Ts. Wealdy similar to A46010 X-linked	4.0 3.9	2.6 21.7
50	441005	Z41305	Hs.303172		mo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9	2.2
	412677	AW029608 AI758912	Hs.17384 Hs.29634	ES 1 adi	enylyl cyclase-associated protein 2	3.9	7.2
	453341 416854	H40164	Hs.80296	i Pu	rkinje celi protein 4	3.9 3.8	2.2 6.2
35	414666	NM_004456	Hs.76828		rpican 5	3.8	3.2
	418217 421855	A1910847 F06504	Hs.13442 Hs.27384	ES	STs STs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	7 ES	STs	3.8 3.7	10.7 2.7
40	433629		Hs.13359 Hs.46826		STs STs	3.7	2.1
40	424738 407708		Hs.26612		STs. Moderately similar to \$23650 retro	3.7	5.3 53.7
	437268	AI754847	Hs.22757	71 re	gulator of G-protein signaffing 4	3.7 3.7	53.7 21.7
	423135		Hs.26411		STs STs	3.7	2.6
45	446818 427562		Hs.2653		STs	3.6	3.6 34.5
-15	43927	AF086092		2 E	STs STs, Weakly similar to ALU1_HUMAN ALU S	3.6 3.6	6.0
	45238 42289		Hs.2908 Hs.4290		STs	3.6	5.1
	42265		Hs.2115	584 n	eurofilament, light polypeptide (68kD)	3.6 3.6	24.6 5.8
50	41715		Hs.2138 Hs.1608		ISTs ISTs	3.6	6.4
	44717 40 5 97		HS. 1000)93 E	:a18	3.6	3.9
	42356				growth arrest-specific 2	3.6 3.6	2.5 5.4
55	44123				Homo sapiens cDNA: FLJ21268 fis, clone C ESTs	3.6	3.4
33	42677 41483		Hs.774	39	protein kinase, cAMP-dependent, regulato	3.6 3.6	2.8 4.9
	4251	3 AW02319			ESTs	3.5 3.5	9.8
	4464! 4458!		Hs.153 3 Hs.134	123	ESTs Homo sapiens clone 24468 mRNA sequence	3.5	16.6
60	4164		6 Hs.793	306	eukaryotic translation initiation factor	3.5 3.5	5.0 16.0
	4182		Hs.347 Hs.156		ESTs Down syndrome critical region gene 1-lik	3.5	6.2
	4253 4170				triadin	3.5	2.5 5.3
	4083	87 AK00117	7B Hs.444		homolog of rat orphan transporter v7-3 ESTs, Wealdy similar to 138022 hypotheti	3.5 3.5	5.5
65					Home saciens mRNA for KIAA1263 protein.	3.5	23.6
	4532 4193				superiorcervical ganglia, neural specifi	3.5	42.3 3.6
	433	303 AIB2359			ESTs, Weakly similar to KIAA1324 protein	3.4 3.4	4.1
70	4507) 4150				quanylate cyclase 1, soluble, beta 3	3.4	9.8
/	423	326 U20325	Hs.17	07	cocaine- and amphetamine-regulated trans	3.4 3.4	4.7 2.4
	427	173 BE2550	17 Hs.97		ESTs ESTs	3.4	3.5
	446 416				ESTs	3.4	4.5
7:	5 458	234 BE5514	108 Hs.12	27196	ESTs	3.4 3.4	4.5 3.9
	434	053 AW445		34948 288	ESTs visinin-like 1	3.3	42.3
		536 Al1431 1366 Al2675	89 Hs.30	02689	hypothetical protein	3.3	
	425	785 T27017	7 Hs.15	59528 6037	Homo sepiens clone 24400 mRNA sequence	3.3 3.3	
8		1998 AW975 3359 AI9679			ESTs homeo box 03	3.3	4.4
		527 NM_00	1037 Hs.1	70238	sodium channel, voltage-gated, type 1, b	3.3 3.3	
		302 N4805	6 Hs.1	915	folate hydrolase (prostate-specific memb	3.3	

		44053410	U- 02F67 -	t-ashelia	3.3	3.6
	*****			roenkephalin ISTs	3.3	3.0
	444612 415242			STs	3.2	22
	421640	AW966652	q	b:EST378726 MAGE resequences, MAGI Homo	3.2	3.8
5	408806	AW847814		tomo sapiens cDNA: FLJ21532 fs. clone C	3.2	24
	446015	T30968		rypothetical protein FLJ10971	3.2 3.2	3.2 2.2
	425495	AA358454	Hs.78026 E	STs, Wealty similar to similar to ankyr	3.2	2.9
	403092 452971	A1873878	Hs.91789 f	ESTS	3.2	4.5
10	454100	Al693231		tromosome 21 open reading frame 51	3.2	2.7
10	448440	AA173467		p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2	2.8
	421200	AA284811		ESTs .	3.2	2.7 2.1
	440827	AI733110		ESTs Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2 3.2	4.3
15	429809	AL162010 AW449258		ESTs	3.2	19.0
13	420156 457535	AA609685		membrane component, chromosome 11, surfa	3.2	20
	419956	AL137939		ESTS	3.1	8.7
	423930	AA332697		ESTs	31	2.7
20	417868	A1078534		ESTs	3.1 3.1	12.6 12.0
20	423346	A1267677		synaptojanin 1 hypothetical protein FLJ21939 similar to	3.1	4.3
	441921 429470	A1733376 A1878901		quanine nucleotide binding protein (G pr	3.1	5.3
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1	7.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	6.3
25	449078	AK001256	Hs.22975	KIAA1576 protein	3.1 3.1	30.1 2.2
	429608	U49250	Hs.210862	T-box, brain, 1	3.1	3.0
	442308	AA989402	Hs.111 Hs.71346	fibroblast growth factor 9 (glia-actival neurofilament 3 (150kO medium)	3.1	10.9
	411666 427865	AF 106564 AA416931	Hs.126065	ESTs	3.1	7.5
30	430708	U78308	Hs.278485	ollactory receptor, family 1, subfamily	3.1	3.4
-	451829	AW964081	Hs.247377	ESTs	3.0	6.2
	405911				3.0 3.0	2.4 6.2
	418808	AI821836	Hs.10359	ESTs	3.0	5.1
35	452893	H18017 AW877787	Hs.22869 Hs.136102	ESTs, Moderately similar to KIAA1395 pro KIAA0853 protein	3.0	21
33	423952 412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0	2.1
	405793			• •	3.0	2.7
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	14.3 2.1
40	427071	AA397958	Hs.192719	ESTs	3.0 3.0	14.5
40	453534	NM_014796	Hs.33187 Hs.23136	KIAA0748 gene product ESTs	3.0	2.2
	413903 426866	AA496493 UO2330	Hs.172816	neurogulin 1	3.0	11.3
	434945	AB033065	Hs.4280	KIAA1239 protein	3,0	3.5
	412639	AW961284	Hs.296235	ESTs	2.9	4.9
45	453590	AF150278	Hs.33578	KIAA0820 protein	2.9 2.9	33.1 2.3
	414502	AL133721	Hs.224680	ESTs KIAA0893 protein	2.9	23.1
	434367 425121	AB020700 Al797511	Hs.3830 Hs.154679	synaptotagmin I	2.9	8.1
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.9	20.8
50	401213			·	2.9	3.2
	401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9 2.9	3.4 3.0
	415191	AA190381	Hs.120810	ESTs .	2.9	5.6
	449275 419863	AW450848 AW952691	Hs.205457 Hs.93485	perlaxin Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.9	35.0
55	411421	BE272110	Hs.21177	ESTs	2.9	2.0
	430865		Hs.5232	HSPC125 protein	2.9	11.4
	437486			RAB6A, member RAS oncogene family	2.9 2.9	2.2 6.0
	442357		Hs.135708	ESTs gb:yg12g11_r1 Soares infant brain 1NIB H	2.9	2.2
60	408274 444185		Hs.66020	ESTs	2.8	5.0
V	420173		Hs.22999	ESTs	2.8	5.1
	428358			Stargardt disease 3 (autosomal dominant)	2.8	7.0
	447252		Hs.12449	Homo sepiens transmembrane protein HTMP1	2.8 2.8	4.4 10.6
65	440260		Hs.7130	copine IV	2.8	B.4
03	417084 438257		Hs.33067 Hs.224794	ESTS L ESTS	2.8	2.8
	441934		Hs.7344	ESTs	2.8	6.2
	44788		Hs_303172	Homo sapiens mRNA; cDNA OKFZp547G133 (Ir	2.8	3.5
70	42355				2.8	3.4 14.4
70	45094	0 AI744943	Hs.14320		2.8 2.8	21.7
	41001		Hs.57856 Hs.14559		2.8	5.1
	44588 42549		Hs.78026		2.8	2.4
	43820			ESTs	2.8	11.9
75	43519	9 R38946	Hs.12795	1 hypothetical protein FLJ14503	2.8	6.0
	43482		1 Hs.22265	pyruvate dehydrogenase phosphatase	2.8 2.8	2.4 3.4
	41546		Hs.12698 44 Hs.83407	ESTs quitamate receptor, metabotropic 7	2.8 2.8	4.5
	41807 43214				2.8	9.5
80	43037		Hs.24011	2 KIAA0276 protein	2.8	7.0
	43735	7 AL35955	9 Hs.33166	6 Homo sapiens mRNA; cDNA DKFZp76202215 (I	2.7	2.5
	41583		Hs.7093	ESTs	2.7 2.7	3.6 2.5
	43867	75 AA81372	5 Hs.21356	38 ESTs	£./	4.0

					22	3.1
		AW953679 AI949389		b:EST365749 MAGE resequences, MAGC Homo STs	2.7 2.7	4.1
	446318 445183			IAA0417 gene product	2.7	5.3
_	457012	R41480	Hs.127630 E	STs	2.7 2.7	19.0 7.2
5	431988	AC002302		rotein kinase C, beta 1	2.7	2.8
	430223 447932	NM_002514 AAB37474	Hs.235935 of Hs.20021 v	ephroblastoma overexpressed gene esicle-associated membrane protein 1 (s	27	3.8
	450214	BE439763		egulator of G-protein signalling 4	2.7	6.9
	434731	AA648049	Hs.121518 (STs	2.7 2.7	5.0 5.2
10	428839	AI767756		tomo sapiens cDNA FLJ14814 fis, clone NT	2.7 2.7	2.5
	407709	AA456135 U03398		ESTs umor necrosis factor (ligand) superfami	2.7	3.3
	422420 443305	AI050693		ESTs	2.7	5.9
_	435648	H24347	Hs.27524	ESTs	2.7	15.0
15	418407	AL044818		nuclear transcription factor Y, beta	2.7 2.7	2.7 6.0
	436771	AW975687		ESTs suffortranferase (amily 4A, member 1	2.7	4.8
	428689 440503	NM_014351 NM_006539	Hs.189810 Hs.7235	calcium channel, voltage-dependent, gamm	2.7	4.4
	441006	AW605267		CGI-60 protein	2.7	31
20	410330	AW023630	Hs.46786	ESTs	2.6 2.6	29.5 2.6
	434398	AA121098	Hs.3838	serum-inducible kinase	26	7.8
	438831 419066	BE263273 Z98492	Hs.6439 Hs.6975	synapsin II PRO1073 protein	2.6	3.4
	412643	AW971239	Hs.293982	ESTs	2.6	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	2.6 2.6	17.9 2.9
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6	20
	401421 419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	2.6	3.8
30	439203	AA448930	Hs.8453	KIAA1587 protein	2.6 2.6	4.2 5.1
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	2.6	3.7
	444583 417919	AW994403 AI928203	Hs.100861 Hs.86379	hypothetical protein FLJ14600 ESTs	26	3.0
	434293	NM_004445	Hs.3796	EphB6	2.6	3.2
35	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6 2.6	6.4 2.2
	443037	AW500305	Hs.299166	syntaxin 7	2.6	7.1
	440736 404648	D56919	Hs.265848	myomegain	2.6	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
40	436508	AW504381	Hs.121121	ESTs, Wealdy similar to S00755 pleckstri	2.6 2.6	3.9 3.1
	441190	H09073	Hs.25046	ESTs	2.6	2.9
	432278 442731	AL137506 AI868167	Hs.274256 Hs.131044	hypothetical protein FLJ23563 ESTs	2.6	4.1
	416836	D54745	Hs.80247	cholecystokinin	2.6	14.9
45	449071	NM_005872	P Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4 2.8
	436321	AA709133	Hs.180144	ESTs	2.5 2.5	3.6
	439693 443212	Al741816 AW269515	Hs.125897 Hs.102500	ESTs hypothetical protein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664	Homo sapiens mRNA; cDNA DKFZp434A1627 (f	2.5	3.8
50	407868	NM_00095	0 Hs.40637	protine-rich Gla (G-carboxyglutamic acid	2.5 2.5	3.1 27.9
	443992				2.5	5.3
	444124 411379		Hs.6818 Hs.12554	ESTs. Weakly similar to NPL4_HUMAN NUCLE	2.5	38.0
	440474		Hs.7195	gamma-eminobutyric acid (GABA) A recepto	2.5	3.8
55	446277	AJ284218	Hs.159204		2.5 2.5	2.2 3.5
	410111		Hs.189547		2.5	4.8
	445162 410718		Hs.12376 Hs.191435	piccolo (presynaptic cytomatrix protein) i ESTs	2.5	4.5
	41720		Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	29
60	42027	4 AW968000	D Hs.143389	ESTs, Wealdy similar to T14318 ubiquitin	2.5 2.5	2.8 4.7
	43349				2.5	3.3
	43733 43735				2.5	3.0
	44198			5 ESTs	2.5	3.6
65	41002		3 Hs.11359	2 ESTs, Moderately similar to 154374 gene	2.5 2.5	9.2 3.6
	41468				2.5 2.5	23.9
	42995 42902				2.5	2.8
	43810			ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	43978		8	db:Homo sapiens mRNA full length insert	2.5 2.5	2.3 3.9
	44080		Hs.32688	ESTs	2.5 2.5	2.6
	44524			8 ESTs KIAA0378 protein	2.4	23.6
	44015 4327				2.4	2.1
75	4151		Hs.2224	S ESTs	2.4	3.9
	4322	98 AL11881			2.4 2.4	9.8 9.8
	4379				24	2.8
	4213 4271				2.4	2.2
80	4520		35 Hs.2774	7 G protein-coupled receptor 37 (endotheli	24	10.0
	4366	39 D14838	Hs.111	fibroblast growth factor 9 (glia-activat	2.4 2.4	3.5 3.1
	4345	20 AA2052			2.4	3.0
	4115	29 AA4303	48 Hs.3175	DO HOURD SAPERIO CONTRA I'EM 12327 (ID., GADIE) PET		

				- NT -	2.4	2.1
	*****			:STs :alclum binding protein 1 (calbrain)	24	27
	422927			luman ctone 23589 mRNA sequence	2.4	2.8
	444647 415827	H17462		ESTs	2.4	15.0
5	451397	AA017432	Hs.84529	ESTs, Wealty similar to Z202_HUMAN ZINC	2.4	3.9
•	445200	AA084460		somatostatin	2.4	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (I	2.4	2.4
	420328	Y19062	Hs.96870 9	staufen (Orosophila, RNA-binding protein	24	4.3
	432122	AA526514		gb:ni60f02.s1 NCI_CGAP_Ov2 Homo septens	2.4	4.3 3.5
10	444125	AI124882		EST8	2.4 2.4	10.8
	430538	AB032435		differentiation-associated Na-dependent	2.4	2.4
	457519	X69438		early growth response 4	24	21
	409371	R51736		ESTs ESTs	24	3.2
15	456303	AA224872		Homo sepiens clone 23809 mRNA sequence	24	23.4
13	440105 400979	AA694010	13.0302	Takin adjust dang about in a confession	24	4.1
	435296	R49685	Hs.24980	ESTs	2.4	6.5
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	24	18.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	2.2
20	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.4	2.7
	408974	AW015458	Hs.297017	ESTs	2.4	25
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	2.4	2.8 2.5
	413153	N94205		gb:za27a08.r1 Soares fetal liver spleen	2.4 2.4	2.6
25	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	23	3.0
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	6.3
	424940	AA985308	Hs.194327	ESTs adenylyl cyclase-associated protein 2	2.3	4.1
	431706	AI816086	Hs.296341 Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	2.3	2.9
	419125 423641	AA642452 AL1372 5 6	Hs.130489	ATPase, aminophospholipid transporter-li	2.3	8.7
30	436407	T88803	Hs.271507	ESTs, Wealty similar to TIM_HUMAN PROBAB	2.3	3.2
50	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cON	2.3	5.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	23	54.7
	410765	A1694972	Hs.66180	nucleosome assembly protein 1-like 2	2.3	9.1
	422386	AF105374	Hs.115830	heparan suffate (glucosamine) 3-O-suffot	2.3	5.0
35	414828	AA156651		gb:zi05h05.r1 Soares_pregnant_uterus_NbH	2.3	2.4
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3 2.3	8.5 26.3
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	2.3	2.5
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	2.3	7.6
40	423420	A1571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	23	26.3
40	439450	R51813	Hs.125304	ESTs pyruvate dehydrogenase phosphalase	23	2.2
	427127	AW802282 AW015633	Hs.22265 Hs.157299	ES18	2.3	3.8
	447179 414711	AJ310440	Hs.288735		2.3	2.3
	433449	AW772282	rts.2801 33	gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.3	3.8
45	414320	U13616	Hs.75893	ankyrin 3, node of Ranvler (ankyrin G)	2.3	2.5
7.5	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	23	7.8
	425130	AA448208	Hs.99163	ESTs	2.3	4.1
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	2.5
	438283	A1458931	Hs.37282	ESTs	2.3	4.2
50	417455			ESTs, Wealdy similar to CA2B_HUMAN COLLA	2.3 2.3	3.0 3.7
	412100			gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.2
	448981	Al968719	Hs.195387		2.3	6.5
	416101		Hs.268806 Hs.45140	5 ESTs hypothetical protein FLJ14084	2.3	17.8
55	439731 415734			KIAA0237 gene product	2.3	40.1
,,,	424596				2.3	2.9
	420230		Hs.284186		2.3	2.4
	451559		Hs.20935		2.3	5.7
	404835			•	2.3	2.1
60	456765	Al497900	Hs.33067	ESTs	23	4.1
	455517			gb:RC0-HN0006-160300-011-e06 HN0006 Homo	23 22	2.4 18.5
	408208				22	3.9
	411770				2.2	2.6
65	43010		Hs.2540	cholinergic receptor, nicotinic, atpha p	22	4.9
0.5	458694		Hs.13298 Hs.77910		2.2	4.4
	41509		Hs.15396	7 ESTs	2.2	2.4
	43964: 45013:				2.2	4.9
	45422				2.2	3.7
70	40532		. ,	== ==	2.2	2.7
. •	43134		8 Hs.21659	9 ESTs	2.2	5.2
	45310			3 ESTs	2.2	3.3
	40889	7 N50204	Hs.28370		2.2	2.8
~~	45139	8 AJ793124			2.2	4.6
75					22	10.4 6.1
	40844				2.2 2.2	3.1
	41413				2.2	3.9
	44501		Hs.1224 7 Hs.1463		2.2	23
80	42437 42464				2.2	11.7
	40972		Hs.1062		2.2	4.9
	43280			03 ESTs	2.2	19.9
	4228		Hs.7589		2.2	10.4

		AF45335	Hs.184786 T	DO lateractina sentain	2.2	6.5
				BP-Interecting protein pothetical protein DKFZp761M0423	2.2	3.4
			Hs.32501 E	STs	22	3.2 2.0
_	452768	AW069459		STs	2.2 2.2	3.2
5		AB024334		rosine 3-monooxygenase/tryptophan 5-mo xidalion resistance 1	2.2	2.3
	426281 428411	AK000987 AW291464		STS	2.2	23
	413787	AI352558	Hs.75544 I	yrosine 3-monooxygenase/tryptophan 5-mo	2.2	31
	451734	NM_006176		eurogranin (protein kinase C substrate,	2.2 2.2	8.5 7.9
10	439108	AW163034	Hs.6457	rynapiogyrin 3	2.2	24
	405385	Al371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	447285 452667	T87219	Hs.13219	ESTs	2.2	3.1
	422234	AF11981B		discs, large (Drosophila) homolog-associ	2.1 2.1	8.3 3.2
15	410339	AI916499		ESTs	21	4.5
	413231	D87461 R19085	Hs.75244 Hs.210706	BCL2-like 2 Homo sapiens cONA FLJ13182 fis, clone NT	21	2.2
	447104 451952	AL120173	Hs.301663	ESTs	21	36.5
	415841	Z45637	Hs.7093	ESTs	21	2.4 2.2
20	441086	A1928489	Hs.213490	ESTs, Wealthy similar to N33_HUMAN N33 PR	2.1 2.1	6.6
	450407	NM_000810	Hs.24969 Hs.179915	gamma-aminobutyric acid (GABA) A recepto guanine nucleotide binding protein (G pr	2.1	5.3
	427627 449712	R87582 R56545	Hs.6100	ESTs	21	4.5
	409660	AW452065	Hs.258905	ESTs	2.1	21
25	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1 2.1	5.4 3.0
	434138	AA625804	LL- 04C00	gh:zu86h01.s1 Soares_testis_NHT Homo sap nel (chicken)-like 1	21	4.8
	448610 418948	NM_006157 AJ217097	Hs.21602	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	21	2.9
	414876	AW950925	Hs.924	crystallin, mu	2.1	3.4
30	440426	Al159800	Hs.7181	Homo sapiens cDNA FLJ13563 fis, clone PL	2.1 2.1	3.7 4.1
	451249	AA016227	Hs.27280	ESTS	2.1	2.1
	451475 448743	T19093 AB032962	Hs.26450 Hs.21896	KIAA0725 protein KIAA1136 protein	21	29.7
	430814	U89336	Hs.247993	NG5 protein	2.1	2.7
35	426990	AL044315	Hs.173094	Homo sapiens mRNA for KtAA1750 protein,	2.1 2.1	2.3 4.5
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	21	2.2
	427335	AA448542 F13036	Hs.251677 Hs.27373	G antigen 78 Homo sepiens mRNA; cDNA DKFZp56401763 (f	2.1	2.3
	459089 435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	21	5.9
40	446383	T05816	Hs.92511	ESTs	2,1 2,1	29 21
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	2.1	4.2
	453976	BE463830 R39039	Hs.163714 Hs.328455	ESTs EST	2.1	3.3
	415111 452238	F01811	Hs.187931	ESTs	2.1	4.9
45	445279	R41900	Hs.22245	ESTS	2.1	9.8 3.1
	448799	Al937094	Hs.179080	ESTs	2.1 2.1	8.3
	418338	NM_00252		neuronal pentraxin 1 hypothetical protein FLJ 10094	2.1	5.4
	445725 443537	AK000956 D13305	Hs.13209 Hs.203	cholecystokinin B receptor	2.1	4.1
50	454066		Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
	429954		Hs.21374	ESTs	2.1 2.1	7.2 3.9
	415292		Hs.200576 Hs.75209	ESTs protein kinase (cAMP-dependent, catalyti	21	3.1
	423563 424906		Hs.153716		2.1	4.7
55	459309	AA040620	Hs.5672	hypothetical protein AF140225	21 21	2.2 4.7
•	439340			brain-specific Na-dependent inorganic ph	21	5.4
	402598 435408		Hs.3128 Hs.4884	polymerase (RNA) II (DNA directed) polyp calcium/calmodulin-dependent protein kin	ži	6.6
	44879		Hs.12826	ESTs	2.1	4,1
60	44950		5 Hs.12926	ESTs	2.1	2.4 5.8
	44113		Hs.7678	cellular retinoic acid-binding protein 1	2.1 2.1	2.7
	43336		73 Hs.30014 Hs.31092		2.1	5.0
	45294 42616				2.0	2.2
65	45366				2.0	3.1
	42463	2 AB01452	3 Hs.15140	6 KIAA0623 gene product	2.0 2.0	3.5 4.1
	44858				2.0	2.3
	43041 44562			ESTs	2.0	21
70	41709		Hs.1811		2.0	2.5
. •	4536	53 AW5055	54 Hs.1445	59 ESTs	2.0 2.0	4,7 3.7
	4358	50 AF25084			2.0	2.1
	4350		43 Hs.1225 Hs.8417		2.0	21
75	42319 4115				2.0	28
	4316	45 AF0788	49 Hs.2664	83 dynein light chain-A	2.0	2.5 3.6
	4298	34 A192964			2.0 2.0	17.5
	4398				2.0	4.0
80	4080 4303			89 glutaminase	2.0	2.7
30	4196			54 popeye protein 3	2.0	2.6
	4326	60 AJ2884	30 Hs.640		2.0 2.0	2.3 15.9
	4540)48 H05626	i Hs.692	I ESTs	2.0	15.5

	423246 AI 415989 AI	119114 H 267700 H	s.77196 spec ls.317584 EST	ZPS8680923 protein trin, atpha, non-enythrocytic 1 (alp 8 8, Highly similer to SORL_HUMAN SORTI	2.0 2.0 2.0 2.0	3.1 2.9 4.8 5.1				
5	424983 Al 446296 A	1742434 H A985662 H	ls.169911 ES1	s no sapiens cDNA FLJ13155 fis, clone NT	2.0 2.0 2.0	15.9 2.7 3.5				
10	TABLE 118: Pkey: CAT number: Accession:	Gene d	Eos probeset ide iuster number nk eocession num			•				
15	408274 412100	AT Number 104999_1 1277224_1 1277883_1	AW89273 BE18034	43964 AA053547 1 H08502 Z45826 8 BE180347 AW901900 BE180222 BE180218 B 8 RE180223 BE180219 BE180346 BE180343 I	8E160418 BE180223 BE16022	6 AW901899 BE180228 AW901897 BE180224 11 BE180341 AW901894 BE180217 BE180227 AW901891				
20	413510 414828	BE 180345 AW893614 AW893615 H85799 H83501 BE 180220 413153 1350849_1 N94205 BE067555 BE067556 BE06756								
25	419558 421249	185904_1 200649_1 204833_1 311738_1 314437_1	AA28536 AW9666 AA46357	19 AW953580 AA24436 HB2527 AA361046 A 2 AW752386 AW847156 AA265373 AW879575 52 AW956653 AA294989 AA385977 1 AI277645 AL118763 13 AI718503 AA469225	624443 HISZES 5 AW879558					
30	432122 433449 434138 437483	341756_1 366532_1 380572_1 43756_1	AA5265 AW7722 AA6258 AL3901	4 AW973343 AA554293 82 AA592974 34 AW418787 AW074833 AI675642 AI393368 74 AW898817 36 R23665 R26578		·				
35	439780 452502 455517 456407	47673_1 919733_1 1321782_1 184986_1	A190425 AW984	6 BE007223 R30687 68 AW984072 AW984077 514 AA243209 AA281411						
40	TABLE 116 Pkey: Ref: Strand: Nt_position	Uniq Sequ sequ Indic	uence source. To sence of human o cates DNA strand	ponding to an Eos probeset to 7 digit numbers in this column are Genbank I thromosome 22" Dunham, et al. (1999) <u>Nature</u> 4 from which exons were predicted. solitions of predicted exons.	dentifier (Gi) numbers. *Dunha 02:489-495.	m, et al." refers to the publication entitled "The DNA				
45	Pkey 400979 401213 401421	Ref 8072554 9858408 7452889	Strand Plus Plus Minus	NI_position 160842-161028 98243-98380,98489-98619 142291-142461		·				
50	403092 404548 404793 404835 405326	8954241 9796894 7232206 6970743 4375975	Plus Minus Minus Plus Plus	174720-175016,175104-175406,175508-1758/ 115334-116020 61087-61590 85462-85684,88139-88287,90338-91018,9482 10633-10709,30805-30893,38078-38253.5511	17-94990	56841				
55	405385 405793 405911 405977	6552772 1405887 6758795 8247789	Plus Minus Plus Minus	48332-48454 89197-89453 101008-101643 135548-136177						
60	Table 12 the Affyr	A lists about 67 netrix/Eos Hu0:	8 genes up-regu 3 GeneChip array	SUCH (that the ratio or average LOG to average	ge" CNS tissues was greater th	CENTRAL NERVOUS SYSTEM ystem (CNS). These were selected from 59680 probesets on an or equal to 2.5. The "average" LGG level was set to the 85° various CNS tissues. In order to remove gene-specific obtracted from both the numerator and the denominator before				
65	the ratio Pkey: ExAcch: Unigene	was evaluated Ui E: ID: Ui	nique Eos probes xemplar Accessio nigene number	et identifier number n number, Genbank accession number	• • • • • • • • • • • • • • • • • • • •					
70	Unigene R1:	Title: U	nigene gene title atio of LOWER (RADE GLIOBLASTOMA to normal CNS						
	Pkay 412420	ExAcon AL035668	UnigenelD Hs,73853	Unigene Title bone morphogenetic protein 2	R1 20.3					
75	424800	AL035588 U23752	Hs.153203 Hs.32964	MyoD family inhibitor SRY (sex determining region Y)-box 11 Yarget Exon cysteine and glycine-rich protein 2	19.5 18.5 16.9 15.0					
80	409638 443731	AW45042 AI083928 BE25915 AI199268 AF21751	Hs.21335 Hs.145418 Hs.127792 Hs.19322 Hs.27990	ESTs ESTs delta (Drosophila)-like 3 Home sapiens, Similar to RIKEN cDNA 2011 clone HQ0310 PRO0310p1	14.0 14.0 13.6 12.7 10.3 9.5) 5 1				
					203					

	425187			ESTS	9.0 8.8
				ESTs	8.4
		N66037 AA742643	Hs.38173	ESTs gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	8.2
5	437034 449539	W80363	Hs.58446	ESTs	8.1
-	417061	AI875944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.0
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	7.8 7.7
	414217	Al309298 Al656969	Hs.279898 Hs.346514	Homo sapiens cDNA: FLJ23165 fis, done L ESTs	7.6
10	449300 449969	AW295142	Hs.180187	Horno sepiens cDNA FLJ14337 fis, clone PL	7.5
10	452372	A1885742	Hs.228474	ESTs	7.2
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	7.2 7.2
	417308	H60720	Hs.81892 Hs.157539	KIAA0101 gene product ESTs	7.1
15	447004 418113	AW296968 Al272141	Hs.83484	SRY (sex determining region Y)-box 4	7.1
12	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	7.1
	406478			Target Exon	7,1 6,9
	428728	NM_016625	Hs.191381 Hs.77256	hypothetical protein enhancer of zeste (Orosophila) homolog 2	6.9
20	414761 428037	AU077228 N47474	Hs.89230	notassium intermediate/small conductance	6.7
20	423343	AA324643	Hs.246106	ESTs	6.7
	418097	R45137	Hs.21868	ESTs	6.7 6.6
	431553	X78075	Hs.2799 Hs.73817	cartilage linking protein 1 smati inducible cytokine A3 (homologous	6.6
25	412326 425397	R07566 J04088	Hs.156346	topoisomerase (ONA) II alpha (170kD)	6.4
23	419169	AW851980	Hs.262346	ESTs, Wealdy similar to S72482 hypothe6	6.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.4 6.3
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence NM_001839":Homo sapiens calponin 3, acid	6.2
30	402855 424009	F11690		gb:HSC300041 normalized infant brain cDN	6.2
50	400419	AF084545		Target	6.2
	446584	U53445	Hs.15432	downregulated in overian cancer 1	6.0 6.0
	414020	NM_002984	Hs.75703 Hs.343768	small inducible cytotime A4 (homologous Homo sapiens clone 25119 mRNA sequence	5.9
35	426140 427144	AF131798 X95097	Hs.2126	vasoactive intestinal peptide receptor 2	5.9
. 55	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.8
	405238			Target Exon	5.7 5.7
	421977	W94197	Hs.110165	ribosomal protein 1.26 homolog C7001664:pij12698081 dbj BAB21849.1 (AB	5.6
40	405348 428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyli	5.4
70	422672	X12784	Hs.119129		5.3
	403349	NM_001406		ephrin-B3	5.3 5.2
	453941	U39817	Hs.36820 Hs.66087	Bloom syndrome ESTs	5.2
45	429139 454860	F09092 AW835767	PIS.0000/	gb:QV4-LT0016-240200-110-b08 LT0016 Homo	5.2
7.5	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.1
	418030	BE207573	Hs.83321	neuromedin 8	5.1 5.1
	429469	M64590 AI7031B6	Hs.27 Hs.27717	glycine dehydrogenase (decarboxylating: I ESTs	5.1
50	450639 412811	H06382	113.27711	ESTs	5.1
-	442832		Hs.25356	ESTs	5.1
	436608			down syndrome critical region protein DS	5.1 5.1
	408161		Hs.30038		5.1
55	443744 447497				5.0
•	450811	A1739486	Hs.24549		5.0
	433244		Hs.27128	5 KIAA1510 protein gb:EST387294 MAGE resequences, MAGN Homo	4.9 4.9
	438458 438456				4.9
60	411048			hypothetical protein DKFZp434G0522	4.9
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.9 4.9
	442547				4.8
	419991 402274		FIS.34211	C19000498*:gij4567179tgbjAAD23607.1JAC00	4.8
65	42009			S ESTs	4.8
	43628		Hs.2721		4.8 4.8
	43080			09 ESTs, Moderately similar to 138022 hypot gb:RC1-BT0313-110300-015-f06 BT0313 Homo	4.8
	45510 40396		,	Target Exon	4.8
70	42495		46 Hs.1846	tumor protein pS3 (U-Fraumeni syndrome)	4.8
	41482	5 X06370	Hs.7743		4,8 4.7
	44789		Hs.6498 Hs.1204		4.7
	42352 42273		Hs.1196		4.7
75	42273		Hs.1907	787 tissue inhibitor of metalloproteinase 4	4.6
	43769	98 R61837	Hs.799	ESTs, Moderately similar to 184505 calci	4.6 4.6
	4034		91 Hs.270	Target Exon 149 ESTs, Weakly similar to 2109260A B cell	4.6
	4260 4221				4.6
80	4183		Hs.203	933 ESTs	4.6
	4064	81		Target Exon	4.5 4.5
	4560				4.5
	4231	10 1000314	y 113,124	and intermediate transfer and a second of the second of the	

					4.5
			Hs.71132	neuroligin 1 Homo sapiens cDNA: FLJ22669 fis, clone H	4.5
			Hs.44653	ESTs, Moderately similar to T03094 A-kin	4.5
	432625 452994	AI243596 AW962597	Hs.94830 Hs.31305	KIAA1547 protein	4.5
5	449961	AW265634	Hs.133100	ESTs	4.4
•	401454			NM_014226*:Homo sapiens renal tumor anti	4.4 4.4
	406395			Yarget Exon	4.4
	432281	AKD01239	Hs.274263 Hs.254129	hypothetical protein FLJ 10377 KIAA1678	4.4
10	453792 415131	AL134539 D61119	NS.204143	gb:HUM158C11B Clontech human fetal brain	4.4
IU	437695	AA769202	Hs.192142	ESTs	4.4
	422081	AW136820	Hs.196011	ESTs	4.4 4.3
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.3
	433323	AA805132	Hs.159142	gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3
15	420352	BE258835 AF070641	Hs.10584	Homo sapiens clone 24421 mRNA sequence	4.3
	444218 441035	AI594309	Hs.126458	ESTs	4.3
	443836	BE221613	Hs.140553	ESTS	4.3 4.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeal (LRR) protein	4.3
20	450166	AA429504		ESTs	4.2
	429149	AW193360	Hs.197962 Hs.34574	ESTs. Wealthy similar to 138022 hypotheti ESTs. Wealthy similar to ALU1_HUMAN ALU S	4.2
	422798 451254	R92347 AI571016	Hs.172967	ESTs	4.2
	409189	AA125984	110.11.200.	gb:zn27h06.r1 Stratagene neuroepithelium	4.2
25	445118	AI208762	Hs.345572	ESTs	4.2 4.2
_	444326	AI939357	Hs.270710	ESTs Homo sapiens cDNA FLJ12284 fis, clone MA	4.2
	456060	C14904	Hs.45184	C5000537":gij3298595jgbjAAC41376.1] (AF0	4.2
	404120 436899	AA764852	Hs.291567	ESTs	4.1
30	407624	AW157431	Hs.248941	ESTs	4.1
50	453361	AA035197	Hs.107375	ESTs	4.1 4.1
	447439	AA313565	Hs.145020		4.1
	438372	AI140189	Hs.123191		4,1
35	438624	AA889055 AW474183	Hs.123468 Hs.250173	hypothetical protein FLJ13158	4.1
33	422493 406872	AI760903	113.250170	gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.1
	425295	AA431366	Hs.37251	ESTs	. 4.1 4.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	4.0
40	434206	AW136973	Hs.180479	ESTs, Wealdy similar to S69890 mitogen i regulator of G-protein signaffing 20	4.0
40	420602	AF060877	Hs.99236	Tamel Fron	4.0
	400645 456306	AA225313	Hs.22288	S ESTs, Weatly similar to TRHY_HUMAN TRICH	4.0
	419326		Hs.42419		4.0
	414948	C15240	Hs.18215		4.0 4.0
45	423198		Hs.1634	cell division cycle 25A gb:MR0-BT0551-060300-102-e05 BT0551 Homo	4.0
	411537		Hs.10630		3.9
	421637 439231				3.9
	429433			8 ESTs, Weakly similar to KIAA1353 protein	3.9 3.9
50	424188	A1536021	Hs.28870		3.9
	449932		Hs.26302		3.9
	434072 434784		Hs.2830! Hs.1640!		3.9
	42514			gb:EST366697 MAGE resequences, MAGC Homo	3.9
55	42853) Hs.9864	3 ESTs	3.9 3.9
	44331		Hs.1331	41 ESTs	3.9
	41685			53 ESTs gb:EST365510 MAGE resequences, MAGB Horno	3.9
	41168 44734				3.9
60	42590			84 novel C3HC4 type Zinc finger (ring finge	3.8
• • •	40369			C4001100°:gi[5852342]gb[AAD54015.1] (AF0	3.8 3.8
	41588		Hs.1347	11 ESTs gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	43264				3.8
65	44705 40081		115.1371	Target Exon	3.8
05	4413		5 Hs.4683		3.8
	4166	64 H72780	Hs.202	B9 ESTs	3.8 3.8
	4260			290 ESTs	3.8
70	4556		ZU	gb:RC4-BT0311-241199-012-c08 BT0311 Homo 66 ets variant gene 1	3.8
70) 4190 4450		Hs.895 7 Hs.344		3.8
	4572			99 ESTs, Wealthy similar to S51797 vasodilat	3.8
	4200		32 Hs.164	039 ESTs, Moderately similar to 138022 hypot	3.8
	4280	60 AA4206		483 ESTs	3.7 3.7
75					3.7
	4530 4049		5 115.20	Target Exon	3.7
	447		408 Hs.15		3.7
_	453	438 AI4699	35 Hs.22	792 ESTs	3.7 3.7
86					3.7
	458			ESTs	3.7
		660 M7908: 188 Al3629			3.7

	430744			STS	3.7 3.7
	454392 454457	BE260893 AW753456	Hs.236131	omeodomain-interacting protein kinase 2 p:QV2-CT0261-261099-011-d11 CT0261 Homo	3.7
_	435095	AA021160	Hs.4750	hypothetical protein OKFZp564K0822	3.7 3.7
5	438206	AA780385 NM_001725		ESTs pactericidal/permeability-increasing pro	3.7
	418967 427809	M26380	Hs. 180878	Spoprotein Spase	3.7 3.7
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116 gb:HSC1FC021 normalized infant brain cDN	3.7
10	413986 438898	Z43567 AIB19863	Hs.106243	ESTs	3.7
10	418483	W26076	Hs.221847	ESTs	3.7 . 3.6
	415849	R20529 T06430	Hs.6806 Hs.6194	ESTs chondroitin sulfate proteoglycan BEHAB/b	3.6
	438380 440296	030829	Hs.180610	splicing factor proline/glutamine rich (3.6
15	438025	AW501360	Hs.258910	ESTs	3.6 3.6
	458970 448002	AW246119 Y15227	Hs.25300 Hs.20149	phosphatidylinositol 4-kinase type II deleted in lymphocytic teukemia, 1	3.6
	432058	AW665996	Hs.130729	ESTS, Weatly similar to ALU1_HUMAN ALU S	3.6 3.6
20	409557	BE182896	Hs.211193 Hs.190488	ESTs Homo sapiens, Similar to nuclear localiz	3.6
20	418049 425331	AA211467 AW962128	MS.13U400	ob:EST374201 MAGE resequences, MAGG Homo	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6 3.6
	404185	AA644142	Hs.7107	Target Exon ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.6
25	427517 421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.6 3.6
	440388	AI693520	Hs.223000	ESTs phospholipase A2, group iB (pancreas)	3.6
	415934 408292	NM_000928 AW178363	Hs.992	gb:RC3-HT0105-010999-002-H06 HT0105 Homo	3.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.6 3.6
30	451826	AA020741	Hs.171611 Hs.177536	ESTs metallocarboxypeptidase CPX-1	3.6
	427375 419485	AL035460 AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.6
	416370	N90470	Hs.203697	ESTs. Wealdy similar to 138022 hypotheti	3.6 3.6
35	418400 436674	BE243026 AA725002	Hs.301989 Hs.272018	KIAA0246 protein low molecular mass ubiquinone-binding pr	3.5
33	407013	U35637	, 4	qb:Human nebutin mRNA, partial cds	3.5 3.5
	403108	A14.40000	Hs.222120	ENSP00000241415*:Hypothetical 67.7 kDa p ESTs	3.5
	422564 450297	Al148008 AW901347		hypothetical protein FLJ23342	3.5
40	436338	W92147	Hs.11839		3.5 3.5
	447458 457364		Hs.15896	ESTs gb:EST383123 MAGE resequences, MAGK Homo	3.5
	458814		Hs.17086	ESTs, Weakly similar to Z195_HUMAN ZINC	3.5 3.5
45	441701		Hs.12749		3.5
45	405558 452682		Hs.9071	Target Exon progesterone membrane binding protein	3.5
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.5 3.5
	443282 405183		Hs.13291	7 ESTs NM_016358":Homo sapiens iroquois homeobo	3.5
50	41006		Hs.19546	4 filamin A, alpha (actin-binding protein-	3.5 3.5
	42523		5 Hs.1659	9 ESTs, Wealdy similar to 138022 hypotheti Target Exon	3.5
	40427 42880		7 Hs.1887	O ESTs	3.5
	44744	4 AK000318			3.5 3.4
55	45047 45445			15 ESTs gb:QV3-CT0192-211099-008-g02 CT0192 Homo	3.4
	40037	9 NM_0184	32	Horno sapiens ovarian cancer related prot	3.4 3.4
	44094				3.4
60	44961 44566		Hs.2823	86 ESTs	3.4 3.4
	4458		Hs.8190 Hs.1697		3.4
	4375 4429				3.4
,,	4511	30 A1762250) Hs.345		3.4 3.4
65	4547 4592		29 Hs.301		3.4
	4337		52 Hs.112	'18 ESTs	3.4 3.4
	4449		Hs.250	xanthene dehydrogenase hypothetical protein from EUROtMAGE 2168	3.4
70	4397 4409		7 Hs.142	979 ESTs	3.4
, ,	4477	26 AL1376		68 matrilin 2	3.4 3.4
	4038 4224		83 Hs.116	Target Exon 385 hypothetical protein FLJ 10521	3.3
-	439	533 W76021	1	gb:zd64c04.r1 Soares_fetal_heart_NbHH19W	3.3 3.3
7:	5 416	422 H60457		ESTs, Moderately similar to ZN91_HUMAN Z 313 ESTs	3.3 3.3
	441 432	668 A161197 890 NM_01		751 siatic acid binding Ig-like lectin 8	3.3
	412	135 AW895	309	gb:QV4-NN0038-300300-155-e07 NN0038 Hor	no 3.3 3.3
8	0 417	130 AW276 854 AW138			3.3
0		048 BE281)408 ESTs, Moderately similar to A47582 B-cel	3.3 3.3
		632 565 AW851	1728	NM_022490:Homo sapiens hypothetical prol gb:MR2-CT0222-011199-007-d06 CT0222 Hor	
	411	565 AW851			

	436267	AW450938	Hs.180115 E	STs	3.3
				erologically defined colon cancer antig	3.3
	401272			29000559*:gij12314195 emb CAB99338.1 (A	3.3
_	433128	AB021923		ST-YO1 protein	3.3 3.3
5	401702			IM_001171*:Homo sepiens ATP-binding cass	3.3 3.3
	454363			rypothetical protein FLJ12973 ESTs	3.3
	440332	AI218517 AW807321	ns.100031 t	b:MR4-ST0062-240300-003-g05 ST0062 Hamo	3.3
	454177 423784	AK000039	Hs.132826	forno sepiens cDNA FLJ14913 fis, clone PL	3.3
10	440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	3.3
	410267	AW978005	Hs.12600	N-ethylmaleimide-sensitive factor attach	3.3
	455778	BE088746	9	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3 3.2
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.2 3.2
1.6	451597	AW295250		ESTs hypothetical protein MGC2628	3.2
15	451446	A1826288		ESTs	3.2
	421353 442710	AW292857 At015631		ESTs	3.2
	420560	AW207748		EST8	3.2
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2
20	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo saplens	3.2 3.2
	430694	AA810624	Hs.30936	ESTs, Wealdy similar to H2BH_HUMAN HISTO	3.2 3.2
	412021	AW885592	Hs.20654	gb:RC4-OT0071-090300-011-g11 OT0071 Homo ESTs	3.2
	443431 445774	A1056847 A1254165	Hs.20034 Hs.339968	ESTS	3.2
25	413335	AI613318	Hs.48442	ESTs	3.2
20	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.2
	411571	BE049094		ESTs	3.2
	404592			NM_022739*:Homo saptens E3 ubiquitin lig	3.2 3.2
20	402747			Target Exon	3.2
30	428600	AW863261	Hs.242413 Hs.127573	hypothetical protein DKFZp434K1421 Homo sepiens FKSG41 (FKSG41) mRNA, compl	3.2
	420300 445347	AA258245 AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	3.2
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.2
	442314	AJ311854	Hs.129220	ESTs	3.2
35	435291	BE568452	Hs.344037	protein regulator of cytokinesis 1	3.2
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	3.2 3.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.2
	403291	AI825420	Hs.197824	Target Exon ESTs	3.2
40	436210 418079	R40058	Hs.6911	ESTs	3.2
70	413951	AW051200	Hs.75640	natriuretic peptide precursor A	3.2
	435828	AA700705	Hs.13852	ESTs	. 3.2
	437722	AW292947	Hs.122872	ESTs, Wealdy similar to JU0033 hypotheti	3.2
40	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.2 3.1
45	405046	202000	20020	C3000978:gij9280045 dbj BAB01579.1 (AB0 ESTs	3.1
	444315 453096	R07860 AW294631	Hs.20039 Hs.11325	ESTS ESTS	3.1
	433835	A1806185	113,11020	gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.1
	430608	R45584	Hs.23025	ESTs. Weakly similar to ALUS_HUMAN ALU S	3.1
50	453324	W26592	Hs.232089	ESTs	3.1
	414884	R54418	Hs.183745		3.1 3.1
	446862	AV660697	Hs.282700		3.1
	427241	AA399988 H81336	Hs.112087 Hs.37560	ESTs	3.1
55	416486 429940		12.01000	gb:zb87a09.r1 Soares_senescent_fibroblas	3.1
	430535			gb:EST380561 MAGE resequences, MAGJ Horno	3.1
	439544		Hs.28891	hypothetical protein FLJ11350; artemis p	3.1
	437083				3.1 3.1
60	435677		Hs.293726		3.1
00	458810 443484		Hs.231510 Hs.134559		3.1
	427581				3.1
	444016			gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
	423337			7 axin 2 (conductin, axii)	3.1
65	403288			C1001737":gi[7511201[pir]]T27904 hypothe	3.1 3.1
	45012				3.1
	43813		Hs.17750		3.1
	43622		Hs.12281 Hs.30166		3.1
70	44343 44372			growth arrest and DNA-damage-inducible,	3.1
, ,	43204			gb:EST384819 MAGE resequences, MAGL Homo	3.1
	40576	0		Target Exon	3.1
	42378	9 AK002084			31
75	41160				3.1 3.1
75					3.1
	44924				3.1
	42952 45664				3.1
_	41249				3.1
80	4216	79 AI475110	Hs.2039	33 ESTs	31
	43450	D3 T96231	Hs.1776	2 ESTs	3.1
	4507				3.1 3.0
	4152	93 R49462	Hs.1065	41 ESTs	3.0

	403212			NM_019595:Homo sapiens intersectin 2 (IT	3.0
	422757	AI909935	Hs.65551	Horno sepiens, Similar to DNA segment, Ch	3.0
	427624	AA406245	Hs.24895	ESTs	3.0
5	449256	AA059050	Hs.59847	ESTs	3.0
,	411543 409112	AW851248 BE243971	He EDGAD	gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	414403	AW969551	Hs.50649 Hs.76064	quinone oxidoreductase homolog	3.0
	427418	AA402587	Hs.325520	ribosomal protein L27a	3.0
	455481	AW948317	113.323320	LAT1-3TM protein gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
10	444396	T65213	Hs.4257	ESTs	3.0 3.0
	407235	020569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	451391	AAD17410	Hs.40568	ESTs	3.0
	430251	AA609246	Hs.181451	ESTs .	3.0
15	420658	AW965215	Hs.130707	ESTs	3.0
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	3.0
	440897	AW104275	Hs.148348	ESTs	3.0
	444609	AW571659	Hs.278081	ESTs	3.0
	433062	AK001757	Hs.281348	hypothetical protein FU10895	3.0
20	408523	AW833259	Hs.314287	ESTs	3.0
	443477	R32325	Hs.221794	ESTs .	3.0
	423869	BE409301	Hs.134012	C1q-related factor	3.0
	405488			ENSP00000220888*:ZINC FINGER TRANSCRIPTI	3.0
25	414988	C17535		gb:C17535 Human placenta cONA (TFujiwara	3.0
25	440471	AA886146	Hs.307944	ESTS	3.0
	416355	H49875	Hs.268906	ESTs	3.0
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.0
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 ffs, clone Y7	2.9
30	438201	AA780243	Hs.54647	EST8	2.9
50	413851 402229	AW897510 BE262804	Hs.137387	ESTs	2.9
	444145	BE153823	U- 202205	mitochondrial ribosomal protein S2	2.9
	423770		Hs.282385	ESTs, Weakly similar to 2004399A chromos	2.9
	439627	AW976766 BE621702	Hs.132776 Hs.29076	Homo sapiens cDNA FLJ10077 fis, clone HE	2.9
35	414232	W86946	Hs.238246	hypothetical protein FLJ21841	29
-	400533	***********	15.230240	hypothetical protein FLJ22479	29
	440483	A1200835	Hs.150386	ENSP00000209376*:PRED65 protein (Fragmen ESTs	2.9
	443502	AI074528	Hs.133949	ESTS	2.9
	449667	AB023227	Hs.23860	KIAA1010 protein	2.9 2.9
40	446809	AW590171	Hs.101413	ESTs	2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-102O5 from Y	2.9
	413627	BE182082	Hs.246973	ESTs	2.9
	449655	AI021987	Hs.59970	ESTs	2.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.9
45	400090			Eas Control	2.9
	454968	AW849046		gb:fl.3-CT0214-150300-085-H06 CT0214 Homo	2.9
	423352	AA324808	Hs.193576	ESTs	2.9
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.9
50	452102	U04343	Hs.27954	CD85 antigen (CD28 antigen ligand 2, B7-	2.9
50	415346	Z43108		gb:HSC13E071 normalized infant brain cDN	2.9
	435726	AA324975	Hs.198689	ESTs, Wealdy similar to T00079 hypotheti	2.9
	442513	AF 150207	Hs.207949	ESTs .	2.9
	425012	177666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	29
55	402322 427235	A1426200	11- 400000	Target Exon	2.9
55	456412	AI126288	Hs.192232	ESTs TOSA total and the second	2.9
	431196	AW749617 AW974436	Hs.280776 Hs.154929	tankyrase, TRF1-interacting ankyrin-rela	2.9
	439379	AA835002	Hs.125611	ESTs ESTs	2.9
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	2.9
60	446134	AW161234	Hs.13993	TBP-like 1	2.9
	435645	AI052789	Hs.133263	ESTa	2.9 2.9
	449385	AI650471	Hs.347290	ESTs	2.9
	444161	N52543	Hs.142940	ESTs	2.9
	406635	U07162		gb:Human clone LNA11 autoantibody to hea	2.9
65	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, ctone C	2.9
	458760	AJ498631	Hs.111334	ferritin, light polypeptide	2.9
	427245	AA421022	Hs.97739	ESTs	2.9
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	2.9
70	430701	AI760833	Hs.293971	ESTs	2.9
70	435294	T84084	Hs.196008		29
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.9
	446160	AW392197	Hs.218003	ESTs .	2.9
	420674	NM_000055	Hs.1327	butyrylcholinesterese	29
75	424330	AW073953	Hs.333396		2.9
13	418915	A1474778	Hs.118977		2.9
	425922	AL157466	Hs.162751		2.9
	447512	AW958148	Hs.129454		2.9
	449990	AJ279010 AVA071837	Hs.48821	ESTS	2.8
80	423779 427395	AW071837 AW298741	Hs.57971	ESTs	2.8
	416188	BE157260	Hs.97861	ESTs, Moderately similar to 138022 hypot	2.8
	426745	J03626	Hs.79070 Hs.2057	v-myc avian myelocytomatosis viral oncog	2.8
	400352	AF068294	Hs.272414	uridine monophosphate synthetase (crotat Homo sapiens HDCMB45P mRNA, partial cds	2.8
	70002	THE SHOPPING	15.41414	Latrice archeria Litzouranas, Litzurar bautai cos	2.8

	457579	AB030816	Hs.36761 I	(RAS-like suppressor	2.8
			Hs.267150 I	QAA1409 protein	2.8 2.8
	403903			25001632*:gij10645308 gb AAG21430.1 AC00	2.8
5	444491 455899	AI151091 BE155112	Hs.270714	EST8 pb:PM1-HT0350-151 299-0 03-a03 HT0350 Homo	2.8
,	457292	A1921270	Hs.281462	hypothetical protein FLJ14251	28
	428305	AA446628	Hs.2799	cartilage linking protein 1	2.8 2.8
	435375	AI733610		ESTs	2.6 2.8
10	409078	AW327515		ESTs hypothetical protein MGC15729	2.8
10	436109 444656	AA922153 AJ277924		ESTs	2.8
	426384	AJ472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	28
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	2.8 2.6
15	438243	AI581311	Hs.186256	ESTs ESTs	28
15	434012 402711	AA621425	ns.100230	Target Exon	2.8
	442955	AI683534	Hs.131583	ESTs	2.8
	418319	AW611703	Hs.190173	ESTs, Wealtly similar to A46010 X-linked	28
~~	438934	BE220137	Hs.124323	ESTs	2.8 2.8
20	438689	AW129261 AA478847	Hs.181672 Hs.42484	ESTs hypothetical protein FLJ10618	2.8
	420083 400315	U46120	Hs.193392	Human expressed unknown mRNA	2.8
	433563	AI732637	Hs.277901	ESTs	2.8
	458093	AJ207788	Hs.343628	sialytransferase 48 (beta-galactosidase	2.8 2.8
25	409157	AA064631	LL- 207077	gb:z/72c03.s1 Soares_pineal_gland_N3HPG ESTs	2.8
	450597 425300	AI701635 AW601773	Hs.207077 Hs.270259	ESTs	2.8
	458817	Z25900	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.8
	418312	AW972468	Hs.170307	Ral guanine nucleotide exchange factor R	2.8 2.8
30	430335	D80007	Hs.239499	KIAA0185 protein gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	454581 419735	AW809189 AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	2.8
	436265	AA731331	Hs.190668	ESTs	2.8
	439481	AF086294	Hs.125844	ESTs	2.8
35	441964	AA972619	Hs.20506	ESTs. Wealdy similar to 138022 hypotheti	2.8 2.8
	422648 430503	D86983 AA533574	Hs.118893 Hs.152274	Melanoma associated gene ESTs	2.8
	403942	AAGGGGG/4	115.152214	Target Exon	2.8
	420565	AI806770	Hs.30258	ESTs	2.8
40	439069	H63144	Hs.184178	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.8 2.8
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel KIAA1708 protein	2.8
	408137 451692	A1694131 AL137422	Hs.29002 Hs.26849	Homo saplens mRNA; cDNA DKFZp761A1623 (f	2.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	2.8
45	452526	W38537	Hs.280740		2.8 2.8
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	405941	742.0.02	12	Target Exon	2.7
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	450651	W79000	Hs.44545 Hs.172108	ESTs, Weakly similar to B34087 hypotheti nucleoponin 88kD	27
	426765 418886	AA743603 AA993982	Hs. 130856		2.7
	429483		Hs.12870		2.7
55	430426	AA478807	Hs.12517		2.7 2.7
	439019		Hs.27173	7 EST6 Target Exon	2.7
	400924 458070		Hs.20940		2.7
	427299				2.7
60	442621	Al004333	Hs.13055	3 ESTs, Weakly similar to ALUA_HUMAN !!!!	2.7 2.7
	437643			gh:Homo sapiens mRNA full length insert 9 Homo sapiens cDNA: FLJ22373 fis, clone H	27
	426925 443397		98 Hs.31568 Hs.29342		2.7
	42997		Hs.23451		2.7
65	438879	5 AA827640			2.7 2.7
	42255			gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	44613		Hs.39749 3 Hs.2890		2.7
	42911 42861				2.7
70	43994			astrotactin	2.7
· -	43969	9 AF08653	4 Hs.1875		2.7 2.7
	43833				2.7
	45668 41207		Hs.7313		2.7
75	41222			gb:QV0-NN1022-170400-193-c02 NN1022 Homo	27
	43880	1 AA82597	'1 Hs.1242		2.7
	44289				2.7 2.7
	43299		15 Hs.2798	165 trans-prenyltransferase NM_001334*:Homo sapiens eathepsin O (CTS	27
80	40379 4003		Hs.2480		2.7
-	4154		Hs.2602	274 ESTs	2.7
	4287	15 AW2937			2.7 2.7
	4577	50 AI65147	4 Hs.163	944 ESTs	2.1

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				ESTs hypothetical protein FLJ23109	2.7 2.7
	444822 432651			ESTs	2.7
_	439823	AW665287	Hs.124514	ESTs	2.7 2.7
5	457021			Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	440026 446960			ESTs ESTs	2.7
	435046		Hs. 174330	ESTs, Wealty similar to ALU1_HUMAN ALU S	2.7
	431999	AL133573		Homo sepiens mRNA; cDNA DKFZp434J2235 (I	27 27
10	458527		Hs.224875	ESTs	27
	445899 404254	AI263738	Hs_145626	ESTs ENSP0000082468*:DJ45P21.3 (butyrophilin	2.7
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	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	2.7 2.7
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20	403431			Target Exon	2.7
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	435143 416569	H64891	ns.134000	gb:yr68h03.r1 Soares fetal liver spieen	2.7
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25	425128	BE561929	Hs.154718	tumor protein 052-like 2 ESTs	2.7
25	443361 404053	AJ792628	Hs.133273	Target Exon	2.7
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30	413098 444884	BE065279 AI201094	Hs.148540	gb:RC1-BT0314-030500-016-b09 BT0314 Homo ESTs	2.6
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	423234	AA323534	Hs.296162	AD037 protein	2.6 2.6
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35	428670 408371	AA431682 AF161545	Hs.134832 Hs.44439	ESTs hypothetical protein	2.6
33	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	2.6
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45	430147 425480	R60704 AB023198	Hs.158135		2.6
73	407182	AA312551	Hs.230157	ESTs	2.6
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55	400780)		NM_007325":Homo sapiens glutamate recept	2.6 2.8
	429258			gb:zx10e09:r1 Soares_total_fetus_Nb2HF8_ gb:UI-H-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su	2.6
	448970 40261			C1003844*:gi[6912550]ref[NP_036483.1] ol	2.6
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	41258 44363		Hs.1342		2.6
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65	43325		Hs.2073		26
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	44521			48 ESTs, Wealdy similar to YC18_HUMAN HYPOT	2.6
	40442	23		C8000067*:gij10432400jembjCAC10290.1j (A	2.6 2.6
70		3 AI767087	Hs.1141 Hs.1197		2.6
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	4502	02 AW9697		45 ESTs, Weakly similar to B49647 GTP-bindi	2.6
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	443021	AA368546	Hs.8904	lg superfamily protein	2.6
	427005	AA394228	Hs.97494	ESTs	26
	437085 408603	AA743935 R25283	Hs.202329 Hs.326416	ESTs Homo saplens mRNA; cDNA DKFZp564H1916 (f	2.6 2.6
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42	455276 416665	BE 176479 H72974		gb:RC3-HT0585-160300-022-b09 HT0585 Homo gb:yu28a10.s1 Soares fetal tiver spleen	2.5 2.5
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55	422752 413786	BE247253 AW613780	Hs.21263 Hs.13500	suppressor of potassium transport defect ESTs	2.5 2.5
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.5
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                                                                                               15739-15951,16165-16779
                      402229
                                           9965022
                                                                      Minus
                                           2935596
                      402274
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                                                                                               5604-6527
                                            7630359
                                                                      Minus
                                                                                              75078-75203
76812-79040
                      402322
                      402344
                                           8099256
                                                                      Mirus
                                                                                               37870-37923,39664-39717,71711-71764
                      402595
                                            7705171
                                                                      Plus
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                      402604
402605
                                           9909420
9909420
                                                                      Plus
                                                                                               20393-20767
47680-47973
                                                                      Minus
                                            9926801
8901247
                                                                                               131390-132157
114306-115418
                                                                      Plus
                       402711
                                                                      Minus
                                                                                                7105-7357
59763-59909
                       402747
                                            9212492
                                                                       Minus
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                                            9882953
                       402855
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                        402936
                                                                                                51655-51771
                       402981
403108
                                             9944246
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Minus
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156037-156210
                                             8980955
                                             7630897
                        403212
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19288-20076
                                             8081479
                        403288
                                            8083176
7230870
                        403290
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                        403291
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                        403349
403431
                                             8569773
7139839
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                                             9965004
3135242
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                                              8084957
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                         403790
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                          403849
                                              7708855
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99606-99757
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                                              7711825
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61797-64205
                          403961
                                               7596976
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                                               7342152
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                                              4572584
9367203
                          404185
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Plus
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83207-83355,84358-84496,90519-90720,91371-91447
                          404254
                                               9885189
7407959
                          404272
                                                                                                   34438-34618
                          404423
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                           404584
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4373-4528
                           404632
                                                9796668
                           405046
                                                7596829
                           405183
                                                                                                    12335-12653
                           405238
405239
                                                7249119
                                                                                                   51728-51836
                                                                           Minus
                                                                                                   144345-144464, 144690-144836, 151750-151883, 152407-152484
43310-43462
                                                7249119
       70
                           405348
405488
                                                2914717
7131455
                                                                           Minus
                                                                                                    75771-75883,105295-105398,134754-134875
4502-4644,5983-6083
                                                                           Minus
                           405558
405717
                                                1621110
9588573
                                                                           Plus
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                            405760
                                                6056938
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                                                                                                    37424-38045
       75
                                                7657810
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                                                                           Plus
                            405863
                            405941
                                                6758796
9256242
                                                                           Plus
                                                                                                    2798-3444
20805-20960
                            406395
                                                                            Mirus
                                                                                                     68314-68523,68853-68950
                            406478
                                                 9857502
                                                                                                     91439-91579
                                                    9864741
                            406481
        80
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TABLE 13A: 964 GENES UP-REGULATED IN LOWER GRADE GUOSLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59660 probasets on the
Allymetric/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG tevel was set to the 85h

PCT/US02/29560 WO 03/025138

percentite amongst various LGG tumors. The "average" normal tissue level was set to the 85° percentile amongst various non-malignant adult tissues. In order to remove genespecific background levels of non-specific hybridization, the 10° percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the
denominator before the ratio was evaluated.

Unique Eos probeset identifier number
Exacon: Exemplar Accession number, Genbank accession number
UniquelD: Unique number
Unique Title: Unique gene title
R1: Ratio of LOWER GRADE GLIOBLASTOMA to NORMAL ADULT TISSUES

5

	KI.				
10	Pkey	ExAcon	UnigenelD	Unigene Tide	R1
10		AI880044	H= 176977	aratein kinase C binding protein 2	67.6
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	58.2 53.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, ZXV	53.8 50.6
	431917	D16181	Hs.2868	peripheral myelin protein 2	48.3
15	428321	AI699994	Hs.2868	peripheral myelin protein 2	44.3
	426325	O28114	Hs.169309	myelin-associated oligodendrocyte basic	44.2
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (I	43.8
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	40.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-1	40.1
20	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	38.8
	417183	R52089	Hs.172717	ESTs	36.8
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	34.9
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	34.4
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015 G protein-coupled receptor 51	34.2
25	429276	AF056085	Hs.198612	myelin oligodendrocyte glycoprotein	33.9
	424140	Z48051	Hs.141308	ESTs	33.8
	450133	AW969769	Hs.105201 Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (I	32.8
	423849	AL157425	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
20	413333	M74028 AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	31.3
30	449494	AW23/014	16.51000	Target Exon	30.3
	402604	AA984472	Hs.74554	KIAA0080 protein	28.8
	412733	AB013805	Hs.80220	catenin (cadherin-associated protein), d	28.2
	416829	AI031540	Hs.235331	ESTs	27.9
35	439239 444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	27.1
22	439415	F05538	Hs.4273	ESTs	· 26.2
	425048	H05468	Hs.164502	ESTs	25.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	25.3
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	24.0 23.5
40	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein.	23.5
-10	447359	NM_012093	Hs.18268	adenylata kinase 5	23.2
	425842	AI587490	Hs.159623	NK-2 (Drosophila) hornolog B	23.2
	423853	AB011537	Hs.133466		22.9
	435708	AI362949	Hs.75169	ESTs	21.6
45	437268	A1754847	Hs.22757		21.1
	409395	U46745	Hs.33667	B dystrobrevin, alpha	20.4
	441285	NM_00237		microtubule-associated protein 2	20.0
	422656	AI870435	Hs.1569	LIM homeobox protein 2	19.7
	425523	AB007948	Hs.15824	4 KIAA0479 protein	19.5
50	437204	AL110216	Hs.22826		19.4
	416370	N90470	Hs.20369		19.3
	441497		Hs.23172		19.1
	453392		Hs.32964 Hs.21929		18.9
55	408604				18.8
23	413597		Hs.7672	CCAATenhancer binding protein (C/EBP),	18.8
	422980 428392		Hs.2255	secretory granute, neuroendocrine protei	18.6
	429466		Hs.1282	7 FSTR	18.2
	448307		Hs.1829		18.2
60	439199		Hs.2629		17.4
00	44874				17.4
	41833			4 neuronal pentraxin I	17.3 17.2
	44451			glutamate receptor, ionotropic, AMPA 1	17.1
	44478			aniilin (Drosophila Scraps homolog), act	16.8
65	44700			i39 ESTs	16.5
-	42598				16.1
	44867	2 AI955511	l Hs.225		15.8
	45237	2 AI885742	2 Hs.228		15.7
	42412	O T80579	Hs.290	270 ESTs	15.6
70) 42458	31 M62062	Hs.150	917 caterin (cadherin-associated protein), a	15.4
	42479	90 AL11934		26 ESTs, Wealdy similar to 2004399A chromos	15.2
	4262		Hs.168	950 Homo sapiens mRNA; cDNA DKFZp566A1046 (I	15.2
	4466			Homo sapiens mRNA for KIAA1763 protein.	14.9
-	4536				14.7
7:					14.6
	4414				14.6
	4299			22 Boggyrans cyclesic o (ordan) 06 ESTs	14.4
	4158			7754 hypothetical protein FLJ22202	14.2
8	A181	10 R43523			14.0
ō					14.0
	4096				13.9
	441; 415;				13.7
	410	(414.70)		216	

	424945	AI221919		hunathatical contrib FL 146502	42.0
	426344	H41821	Hs.322469	hypothetical protein FLJ10582 transcriptional activator of the c-tos p	13.6 13.4
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	13.3
_	429946	R49390	Hs.254129	KJAA1678	13.3
5	444119 438380	R41231 T06430	Hs.184261 Hs.6194	ESTs, Weakly similar to T26686 hypotheti	13.3
	415910	U20350	Hs.78913	chondraitin sulfate proteoglycan BEHAB/b chemokine (C-X3-C) receptor 1	13.2 13.2
	412266	N59006	Hs.26133	ESTs	13.2
10	43687B	BE465204	Hs.47448	EST8	13.1
10	428536	Al143139	Hs.2288	visinin-like 1	13.1
	425649 428982	U30930 NM_005097	Hs.158540 Hs.194704	UDP glycosyttransferase 8 (UDP-galactose	13.1
	437948	AA772920	Hs.303527	leucine-rich, glioma inactivated 1 ESTs	13.0 13.0
	444124	R43097	Hs.6818	ESTs	12.9
15	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.7
	419249 412959	X14767 D87458	Hs.89768 Hs.75090	gamma-aminobutyric acid (GABA) A recepto	12.7
	419863	AW952691	Hs.93485	KIAA0282 protein Homo sapiens mRNA, cDNA DKFZp761D191 (fr	12.6 12.6
•	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	12.6
20	431019	NM_005249	Hs.2714	forkhead box G18	12.4
	420547	AF1\$\$140	Hs.98738	gonadotropin-regulated testicular RNA he	12.4
	430091 448595	AB032958 AB014544	`Hs.233023 Hs.21572	KIAA1132 protein KIAA0644 gene product	12.4 12.2
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.2
25	409049	AI423132	Hs.146343	ESTs	12.0
	421264	AL039123	Hs.103042	microturbule-associated protein 18	11.9
	451952 411305	AL120173 BE241596	Hs.301663 Hs.69547	ESTs myelin basic protein	11.9
	433551	AI985544	Hs.12450	protocadherin 9	11.8 11.6
30	431988	AC002302	Hs.77202	protein kinase C, beta 1	11.6
	415170	R44386	Hs.164578	ESTs	11.5
	408562 435501	AI436323	Hs.31141	Horno sapiens mRNA for KIAA1568 protein,	11.4
	429656	AW051819 X05608	Hs.129908 Hs.211584	KIAA0591 protein neurofilament, light polypeptide (68kD)	11.4 11.1
35	423419	R55336	Hs.23539	ESTs	11.1
	424432	AB037821	Hs.146858	protocadherin 10	10.9
	433896	AW294729	Hs.274461	ESTs	10.9
	415293 447101	R49462 N72185	Hs.106541 Hs.44189	ESTs ESTs	10.9
40	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	10.9 10.9
	438054	AA776626	Hs.169309	ESTs	10.8
	433597	AA708205	Hs.100343	ESTs	10.7
	421659	NM_014459	Hs.106511	protocadherin 17	10.6
45	445102 425154	AW204610 NM_001851	Hs.22270 Hs.154850	EST8	10.6
75	451625	R56793	Hs.106576	collagen, type tX, alpha 1 alanine-glyoxylate aminotransferase 2-li	10.6 10.6
	435191	R15912	Hs.4817	Homo sepiens clone 24461 mRNA sequence	10.6
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	10.5
50	407886 420345	AW969688 AW295230	Hs.100826	ESTS	10.4
50	428728	NM_016625	Hs.25231 Hs.191381	ESTs hypothetical protein	10.4 10.3
	424997	AL138167	Hs.96920	ESTs .	10.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	10.2
55	419078	M93119	Hs.89584	insulinoma-associated 1	10.2
75	445495 416857	8E622641 AA188775	Hs.38489 Hs.292453	ESTs, Wealdy similar to (38022 hypotheti ESTs	10.1
	445041	T64183	Hs.282982	solute carrier	10.0 10.0
	419271	N34901	Hs.238532	ESTs	9.8
60	446711 426847	AF169692	Hs.12450	protocadherin 9	9.8
00	420047	S78723 AA761526	Hs.298623 Hs.163853	5-hydroxytryptamine (serotonin) receptor ESTs	9.7
	418097	R45137	Hs.21868	ESTs	9.7 9.7
	449300	A1656959	Hs.346514	EST ₅	9.7
65	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	9.7
UJ	443785 415486	AW449952 H12214	Hs.190125 Hs.13284	basic-helix-loop-helix-PAS protein	9.5
	453220	AB033089	Hs.32452	ESTs, Wealdy similar to 2109260A B cell Homo saplens mRNA for KIAA1263 protein,	9.5 9.5
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.4
70	424028	AF055084	Hs.153692		9.4
70	419683	AA248897	Hs.48784	ESTS	9.4
	414175 400292	AJ308876 AA250737	Hs.103849 Hs.72472	hypothetical protein DKFZp761D112 BMP-R1B	9.2
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	9.2 9.2
76	454048	H05626	Hs.6921	ESTs	9.2
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.1
	441016	AW138653	Hs.25845	ESTs	9.0
	425187 445568	AW014486 H00918	Hs.22509 Hs.268744	ESTs KJAA1796 protein	9.0 8.9
~~	453941	U39817	Hs.36820	Bloom syndrome	8.9
80	422411	AW749443	Hs.22511	ESTs	8.8
	447350	AI375572	Hs.172634		8.8
	424481 448902	R19453 Z45998	Hs.1787 Hs.22543	proteolipid protein 1 (Pelizaeus-Merzbac Homo sapilens mRNA; cDNA DKFZp761I1912 (f	8.7
	-10302	2-10000		recoverable inches, control District 1915 (t	8.7

	448986	H42169	Hs.347310	houseth offered months for the second	
	423135	N67655	Hs.26411	hypothetical protein FLJ14627 ESTs	8.6
	418030	BE207573	Hs.83321	neuromedin B	8.5 8.4
_	448769	N66037	Hs.38173	ESTs	8.4
5	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	8.3
	400293 415279	N51002 F04237	Hs.306480 Hs.1447	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	8.3
	451516	AI800515	Hs.12024	glial fibrillary acidic protein ESTs	8.2
	419629	AB020695	Hs.91662	KIAA0888 protein	8.2 8.2
10	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GC81 Homo sapiens	8.2
	456965	AW131888	Hs.172792	ESTs. Weakly similar to hypothetical pro	8.1
	417417 452279	F05745 AA286844	Hs.89512 Hs.61260	ATPase, Ce transporting, plasma membrane	8.1
	422864	AA318323	Hs.12827	hypothetical protein FLJ13164 gb:EST20390 Retina II Homo sapiens cDNA	8.1
15	452526	W38537	Hs.280740	hypothetical protein MGC3040	8.1 8.0
	435793	AB037734	Hs.4993	KIAA1313 protein	7.9
	415669 407168	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	7.9
	447414	R45175 D82343	Hs.117183 Hs.74376	ESTs neuroblastoma (nerve tissue) protein	7.9
20	442710	AI015631	Hs.23210	ESTs	7.8 7.8
	416836	D54745	Hs.80247	cholecystokinin	7.8
	419721	NM_001650	Hs.288650	aquaporin 4	7.7
	438080 436109	AA777381 AA922153	Hs.291530 Hs.132760	ESTs, Wealty similar to ALUC_HUMAN !!!!	7.7
25	428845	AL157579	Hs.153610	hypothetical protein MGC15729 KIAA0751 gene product	7.7 7.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coti like	7.7
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	7.6
	443392 429038	AI055821 AL023513	Hs.293420 Hs.194766	ESTs	7.6
30	418738	AW388633	Hs.6682	seizure retated gene 6 (mouse)-like solute carrier family 7, (cationic amino	7.5 7.5
	423361	AW170055	Hs.47628	ESTS	7.5 7.5
	447198	D61523	Hs.283435	ESTs	7.5
	448555 458332	AI536697 AI000341	Hs.159863 Hs.220491	ESTs ESTs	7.5
35	407034	U84540	110.220431	gb:Human dystrobrevin isoform DTN-3 (DTN	7.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	7.4 7.4
	426814 448507	AF036943 AL133109	Hs.172619	myelin transcription factor 1-like	7.4
	439845	AL355743	Hs.21333 Hs.56663	Homo sapiens mRNA; cDNA DKFZp566N1047 (f Homo sapiens EST from clone 41214, full	7.4
40	449078	AK001256	Hs.22975	KIAA1576 protein	7.4 7.3
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	7.2
	425741 440210	AF052152 AW674562	Hs.159412 Hs.125296	Homo sapiens clone 24628 mRNA sequence ESTs	7.2
	415651	AI207162	Hs.3815	stathmin-tike-protein RB3	7.2
45	428409	AW117207	Hs.98523	ESTs	7.2 7.1
	413409 443992	AI638418 AW022228	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	455601	A1368680	Hs.322922 Hs.816	ESTs SRY (sex determining region Y)-box 2	7.1
60	427540	R12014	Hs.20976	ESTs	7.1 7.0
50	439979	AW500291	Hs.6823	hypothetical protein FU10430	7.0
	424893 452355	AW295112 N54926	Hs.153648 Hs.29202	Homo sapiens cDNA FLJ13303 fis, clone OV	7.0
	414696	AF002020	Hs.76918	G protein-coupled receptor 34 Niemann-Pick disease, type C1	7.0 7.0
55	440152	AB002376	Hs.7006	KIAA0378 protein	7.0
55	454293 425782	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	416805	U66468 F13271	Hs.159525 Hs.79981	cell growth regulatory with EF-hand doma	7.0
	419991	AJ000098	Hs.94210	Human ctone 23560 mRNA sequence eyes absent (Drosophila) homotog 1	7.0
60	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	7.0 6.9
60	408369 449605	R38438 AW138581	Hs.182575	solute carrier family 15 (H??? transport	6.9
	444396	T65213	Hs.198416 Hs.4257	ESTs ESTs	6.9
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	6.9 6.9
65	414245	BE148072	Hs.75850	WAS protein family, member 1	6.9
U.S	412155 424624	R38167 AB032947	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.9
	448681	AL109781	Hs.151301 Hs.21754	Ca2+dependent activator protein for secr Homo saplens mRNA full length insert cON	6.9
	411379	AI816344	Hs.12554	ESTs, Wealthy similar to NPL4_HUMAN NUCLE	6.9 6.9
70	446782	A1653048	Hs.144006	ESTs	6.8
70	426919 423346	AL041228 Al267677	Lb- 12741C	ELAV (embryonic lethal, abnormal vision,	6.8
	436643	AA757626	Hs.127416 Hs.10941	synaptojanin 1 ESTs, Wealdy similar to IPP1_HUMAN PROTE	6.8
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	6.8 6.8
75	410037	AB020725	Hs.58009	KIAA0918 protein	6.8
	442613 413589	A!004002 AW452631	Hs.130522 Hs.313803	Ky channel-interacting protein 1	6.8
	422175	N79885	Hs.6382	ESTs, Highly similar to AF157833 1 noncl ESTs, Highly similar to T00391 hypotheti	6.8 6.8
	421141	AW117261	Hs.125914	ÉST8	6.7
80	452786 441916	R61362 AA993571	Hs.106642 Hs.129075	ESTs, Weakly similar to T09052 hypotheti ESTs	6.7
-	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	6.7 6.7
	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7
	423343	AA324643	Hs.246106	ESTs	6.7

	466727	243902	Hs.4748 ;	adenytate cyclase activating polypeptide	6.7
	456723 414214	D49958	Hs.75819	pycoprotein M6A	6.7
	434811	AW971205	Hs.114280	STS	6.7
•	424922	BE386547		hypothetical protein MGC10825	6.7 6.6
5	449328 431553	AI962493 X78075		ESTs cartilage linking protein 1	6.6
	420156	AW449258		ESTs	6.6
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.6
10	422960	AW890487		cadherin 13, H-cadherin (heart)	6.6 8.5
10	429239	AA448419 R49295		ESTs ESTs	6.5
	453924 433929	AI375499		ESTs	6.5
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	6.5
	414683	S78295	Hs.76888	hypothetical protein MGC12702	6.4 6.4
15	409746	NM_004794	Hs.56294 Hs.262346	RAB33A, member RAS oncogene family ESTs, Wealdy similar to S72482 hypotheti	6.4
	419169 453590	AW851980 AF150278	Hs.33578	KIAA0820 protein	8.4
	422263	AA307639	Hs.129908	KIAA0591 protein	6.4
	421688	AK000307	Hs.106825	hypothetical protein FLJ 20300	6.4
20	447197	R36075	14- 40007	gb:yh88b01.s1 Soares placenta Nb2HP Homo	6.3 6.3
	425588 410366	F07396 A1267589	Hs.46627 Hs.302689	ESTs hypothetical protein	6.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	6.3
	445997	AA383439	Hs.16758	Spir-1 protein	6.3
25	427958	AA418000	Hs.98280	potassium intermediate/smail conductance	6.3 6.3
	445908 412068	R13580 S72043	Hs.13436 Hs.73133	Homo sapiens clone 24425 mRNA sequence metallothionein 3 (growth inhibitory fac	6.3
	452834	AI638627	Hs.105685	KIAA1688 protein	6.3
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor.	6.3
30	418512	AW498974		diacylglycerol kinase, zeta (104kD)	6.2 6.2
	410099 452744	AA081630 Al267652	Hs.246107	KIAA0036 gene product Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	6.2
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.2
35	439274	AFD86092	Hs.48372	E\$Ts	6.2 6.2
	431552	AI815863 BE540565	Hs.259873 Hs.159460	axonal transport of synaptic vesicles ESTs	6.2
	439607 408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	6.2
	412709	AL022327	Hs.74518	KIAA0027 protein	6.2
40	435624	AF218942	Hs.24889	formin 2	6.1 6.1
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1
	420077 457005	AW512260 AJ007421	Hs.87767 Hs.172597	ESTs sal (Drosophila)-like 3	6.1
	440471	AA886146	Hs.307944	ESTS	6.1
45	423770	AW976766	Hs.132776	Homo sepiens cDNA FLJ10077 fis, clone HE	6.1
	438624	AA889055	Hs.123468	ESTs	6.1 6.1
	452752 438208	AW044058 AL041224	Hs.33578 Hs.65379	KIAA0820 protein ESTs	6.1
	416072	AL110370	Hs.79000	growth associated protein 43	6.1
50	407808	AA663559	Hs.279789		6.1
	433701	AW445023	Hs.15155	ESTs	6.1 6.1
	419704 429250	AA429104 H56585	Hs.45057 Hs.198308	ESTs tryptophan rich basic protein	6.1
	433244	AB040943	Hs.271285		6.0
55	422544	AB018259	Hs.118140	KIAA0716 gene product	6.0
	420133	AA426117	Hs.155543		6.0 6.0
	440491 422728	R35252 AW937826	Hs.130558 Hs.103262		6.0
	415257		Hs.27513	ESTs	5.9
60	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.9
	430188				5.9 5.9
	437372 430471				5.9
	433523		113.24132	ESTs	5.9
65	408926				5.9
	427317				5.9 5.9
	426140 409892			8 Homo sapiens clone 25119 mRNA sequence gb:EST368183 MAGE resequences, MAGD Homo	5.8
	459516				5.8
70	442910	Al365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.8
	41473				5.8 5.8
	42433		Hs.10161	5 ESTs NM_002706*:Homo seplens protein phosphat	5.8
	40314 42011		2	gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.8
75	45081				5.8
	40214	5		Target Exon	5.8
	43479				5.8 5.8
	42242 44574				5.8
80	42060				5.8
	45140	7 AA13137	6 Hs.3438	09 fibroblast growth factor 128	5.7
	44110			intermediate filament protein syncollin	5.7 5.7
	42456	30 AA15872	7 Hs.1505	55 protein predicted by clone 23733	3.7

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	430287	AW182459	Hs.125759	ESTs, V	Vealdy similar to LEUS_HUMAN LEUKE	5.7
	405238			Target I	Exon	5.7 5.7
					sid binding Ig-like lectin 8 Bical protein DKFZp547J036	5.7
5		R39127 Q87470			80 protein	5.7
,	427624	AA406245		ESTs		5.7
	418079	R40058	Hs.6911	EST8	1.4.4.4	5.6 5.6
	424458	M29273	Hs.1780	myelin	associated glycoprotein etical protein FLJ10392	5.6
10	448299	AA497044 A1685086	Hs.20887 Hs.26339	FSTs.	Wealdy similar to S21348 probable	5.6
10	429698 430228	AW950939	Hs.6382	ESTs.	Highly similar to T00391 hypotheti	5.6
	445255	NM_014841	Hs.12477	synapi	osomal-associated protein, 91 kDa	5.6 5.6
	436887	AW953157	Hs.193235		etical protein DKFZp547D155	5.6
15	452898	AA814497 AB011540	Hs.78792 Hs.4930	ESTs low de	nsity Epoprotein receptor-related	5.6
15	435638 436035	AA703679	Hs.106999	ESTs.	Weekly similar to SYT5_HUMAN SYNAP	5.5
	412190	R16180	Hs.274461	EST8		5. 5 5.5
	459278	AW294659	Hs.34054		sapiens cDNA: FLJ22488 fs, clone H	5.5
20	416490	AF090116 Al497900	Hs.79348 Hs.33067	ESTs	tor of G-protein signalling 7	5.5
20	423449 440856	AI703103	Hs.271360		hetical protein MGC16275	5.5
	432154	AI701523	Hs.112577	FSTs	•	5.4 5.4
	423476	AL035633		Huma	an DNA sequence from clone RP5-1046G1	5.4
25	428588	F12101	Hs.185701 Hs.36790	FST	o saplens mRNA full length insert cDN , Wealdy similar to putative p150 (H	5.4
23	447773 436936	AJ423930 AL134451	Hs.197478			5.4
	427250	R35941	Hs.25418	EST		5.4 5.4
	427302	AA400540	Hs.135282	Hom	o sapiens cDNA FLJ11554 fis, clone HE	5.4
20	452856	AF034799	Hs.30881 Hs.97469	Prote	tin tyrosine phosphatase, receptor t s, Highty similar to A39769 N-acetyl	5.4
30	428795 407385	R45503 AA610150	Hs.272072	EST	s. Weakly similar to 138022 hypotheti	5.4
	405348	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		Ç70	01684:gi 12698061 dbi BAB21849.1 (AB	5.4 5.3
	438330	AW450572	Hs.257316	EST	s ST93093 Skin tumor I Homo sapiens cD	5.3
35	426503	AA380153	Hs.20509	GO:F	pX associated protein-8	5.3
33	44B14B 410386	NM_016578 W26187	Hs.3327	Hon	no sapiens cDNA: FLJ22219 fis, clone H	5.3
	445225	AI216555	Hs.202398	ES1	's	5.3 5.3
	428784	Y12851	Hs.193470		nergic receptor P2X, ligand-gated to	5.3 5.3
40	410759	AA227879	Hs.187621		get Exon	5.3
40	402605 412046	Y07847	Hs.73088		S-related on chromsome 22	5.3
	423869	BE409301	Hs.13401	2 C1	related factor	5.2 5.2
	430130	AL137311	Hs.23407		no sapiens mRNA; cDNA DKFZp761G02121 (5.2 5.2
15	453096	AW294631 AW805634				5.2
45	450475 429139		Hs.65087			5.2
	451783		Hs.21086	2 T-I	oox, brain, 1	5.2 5.2
	436568		Hs.91564	ES	iTs mo sapiens cDNA FLJ13596 fis, clone PL	5.2 5.2
50	424330		Hs.33339 Hs.45127	ab HK 7 eh	ondroitin sulfate proteoglycan 5 (neur	5.2
50	408453 447499			74 pn	otocadherin beta 16	5.2
	402855	;		N	4_001839°:Homo sapiens calponin 3, acid	5.2 5.2
	420805		Hs.9994		ticulon 1	5.2
55	426457 417355		7 Hs.1699 Hs.8200	00 G 2 Ar	imerin (chimaerin) 1 idothelin receptor type B	5.1
))	429469		Hs.27	gl	ycine dehydrogenase (decarboxylating;	5.1
	45063		Hs.2771	74 È	STs	5.1 5.1
	41281		22	E	STs omo sapiens ovarian cancer related prot	5.1
60	400379 44186				untingtin-associated protein interactin	5.1
00	44283			69 E	STS	5.1 5.1
	42270	9 AA31533			STs	5.1 5.1
	41155		7 Hs.7066 Hs.8956		IMP19 protein ts variant gene 1	5.0
65	41904 43097			110 F	STe	5.0
0,5	45132				liacylglycerol kinase, zeta (104kD)	5.0
	42367			7 i	STs	5.0 5.0
	42991			383 I	ESTs erythroid differentiation and denucleati	5.0
70	45276 45312		T	91	acytohosphatase 2, muscle type	5.0
/ \	4280		Hs.219	907	ESTs. Moderately similar to Transforming	5.0
	4301	83 BE0100	38		pb:PM3-BN0176-100400-001-g04 BN0176 Horno	5.0 5.0
	4499				Homo sapiens cDNA FLJ14337 fls, clone PL	5.0
75	4391			17 2047	synaptogyrin 3 chondroitin sutfate proteoglycan 3 (neur	5.0
/.) 4262 4517				KIAA1171 protein	5.0
	4205	78 AA8135	46 Hs.990	334	GTP-binding protein Rho7	4.9
	4273	15 AA1799			Homo saplens mRNA; cDNA DKFZp564N0763 (f	4.9 4.9
80	4281		300 Hs.299 546 Hs.199		mannosidase, alpha, class 2A, member 2 ESTs	4.9
81	U 4451 4103				ESTs	4.9
	4271	44 X95097	Hs.21	26	vasoactive intestinal peptide receptor 2	4.9 4.9
	448		Hs.21	413	solute carrier tarnily 12, (potassium-chi	4.9
					220	

	457561	AA331517	Hs. 286055	chimerin (chimaerin) 2	4.9
	409100 437117	H98216 AL049256	Hs.42245 Hs.122593	ESTs, Moderately similar to 138022 hypot ESTs	4.9
	415101	R45531	Hs.144534	ESTs	4.9
5	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.9
-	442026	AJ243749	Hs.8074	brain-specific angiogenesis inhibitor 3	4.9 4.9
	438283	AI458931	Hs.37282	ESTs	4.9
	449714	AB033015	Hs.23941	KIAA1189 protein	4.9
• •	420871	AA702972	Hs.65300	ESTs	4.9
10	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.9
	424001	W67883	Hs.137476	paternally expressed 10	4.9
	419103	240229	Hs.96423	hypothetical protein FLJ23033	4.B
	446727	AB011095	Hs.16032	KIAA0523 protein	4.8
15	408670 428189	AF160967 AA424030	Hs.46784 Hs.46627	potassium large conductance calcium-acti	4.8
13	420092	AA814043	Hs.88045	ESTs ESTs	4.B
	410631	AA086469	Hs.47171	ESTs	4.8
	449277	AA001064	Hs.43670	ESTs	4.8 4.8
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.8
20	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
	438703	AI803373	Hs.31599	ESTs	4.8
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.8
	445890	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence	4.7
25	438734	Al937612	Hs.273758	hypothetical protein FLJ23112	4.7
23	408177	A1241733	Hs.43871	ESTs	4.7
	445740 450627	178281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	4.7
	459527 445523	AW977558 Z30118	Hs.291735 Hs.293788	ESTs, Wealthy similar to 178885 serine/th	4.7
	409172	Z99399	Hs.122593	ESTs, Moderately similar to unnamed prot ESTs	4.7
30	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.7
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7 4.7
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	4.7
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.7
25	447891	R41754	Hs.6496	ESTs	4.7
35	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	4.7
	404819			NM_002688*:Homo sapiens peanut (Drosophi	4.7
	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7
	437762 441668	T78028	Hs.154679	synaptotagmin I	4.7
40	444190	AI611973 AI878918	Hs.136313 Hs.10526	ESTs	4.7
	429269	AA449013	Hs.99203	cysteine and glycine-rich protein 2 ESTs	4.6
	433009	AA761668	113.53203	gb:nz24c08.s1 NCI_CGAP_GC81 Homo sagiens	4.6
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.6 4.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	4.6
45	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fls, clone PL	4.6
	437698	R61837	Hs.7990	ESTs, Moderately similar to IB4505 calci	4.6
	445813	Z42023	Hs.106576	alanine-glyoxylate aminotransferase 2-li	4.6
50	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	4.6
50	448765 419723	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
	424282	AL120193 R76421	Hs.339810 Hs.135694	longevity assurance (LAG1, S. cerevisiae	4.6
	429401	AW296102	Hs.99272	ESTs ESTs, Wealdy similar to S32567 A4 protei	4.6
	426413	AA377823	119.33474	gb:EST90805 Synovial sarcoma Homo sapien	4.6
55	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	4.5 4.5
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.5
	443731	A1083928	Hs.145418	ESTs	4.5
	449539	W80363	Hs.58446	ESTs .	4.5
60	420362	U79734	Hs.97206	huntingtin interacting protein 1	4.5
UU	443301	AI733614	Hs.220587	ESTs, Moderately similar to ALU5_HUMAN A	4.5
	423178 437933	AI033140 AI276132	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5
	446544	AJ631932	Hs.146155 Hs.7047	ESTs Workly similar to Hattague (N. 1991)	4.5
	411642	NM_014932	Hs.71132	ESTs, Weakly similar to Unknown (H.sapie neuroligin 1	4.5
65	428282	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	4.5 4.5
•	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	4.5
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.5
	436637	AI783529	Hs.26766	ESTs	4.5
70	438456	AA913381	Hs.20594	ESTs .	4.5
70	400533			ENSP00000209376":PRED65 protain (Fragmen	4.4
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.4
	417632	R20855	Hs.5422	. glycoprotein M6B	4.4
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	4.4
75	457211 413812	AW972565 AW188687	Hs.32399 Hs.44748	ESTs. Wealdy similar to S51797 vasoditat	4.4
. 5	448451	AW015994	Hs.345433	ESTS	4.4
	432281	AK001239	Hs.274263	gb:UI-H-BI0p-abh-g-09-0-UI.s1 NCI_CGAP_S hypothetical protein FLJ10377	4.4
	458760	Al498631	Hs.111334	ferritin, light polypeptide	4.4 4.4
00	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
80	447877	AJ435184	Hs.164252	ESTs .	4.4
	431342	AW971018	Hs.21659	ESTs	4.4
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445729	H21066	Hs.13223	Homo sapiens mRNA full length Insert cDN	4.4

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	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.4
	419088 428305	A1538323 AA446628	Hs.52620 Hs.2799	integrin, beta 8 cartilage linking protein 1	4.4 4.4
_	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.4
5	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.4
	451621 424240	AI879148 AB023185	Hs.26770 Hs.143535	fatty acid binding protein 7, brain calcium/calmodulin-dependent protein kin	4.4 4.3
	433932	AW954599	Hs.169330	neuronal protein	4.3
• •	439935	S75105	Hs.8358	glutamate receptor, ionotropic, kainate	4.3
10	436039	AW023323	Hs.121070	ESTs	4.3
	416220 409953	N49776 AA332277	Hs.170994 Hs.57691	hypothetical protein MGC10946 cadherin 18, type 2	4.3 4.3
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	4.3
15	420352	8E258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3
15	454032 421790	W31790 AW896201	Hs.194293 Hs.22654	ESTs, Wealthy similar to I54374 gene NF2 sodium channel, voltage-gated, type I, a	4.3 4.3
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.3
	436391	AJ227892	Hs.146274	ESTs	4.3
20	452106 422465	AI141031 AF073710	Hs.21342 Hs.117149	ESTs regulator of G-protein signalling 9	4.3 4.3
20	439285	AL133916	113.117143	hypothetical protein FLJ20093	4.3
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.3
	424572 449048	M19650 245051	Hs.22920	2,3-cyclic nucleotide 3 phosphodieste	4.3
25	409182	AA064970	Hs.122593	similar to \$68401 (cattle) glucose induc ESTs	4.3 4.3
	444600	R41398	Hs.6996	ESTs	4.3
	408838	AI669535	Hs.40369	ESTs	4.3
	410592 440168	R94088 AA868507	Hs.43569 Hs.126141	ESTs ESTs	4.3 4.2
30	445078	AJ869975	Hs.4775	Junetophilin 3	4.2
	428670	AA431682	Hs.134832	ESTs	4.2
	411666 412505	AF 106564 AA974491	Hs.71346 Hs.21734	neurofilament 3 (150kD medium) ESTs	4.2 4.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.2
35	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	449433 441523	AI672096 AW514263	Hs.9012 Hs.301771	ESTs, Wealth similar to \$26650 DNA-bindi	4.2 4.2
	448243	AW369771	Hs.52620	ESTs, Wealthy similar to ALUF_HUMAN !!!! integrin, beta 8	4.2
40	429149	AW193360	Hs.197962	ESTs, Weakly similar to 138022 hypotheti	4.2
40	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (4.2
	404584 422798	R92347	Hs.34574	Target Exon ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2 4.2
	451254	AI57 1016	Hs.172967	ESTs	4.2
45	428585	AB007863	Hs.185140	KIAA0403 protein	4.2
43	439231 425287	AW581935 R88249	Hs.141480 Hs.155524	Homo sapiens mRNA; cDNA DKFZp434N079 (fr peanut (Drosophila)-like 2	4.2 4.2
	425790	AW136286	Hs.288446	ESTs	4.2
	450407	NM_000810		gamma-aminobutyric acid (GABA) A recepto	4.2
50	425241 445292	AA324624 AV653264	Hs.155247 Hs.13982	aldolase C, tructose-bisphosphate Homo sapiens cDNA FLJ14666 fis, clone NT	4.2 4.1
50	400777	AVOLUZUA	113.1330Z	NM_007325':Homo sapiens glutamate recept	4,1
	422170	A1791949	Hs.112432	anti-Mullerian hormone	4.1
	410765 425402	Al694972 Al215881	Hs.66180 Hs.24970	nucleosome assembly protein 1-fike 2 ESTs, Weakly similar to B34323 GTP-bindi	4.1 4.1
55	438461	AW075485	Hs.286049		4,1
	421268	Al126821	Hs.30514	ESTs	4.1
	416439 419687	AA180363 AJ638859	Hs.118769 Hs.227699		4.1 4.1
	435040	AI932350	Hs.152825		4.1
60	439774	AL360257	Hs.213493		4.1
	458435 410320	AM18718	Hs.144121 Hs.93816		4.1
	436899	AA084071 AA764852	Hs.291567	Homo sapiens mRNA; cDNA DKFZp547N093 (fr ESTs	4.1 4.1
65	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	4.1
65	453118 428771	AW195849 AB028992	Hs.252757		4.1
	444185	AW298350	Hs.193143 Hs.66020	KIAA1069 protein ESTs	4.1 4.1
	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
70	430147 456060	R60704	Hs.234434		4.1
70	433819		Hs.45184 Hs.112765	Homo sapiens cDNA FLJ12284 fs, clone MA ESTs	4.1 4.1
	415827	H17462	Hs.23079	ESTs	4,1
	437397		Hs.4221	hypothetical protein OKFZp761H039	4.1
75	441390 440483		Hs.131175 Hs.150386		4.1 4.0
. •	435294	T84084	Hs.196008		4.0
	447397	BE247676	Hs.18442	E-1 enzyme	4.0
	425390 432022		Hs.156114 Hs.272348	The second secon	4.0
80	420602		Hs.99236	3 Homo sapiens mRNA; cDNA DKFZp761L1212 (f regulator of G-protein signalling 20	4.0 4.0
	408081	AW451597	Hs.167409	ESTS	4.0
	453313 436511		Hs.153746 Hs.291503		4.0 4.0
	-00311	PANT & TEUR	110.43130		4.0
				222	•

	448944 419412	AB014605 AW161058	Hs.22599 Hs.90297	strophin-1 interacting protein 1; activi	4.0
	409091	AW970386	Hs.269423	synuclein, beta ESTs	4.0 4.0
_	453438	AI459935	Hs.22792	ESTs	4.0
5	450582	AJ339732		G-rich RNA sequence binding factor 1	4.0
	440553 437449	AA889416 AL390153	Hs.344043 Hs.208339	Homo sapiens cDNA FLJ14459 fis, clone HE Homo sapiens mRNA; cDNA DXFZp762G113 (fr	4.0 4.0
	445888	AF070564	Hs.13415	Homo saplens clone 24571 mRNA sequence	4.0
10	439450	R51613	Hs.125304	ESTs	4.0
10	453792	AL134539	Hs.254129	KIAA1678	4.0
	459080 438810	AW192083 AW897846	Hs.290855 Hs.6421	ESTs hypothetical protein DKFZp761N09121	4.0 4.0
	446233	AI282028	Hs.25205	ESTs	4.0
15	412754	AW160375	Hs.74565	armyloid beta (A4) precursor-like protein	4.0
15	412326 434859	R07566 BE255080	Hs.73817	small inducible cytokine A3 (homologous	4.0
	423279	AW959861	Hs.299315 Hs.290943	collapsin response mediator protein-5; C ESTs	4.0 4.0
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	3.9
20	410126	BE169274	***	KIAA0036 gene product	3.9
20	431173 446936	AW971198 H10207	Hs.294068 Hs.47314	ESTs ESTs	3.9
	424899	AL119387	Hs.119062	ESTs	3.9 3.9
	419038	AW134924	Hs.190325	ESTs	3.9
25	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	3.9
23	438142 412659	T90309 AW753865	Hs.269651 Hs.74376	ESTs offactomedin related ER localized protei	3.9 3.9
	412788	AA120960	Hs.198416	ESTs	3.9
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALUB_HUMAN A	3.9
30	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
30	432809 424186	AA565509 Al536021	Hs.131703 Hs.288706	ESTs Homo sapiens cDNA FLJ10281 fis, clone HE	3.9 3.9
	425480	AB023198	Hs.158135	KIAA0981 protein	3.9
	449932	AI675444	Hs.263024	ESTs	3.9
35	434072 450590	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
55	419586	A1701507 A1088485	Hs.273740 Hs.144759	ESTs ESTs, Weakly similar to 138022 hypotheti	3.9 3.9
	414040	N58513	Hs.32171	ESTs	3.9
	436480	AJ271643	Hs.87459	putative acid-sensing ion channel	3.9
40	443210 448448	A1692649	Hs.9451	hypothetical protein MGC13168	3.9
40	447067	NM_014954 R42098	Hs.21239 Hs.21964	KIAA0985 protein ESTs	3.9 3.9
	413199	M62843	Hs.75236	ELAV (embryonic lethat, abnormal vision,	3.9
	429421	AL031658		Human DNA sequence from clone RP1-310013	3.9
45	415796 417333	R87548 AL157545	Hs.78854 Hs.173179	ATPase, Na? transporting, beta 2 polypep bromodomain and PHD finger containing, 3	3,8 3.8
	418771	AA807881	Hs.25329	ESTs	3.8
	417565	AJ203405	Hs.47831	ESTs	3.8
	412420 450202	AL035668	Hs.73853	bone morphogenetic protein 2	3.8
50	435312	AW969756 AJ243396	Hs.34145 Hs.4865	ESTs, Wealty similar to 849847 GTP-bindi vollage-gated sodium channel bela-3 subu	3.8 3.8
• •	435832	AA425688	Hs.41641	Bruno (Orosophila) -like 4, RNA binding	3.8
	435854	AJ278120	Hs.4996	pulative ankyrin-repeat containing prote	3.8
	459079 425905	AI821122 AB032959	Hs.318584	gb:ns91g10.y5 NCI_CGAP_Pr3 Home sapiens	3.8 3.8
55	421977	W94197	Hs.110165	novel C3HC4 type Zinc finger (ring finge ribosomal protein L26 homolog	3.8
	437756	AA767537	Hs.197096	ESTs	3.8
	403696	A A 200000	11: 04 400	C4001100* gij5852342 gb AAD54015.1 (AF0	3.8
	453033 441732	AA325869 AW298818	Hs.31463 Hs.127341	KIAA0281 gene product ESTs	3.8 3.8
60	415884	H22966	Hs.13471	ESTs	3.8
	432646	AW753310		gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	451059 447057	AW297465 AI423407	Hs.267150 Hs.157697		3.8
	418915	AI474778	Hs.118977		3.8 3.8
65	441111	AI806867	H\$.126594	ESTs	3.8
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.8
	457183 418358	H91882 L02840	Hs.118569 Hs.84244		3.8
	410711	AB002316	Hs.65746	potassium voltage-gated channel, Shab-re KIAA0318 protein	3.8 3.8
70	428878	AA436884	Hs.48926	ESTS	3.8
	438944	AA302517	Hs.92732	KIAA1444 protein	3.8
	420898 418329	AB002379 AW247430	Hs.100113 Hs.84152	KIAA0381 protein cystathionine-beta-synthase	3.8 3.8
	427209	H06509	Hs.92423	KIAA1566 protein	3.8 3.7
75	445319	AF052108	Hs.12513	Homo sapiens clone 23687 mRNA sequence	3.7
	428841	AI418430	Hs.104935		3.7
	414821 443310	M63835 BE552018	Hs.77424 Hs.133152	Fc tragment of IgG, high affinity ta, re ! ESTs	3.7 3.7
00	407728	AW071502	Hs.175931		3.7
80	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.7
	444127 425652	N63620 AB021742	Hs.13281 Hs.322431	ESTs neurogenic differentiation 2	3.7
	458072	AI890347	Hs.27192		3.7 3.7

	459660	M79082	2020	ESTs	3.7
	432188 437627	A1362952 AW469925	Hs.2928	solute carrier family 7 (cationic amino	3.7
	408508	A1806109	Hs.257837 Hs.135736	ESTs KIAA1580 protein	3.7
5	448999	AF179274	Hs.22791		3.7
•	410623	AW958932	Hs.293833	transmembrane protein with EGF-like and ESTs	3.7
	430744	AA485229	Hs.105649	ESTs	3.7 3.7
	454392	BE260893	Hs.236131	homeodomain-interacting protein kinase 2	3.7
• •	453739	AL120266		ESTS	3.7
10	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.7
	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	3.7
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.7
15	451027	AW519204	Hs.40808	ESTS	3.7
13	415131 443454	D61119 Al057494	LL 122424	gb:HUM158C118 Clontech human fetal brain	3.7
	423779	AW071837	Hs.133421 Hs.57971	ESTS	3.7
	452092	8E245374	Hs.27842	ESTS	3.7
	435910	AI084152	Hs.21782	hypothetical protein FLJ11210 ESTs, Wealty similar to ALU7_HUMAN ALU S	3.7
20	447028	AI973128	Hs.167257	brain link protein-1	3.6 3.6
	452997	N64777	Hs.44656	ESTs	3.6
	408601	U47928	Hs.86122	protein A	3.6
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.6
25	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.6
25	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.6
	421679	AI475110	Hs.203933	ESTs	3.6
	448985	AA324885	Hs.22777	carbonic anhydrase XI	3.6
	414709 411775	AA704703	Hs.77031	Sp2 transcription factor	3.6
30	439099	H08342 AB037800	15.0400	gb:yl87b09.r1 Soares Infant brain 1NIB H	3.6
50	436315	BE390513	Hs.6462 Hs.27935	protein kinase C and casein kinase subst	3.6
	423611	AB011163	Hs.129908	hypothetical protein MGC4837 KIAA0591 protein	3.6
	453169	AB037815	Hs.32156	KIAA1394 protein	3.6
	436954	AA740151	Hs.130425	ESTs	3.6 3.6
35	439249	AF086060	Hs.170053	G-protein coupled receptor 88	3.6
	432058	AW665996	Hs.130729	ESTs, Wealty similar to ALU1_HUMAN ALU S	3.6
	419390	A1701162	Hs.90207	hypothetical protein MGC11138	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
40	409557	BE182896	Hs.211193	ESTs	3.6
40	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.6
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	445105 424051	AF238869 AL110203	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
45	446420	AW015693	Hs.138411 Hs.135614	Homo sapiens mRNA; cDNA DKFZp586J1922 (1	3.6
	428138	AA773842	Hs.293799	ESTs ESTs	3.6
	404185	74.7.0012	115.230733	Target Exon	3.6
	427517	AA644142	Hs.7107	ESTS, Weakly similar to ALU7_HUMAN ALU S	3.6
	443150	AI034467	Hs.34650	ESTs	3.6 3.6
50	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.6
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	3.6
55	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	3.6
55	412350	A1659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.6
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.6
	451734 437056	NM_006176 Al147061	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	438328	AJ492261	Hs.32450	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S ESTs	3.6
60	451489	NM_005503	Hs.26468		3.6
- •	423541	AL137256	Hs.130489	artyloid beta (A4) precursor protein-bind ATPase, aminophospholipid transporter-li	3.6
	434784	AA649051	Hs.164007	ESTs	3.6
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.5 3.5
<i>c</i> =	421183	AL135740	Hs.102447	TSC-22-like	3.5
65	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.5
	425870	R13406	Hs.56782	ESTs	3.5
	425115	R44664	Hs.123956	ESTs	3.5
	444471	AB020684	Hs.11217	KIAA0877 protein	3.5
70	419929	U90268	Hs.93810	cerebral cavernous mailformations 1	3.5
	407792 422564	AI077715 AI148006	Hs.39384	putative secreted ligand homologous to f	3.5
	433323	AA805132	Hs.222120 Hs.159142	ESTs EST-	3.5
	435743	T66861	Hs.12962	ESTs ESTs	3.5
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
75	403341			Target Exon	3.5
	443761	AI525743	Hs.345187	ESTs	3.5 3.5
	458743	R53169	Hs.80712	KIAA0202 protein	3.5 3.5
	447925	AW292271	Hs.250718	EST6	3.5
80	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.5
ου	416874	H98752	Hs.42568	ESTB	3.5
	430456	AA314998	Hs.241503	hypothetical protein	3.5
	419647 412707	AA348947	Hs.91816	hypothetical protein	3.5
	7.2/0/	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	3.5

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	444458	BE041526	Hs.31746	hundhallad amiala DVF 7aF 47FA39	
	451066	AI758660	Hs.206132	hypothetical protein OKFZpS47F072 ESTs	3.5 3.5
	425234	AW152225	Hs.165909	ESTs, Wealthy similar to 138022 hypotheti	3.5
-	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	3.5
5	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.5
	442118	AA976718	Hs.202242	ESTS	3.5
	421686	AB011156	Hs.106794	KIAA0584 protein	3.5
	428966 444326	AF059214 Al939357	Hs.194687	cholesterol 25-hydroxylase	3.5
10	443361	AI792628	Hs.270710 Hs.133273	ESTs ESTs	3.5
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.5
	434542	AA769310	Hs.61260	hypothetical protein FLJ 13164	3.4 3.4
	419235	AW470411	Hs.288433	neurotrimin	3.4
1.5	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4
15	417084	H08370	Hs.33067	ESTs	3.4
	432925	AA878324		ESTs .	3.4
	439920 453710	H05430 AL119136	Hs.288433	neurotrimin	3.4
	412783	BE276738	Hs.236131 Hs.74578	homeodomain-Interacting protein kinase 2	3.4
20	435977	AL138079	Hs.5012	DEAD/H (Asp-Gtu-Ata-Asp/His) box polypep brain-specific membrane-anchored protein	3.4
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	3.4 3.4
	449611	AJ970394	Hs.197075	ESTs	3.4
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cONA DKFZp586P1124 (f	3.4
25	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.4
23	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALUS_HUMAN A	3.4
	412043 445666	BE156622 R59960	Hs.333371	Horno sapiens clone TA40 untranslated mRN	3.4
	412820	BE001236	Hs.282386	ESTs	3.4
	458912	Al911066		gb:CM3-BN0075-240200-101-d11 BN0075 Homo ESTs	3.4
30	452449	AW068658	Hs.20943	ESTs	3.4 3.4
	437085	AA743935	Hs.202329	ESTs	3.4
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.4
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.4
35	435741	A1240668	Hs.113099	ESTs	3.4
55	445828 419347	F05802 C15944	Hs.81907 Hs.90005	ESTs	3.4
	431733	AW298410	Hs.21475	superiorcervical ganglia, neural specifi ESTs	3.4
	415949	H10562	Hs.21691	ESTs	3.4 3.4
40	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	3.4
40	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	3.4
	442593	R39804	Hs.31961	ESTs	3.4
	442927	AI024347	Hs.131519	ESTs	3.4
	429528	AI985303	Hs.99361	ESTs	3.4
45	450756 437387	A1733488 A1198874	Hs.144052	ESTs	3.4
	430347	NM_002039	Hs.28847 Hs.239706	AD026 protein GRB2-associated binding protein 1	3.4
	404283	1111_002003	113.233100	ENSP00000244751*:Copine-like protein KIA	3.4
	433229	AB040925	Hs.91625	KIAA1492 protein	3.4 3.4
60	440274	R24595	Hs.7122	scrapie responsive protein 1	3.4
50	436114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.4
	439690	AA843868	Hs.190567	ESTs	3.4
	450784 417868	AW246803	Hs.47289	ESTs	3.3
	439793	AI078534 AA018825	Hs.122592 Hs.7934	ESTs	3.3
55	456209	W60633	H\$.297792	Kruppel-like factor 4 (gut) ESTs	3.3
	421458	NM_003654	Hs.104578	carbohydrate (keratan sutfate Gal-6) sul	3.3 3.3
	438201	AA780243	Hs.54647	ESTs	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
60	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 ffs, clone C	3.3
UU	423169 415539	8E047009 Al733881	Hs.21837	ESTs, Wealdy similar to KIAA0927 protein	3.3
	450337	AI733881 AI693256	Hs.72472 Hs.202427	BMP-R1B ESTs	3.3
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	3.3
	423420	AI571364	Hs.128382	Homo sepiens mRNA; cDNA DKFZp76111224 (f	3.3 3.3
65	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.3
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	3.3
	453785	AI368238	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	448048	BE281291	Hs.170408	ESTs. Moderately similar to A47582 B-cel	3.3
70	436207 404632	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
	411565	AW851728		NM_022490:Homo sapiens hypothetical prot	3.3
	416845	H95279	Hs.293788	gb:MR2-CT0222-011199-007-d06 CT0222 Homo gb:yu20h02.a1 Soares fetal liver spleen	3.3
	436267	AW450938	Hs.180115	ESTs	3.3
76	426625	T78300	Hs.300642	serologically defined colon cancer antiq	3.3 3.3
75	401272			C9000559*:gij12314195jembjCAB99338.1j (A	3.3
	435071	D60683	Hs.35495	ESTs	3.3
	433128	AB021923	Hs.23367	EST-YD1 protein	3.3
	426920 423668	AA393351 Y10148	Hs.132121 Hs.131138	ESTs	3.3
80	435056	AW023337	Hs.5422	neurotensin receptor 2 glycoprotein M6B	3.3
	445534	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	3.3 3.3
	425010	T16837	Hs.4241	ESTs	3.3
	445260	AI218133	Hs.147617	ESTs	3.3
				225	

	424204	414070202	Lin 200000 a		
	421094 450358	AW978202 AB010098	Hs.289064 Hs.24907	hypothetical protein FLJ22251	3.3
	411048	AK001742	Hs.67991	coronin, actin-binding protein, 2B hypothetical protein DKFZp434G0522	3.3 3.3
_	432488	AA551010	Hs.216640	ESTs	3.3 3.3
5	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.3
	412719	AW016610	Hs.816	ESTs	3.3
	420050	AL118615	Hs.94653	neurochondrin	3.3
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.3
10	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.3
10	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434574 432715	AI424458 AA247152	Hs.33470 Hs.200483	ESTS	3.2
	426757	AW205640	Hs.158206	ESTs, Wealdy similar to KIAA1074 protein ESTs	3.2
	428157	AA770021	Hs.16332	ESTs	3.2 3.2
15	451597	AW295250	Hs.207536	ESTs .	3.2
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.2
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	429550	AW293055	Hs.119357	ESTs	3.2
20	404120	0500000		C5000537":gij3298595 gb AAC41376.1 (AFO	3.2
20	417123 450313	BE326521 A1038989	Hs.159450	ESTs	3.2
	425999	AW513051	Hs.332633 Hs.332981	Bardet-Biedl syndrome 2 ESTs, Wealdy similar to I38022 hypotheti	3.2
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	3.2 3.2
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.2
25	415558	AA885143	Hs.125719	ESTs	3.2
	451996	AW514021	Hs.245510	ESTs	3.2
	420560	AW207748	Hs.59115	ESTs	3.2
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinese/fructose-2,6-bi	3.2
30	417404 414300	NM_007350 AJ304870	Hs.82101	pleckstrin homology-like domain, family	3.2
50	437834	AA769294	Hs.188680 Hs.283854	ESTs gb:nz36g03.s1 NCI_CGAP_GC81 Homo saciens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H28H_HUMAN HISTO	3.2 3.2
	447714	AW296313	Hs.255537	ESTs	3.2
~ ~	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	3.2
35	443431	AI056847	Hs.20654	ESTs	3.2
	445774	AI254165	Hs.339968	ESTs .	3.2
	431327	AW972220	Hs.105426	ESTs	3.2
	413335 430809	AI613318 AI791150	Hs.48442	ESTs	3.2
40	445858	AL133811	Hs.262009	ESTs. Moderately similar to (38022 hypot	3.2
••	450692	H50603	Hs.94037	solute carrier family 1 (glial high affi hypothetical protein FLJ23053	3.2 3.2
	439039	AI656707	Hs.48713	ESTs	3.2
	401720			NM_014587*:Homo sapiens SRY (sex determi	3.2
45	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	3.2
45	451032	W03692	Hs.323079	Homo sapiens mRNA; cONA DXFZp564P116 (fr	3.2
	413834	BE296896 R98299	Hs.224179	ESTs, Weakly similar to I38022 hypotheti	3.2
	438138 436338	W92147	Hs.177502 Hs.118394	ESTS ESTS	3.2
	417169	R13550	Hs.246773	ESTs	3.2 3.2
50	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	3.2
	435767	H73505	Hs.117874	ESTs	3.2
	415314	N88802	Hs.5422	glycoprotein M6B	3.2
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.2
55	414699 438549	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.2
55	453896	BE386801 AW293483	Hs.21858 Hs.255205	trinucleotide repeat containing 3 KIAA1853 protein	3.2
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	3.2 3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threanin	3.1
60	429046	X57436	Hs.194772	oligodendrocyte myelin glycoprotein	3.1
	421896	N62293	Hs.45107	ESTs	3.1
	413995 414734	BE048148 AA151712	Hs.75671 Hs.82572	syntaxin 1A (brain)	3.1
	446147	AL133064	Hs.14051	ESTs Homo sapiens mRNA; cDNA DKFZp434A2417 (f	3.1
65	427712	AJ368024	Hs.283696	ESTs	3.1 3.1
	406481			Target Exon	3.1
	453204	R10799	Hs.191990	ESTs	3.1
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.1
70	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	3.1
70	421030 423603	AW161357	LI. 490000	microtubule-associated protein tau	3.1
	413985	AB007880 AI018666	Hs.129883 Hs.75667	Homo sapiens KIAA0420 mRNA, complete cds	3.1
	431721	A8032996	Hs.268044	synaptophysin KIAA1170 protein	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1 3.1
75	429876	AB028977	Hs.225974		3.1
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.1
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	3.1
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.1
80	453324 424009	W26592 F11690	Hs.232089	ESTs	3.1
Ų.	436222	AI208737	Hs.122810	gb:HSC30D041 normalized infant brain cDN Homo septens cDNA FLJ11489 fis, clone HE	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1 3.1
	446862	AV660697	Hs.282700		3.1
					- , •

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	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	3.6
	455388	AW936234	10.112001	gb:QV0-DT0020-090200-106-g05 DT0020 Homo	3.1 3.1
	415838	R44336	Hs.7093	ESTs	31
5	451692	AL137422	Hs.26849	Homo saplens mRNA; cDNA DKFZp761A1623 (f	3.1
3	445294 434460	Z45978	LL 2053	Human clone 23826 mRNA sequence	3.1
	449919	AA478486 AI674685	Hs.3852 Hs.200141	KIAA0368 protein ESTs	3.1 3.1
	440688	AW404591	Hs.147440	ESTs, Wealthy similar to Z192_HUMAN ZINC	31
	416801	X98834	Hs.79971	sal (Orosophila)-like 2	3.1
10	428060	AA420616	Hs.249483	ESTs	1 1
	423597	AL043117	Hs.129872	sperm associated entigen 9	3.1
	452454 445337	AW820480 NM_013280	Hs.12523	gb:QV2-ST0298-140200-042-110 ST0298 Homo	3.1
	413974	BE208636	Hs.27788	fibronectin leucine rich transmembrane p ESTs	3.1 3.1
15	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	435375	AJ733610	Hs.187832	ESTs	3.1
	450661	AW952160	Hs.83849	ESTs	3.1
20	428647 400658	AA830050	Hs.124344	ESTS ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.1
	443845	AI590084	Hs.148485	ESTs, Weakly similar to A47161 Mac-2-bin	3.0 3.0
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
25	437738	AA766914	Hs.203475	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
23	444772 453825	AW450800 AL157475	Hs.176859	ESTS	3.0
	439971	W32474	Hs.35453 Hs.301746	Homo sapiens mRNA; cDNA DKFZp761G151 (fr RAP2A, member of RAS oncogene family	3.0 3.0
	408449	NM_004408	Hs.166161	dynamin 1	3.0
**	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	3.0
30	453657	W23237	Hs.296162	AD037 protein	3.0
	407235 428862	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.0
	426002 424726	NM_000346 AK001007	Hs.2316 Hs.138760	SRY (sex determining region Y)-box 9 (ca Homo sapiens cDNA FLJ 10145 fis, clone HE	3.0
	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.0 3.0
35	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.0
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.0
	440461	R52728	Hs.7193	KIAA1183 protein	. 3.0
	452850 431431	H23230 AL096711	Hs.22481 Hs.252953	ESTs, Moderately similar to A46010 X-lin	3.0
40	447881	BE620886	Hs.75354	Human DNA sequence from clone RP3-403A15 GCN1 (general control of amino-acid synt	3.0 3.0
	454042	H22570	1-0.1 0004	hypothetical protein FLJ20093	3.0
	429168	AA984682	Hs.146589	ESTs, Weakly similar to JC5238 galactosy	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
45	446377	AW014022	Hs.170953	ESTs	3.0
7.7	430251 420658	AA609246 AW965215	Hs.181451 Hs.130707	ESTs ESTs	3.0
	454119	BE549773	Hs.40510	uncoupling pratein 4	3.0 3.0
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	3.0
50	435321	R16814	Hs.112062	ESTs	3.0
50	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.0
	423858 431242	AL137326 AA987742	Hs.133483 Hs.347534	Horno saplens mRNA; cDNA DKFZp434B0650 (f KIAA1201 protein	3.0
	403022	741501742	110.047.004	C21000178*:gi[7341207 gb]AAF61215.1 AF22	3.0 3.0
	445899	AI263736	Hs.145626	ESTs	3.0
55	440261	M81888	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0
	446809	AW590171	Hs.101413	EST8	3.0
	434269 418951	AK001991 F07809	Hs.3781 Hs.89506	similar to murine leucine-rich repeat pr	3.0
	448499	BE613280	Hs.77550	paired box gene 6 (anindia, keratitis) hypothetical protein MGC1780	3.0 3.0
60	432229	AW290976	Hs.143587	ESTs	3.0
	443726	AI083825	Hs.148382	ESTs	3.0
	TABLE	10.			
	TABLE 1: Pkey:		ua Eas araba	et identifier number	
65	CAT num		e cluster numi		
	Accession		bank accessio		
					
	Pkey 408065	CAT Number		41666454 4 4 6 7 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7	
70	410099	103646_1 117647_1		AI003154 AA059300 AA046911 T09671 A1174264 D93974 AWD50943 AA264693 AA6924	C7 AND 00000 DECORDARY A A 40000 A 100000 A 1000000 A 10000000 A 100000000
, ,	410033	117047_1	T07735 AA	100071 A1179239 D03074 AWS33043 AA304503 AA6934 884549 W60090 D52685 T23811 RE327043 AW001768 D	87 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 E551237 AA917004 AA716027 A4439658 AA283724 A1805992 A1457096
			AA084618	BE467738 Al092635 Al887863 Al697593 AA436618 Al16	7419 Al418634 T31586 AA436630 AA706191 Al041169 Al422304 T03534
			AA211402	AIZU4899 AI366472 AW827081 AA788593 T32736 AI767!	335 AA167791 AA747914 AA663870 AIR65504
75	410126	117761_1	BE169274	AW893230 AA210998 H24222 AA081774 BE000935 BE0	D0834 AA334880
, 5	411585 411775	1249756_1 125757_1		AW851607 AW851621 AW851702 AW851647 AW85172	7 AW851658 AW851617 AW851628
	412021	1272156_1		2430 Z42067 AA095285 AW885594 AW885579 AW885651	
	412799	132817_1		A121045 AA126521	
0.0	412811	132943_1	H06382 AV	V957730 AA352014 R13591 AA121201 D60420 RF26326	3 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
80	440000	4220020 -	HC39881 AA	813482 AWU16452 HU6383 H41807 AL364268 AA620528	AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
	412820 415131	1330039_1 1523680_1	85001236	BE001177 BE001180 BE001234 1508 D81734	
			C01113 D0	TOOL GOTT DE	

	418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074
			AW890649
	420111	190755_1	AA255652 AA280911 AW987920 AA262684
5	420352 421030	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
,	421030	19864_1	AW161357 AIB79062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454
			AI807703 R44253 AA976667 AI985186 AI550254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885
			AUS04013 AUS34765 AI796172 AW157488 AI929191 R85523 D51221 D53851 HR5610 AI740674 F21582 AA323145 AA010127 AA602444 T06748
••			AI699293 HZ9532 AA214029 AA223656 NM 016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 P27671 AARS1920
10			A1990023 A1935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479977 R44570 A1899804 AA29804
	400000	202707.4	AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 RF314R24 W2R930 R44098 R51045
	422890	222707_1	Z43784 R13382 AW572911 AA449369 H17037 R19503 AI532565 AW004030 BE 502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918
			AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI857447 AW204071 AW956110 C15616 D81142 H17038 AW162343 T87230 AI366013 H10064 AI190479 AI093318 AI867923 BE219303 BE048820 AI198397 AA654667 Z39851 F02655 Z28734 F04161 T16575 F10145
15			AA318815 R40898
	423476	22861_1	AL033633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 AL299437 AL133995 AA057405 N78357 AA917450 A1002692 T09262 T65008
	424009		H29290 Al200874 AA894415 Al732887 Al791768 Al733447 AA988785 N62128 T09261 AW956938
	424572	234177_1 24097_1	F11690 AW966370 AA33358 D30830
20	424312	24037_1	M19650 R18810 R18721 AW896146 AW899520 AA192362 AA176814 F12085 BE25S264 BE251393 T65248 AA380565 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303
			AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 AI858240 R73218 H30477 H17776 AA659570 BE276750 AL118657
			AAJ/3851 AAJ52427 AW581695 AI141188 N63474 AA654162 H17659 AL120696 T28867 AW498868 AI355918 AA902349 AAG6909 AI088223
•			A0042604 AA555133 A1183611 A1608822 A1275941 AW316805 AA349486 A1355233 RR5117 AW613696 R49234 AA468846 N20660 N18603 AA077667
25			T15423 AW002084 AI824721 N35242 AA17281 AI018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916639 AI872560 F00482 H45184
			AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL 133684 AI807085 AA808009 AA915914 F00007 AA019749 AL 121560 AW675544 AW090233 AW072071 AI810932 AI089733 AW026222 AA770155 AI089647 AI085733 AW516061 AL037636 AL037636 AL037636 AI683947 H50420
			R11203 AA019133 N94772 N71842 N29047 AA778138 AA554338 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13148 AA349487
			AV077160 BE255671 BE276795 BE250823 AL 120301 BE31 1390 RF2524R3
- 30	424945	245223_1	AJ221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AJ341345 AW298800 AA724961 AA931158 AJ741227
30			AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472555
	425331	250199_1	A1193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665 AW962128 AA355353 AA427363
	426413	266650_1	AA377823 AW954494 AI022588
26	426503	268283_1	AA380153 AA380233 AW963529
35	426919	273507_1	ALD41228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601
	428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340
	429007	298301_1	080642 AA443145 AL119015 AW904500
40	429421	30431_1	AL031658 Al693758 AL040619 AW977914 AA811967 Al352198 AW104364 AA648367 AA897604 AW341668 Al011903 AL040620
40	430183	31412_2	BE010038 AA676833 Al311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 Al936370 AA552514 T67280 AA039909
	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040
	430968	326269_1	AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 AW972830 AA527647 AA489820 AA570362
	432646	351909_1	2007 - 100 -
45	432925	356372_1	AA878324 AI863159 AI619686 AA570406 AI014377
	433009	357371_1	AA761668 AA573621 R92814 R09670
	433523 437034	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	437056	431713_1 432262_1	AA742643 AA808575 AW976668 A1147061 AA743380 AA765223 AW976398 AI803927
50	438458	457837_1	AW975186 AA807807 D29548
	439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552
	444400	£00004 4	Nb2351 Nb9253 AA626243 A1341407 BE175639 AA456968 A1358918 AA457077
	441102 445294	509604_1 6352_1	A4973905 Al299888 A4917019 H63235 T90771
55	713234	0332_1	245978 U79248 T77277 R24952 AA361008 AW953678 T10376 AW860579 AW860657 AW364889 AW860635 AW860658 AW905164 W21226 AA448954 W69484 AA993098 AA287413 AA449682 AI961815 W57612 AW271363 R45215 AW136256 AI865103 W69577 AI961826 AA747542
			AA173746 AI961816 F07706 R39461 F04829 F05938 AA172385
	445858	6525_1	AL133811 M78538 T07792 AW895859 AW895589 AL119422 T79878 R19494 AF131756 H18570 T0R285 F11532 742038 AW081084 AA683201
			M62U92 AL119616 ZZ1141 AA663820 Z19748 H18462 AL120152 R43841 R37594 AA775980 F09194 AI207884 Z38142 F01555 AA020737 AL 120362
60	446692	689623_1	AW952737 T04912 Z44514 AJ352097 AJ803984 AW235923 AW196558 AJ954637 AJ336983
	447197	711623_1	R36075 Al365546 R38167
	448044	747196_1	A458682 H24240 R14537 R18426 AW857082
	450582	83933_1	A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
65	451320	86576_1	AW118072 AI631982 715734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088
0,5			AA224388 A1084316 A1354686 T33652 A1140719 A1720211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 A1222556 T33511 T33785 A1419606 D55612
	452454	918306_1	AW820480 AW820288 AI902522
	453739	979419_1	AL120266 AW269469 AW890114
70	454042	99636_3	H22570 AW292267 AW137298 AW874199 A1206120 H45263 AA788851 R49056 AW241428 AI921013 AW129293 A1684910 BE466753 AA340613
, 0			AWU20309 AU2U2001 AI243913 AW771106 F04969 AI654847 AI494436 AW771447 AW103715 N64350 AA347011 AI431507 AA770107 AAA41106
			A358894 A421678 AI018523 AA707199 AA410309 A366468 AW020049 AI880103 AL119553 R42410 R55722 T66767 R43035 H17396 H45331 F01859 Z38381 AA708686 AI081305 R53955 AA041432 W27787
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
76	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
75	455646	1348557_1	
	458912 459079	823104_1 888710_1	AI911066 AI933734 AI680888 AJ003599 AI821122 AI821866
	-03013	····	THE
00	TABLE 1		
80	Pkey:	Un	rique number corresponding to an Eos probeset
	Ref:	Se	squence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:	90	quence of human chromosome 22' Dunham, et al. (1999) <u>Nature</u> 402:489-495. ficates DNA strand from which exons were predicted.

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	Nt_positio	n: Indic	ates nucleotide	positions of predicted exons.	
	Pkey 400533	Ref 6981826	Strand Minus	Nt_position	
5	400658	8118459	Minus	277132-277595 73525-73644	
_	400777	8131663	Plus	70745-71121	
	401272	9797373	Minus	98374-98509	
	401720	6468551	Plus	7783-8468	
10	402145	8018280	Plus	113086-114800	
10	402604	9909420	Phus	20393-20767	
	402605 402855	9909420 9662953	Minus Minus	47680-47973	
	403022	3132351	Plus	59763-59909 92097-92864	
	403142	9444521	Plus	89286-90131	
15	403341	8569175	Plus	30699-30910	
	403696	3135242	Minus	143467-143634	
	404120	7342152	Plus	135775-136000	
	404185	4572584	Minus	129171-129327	
20	404283 404541	2276311	Minus	99460-99564	
20	404584	831855 9 9857511	Plus Plus	103456-103664	
	404632	9796668	Plus	138651-139153 45096-45229	
	404819	4678240	Plus		075,17170-17287,17389-17529,18261-18357,18443-18578
0.0	405238	7249119	Minus	51728-51838	07.0,11 110-11201,1130-11323,1020 F10331,10405-10316
25	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,1	52407-152484
	405348	2914717	Minus	43310-43462	
	405819 406481	4007557 9864741	Plus	2830-2967	
	******	3004741	Minus	91439-91579	
30					•
	TABLE 14	A: ABOUT 111	1 GENES UP-F	REGULATED IN GLIOBLASTOMA COMPARED TO	NORMAL CENTRAL NERVOUS SYSTEM
	18018 144	111111111111	1 genes up-rea	ulated in clioblastoma compared to cormal central ce	NOUS System (CNS). Those were calculat from EDESD evaluates as the Administration
	1000 061	recipately out	A GUST DIE TRUG	OF EVERAGE GRODIASIDMA to "average" CNS bissues	was creater than or equal to 2.5. The "average" eligible town level was on to the the first
35	percentile	STREET AND A STREET	soran cumors.	I DE "AVERAGE" DOMINAL CINS ESSUE LEVEL WAS SELLE F	TO ROM nemontale amounts undouge CNS fire use. In order to communicate annual a
23	the ratio w	ras evaluated.	specific nyongi	zation, the 10" percentile value amongst various non	malignant tissues was subtracted from both the numerator and the denominator before
	Pkey:		ue Eos probes	et identifier number	
	ExAcon:	Exer	nplar Accession	n number, Genbank accession number	
40	Unigenet	O: Unig	ene number		
40	Unigene 1		ene gene title		
	R1:	Kak	of GLIOBLAS	TOMA to CNS	•
	Pkey	ExAccn	UnigeneID	Unigene Title	· R1
	422737	M26939	Hs.119571	collagen, type till, alpha 1 (Ehlers-Dani	32.8
45	423961	D13666	Hs.136348	periostin (OSF-2os)	28.0
	433001	AF217513	Hs.279905	done HQ0310 PRO0310p1	25.3
	414555 424800	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	24.3
	417308	AL035588 H60720	Hs.153203 Hs.81892	MyoD family inhibitor	22.6
50	449539	W80363	Hs.58446	KiAA0101 gene product ESTs	22.2 20.7
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	18.7
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	18.6
	444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	17.2
55	412420 417130	AL035668	Hs.73853	bona morphogenetic protein 2	16.7
73	414217	AW276858 Al309298	Hs.81256 Hs.279898	S100 calcium-binding protein A4 (calcium	16.7
	431941	AK000106	Hs.272227	Hamo sapiens cDNA: FLJ23165 fis, clone t. Hamo sapiens cDNA FLJ20099 fis, clone CO	14.3
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.3 14.1
<i>c</i> o	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	13.9
60	422672	X12784	Hs.119129	collagen, type IV, alpha 1	13.6
	402604 424635	4 4 400007	11- 445460	Target Exon	13.6
	428330	AA420687 L22524	Hs.115455 Hs.2256	Homo sapiens cDNA FLJ14259 fs, clone PL	13.0
	434078	AW880709	Hs.283683	matrix metalioproteinase 7 (matrilysin, chromosome 8 open reading frame 4	12.9
65	414761	AU077228	Hs.77256	enhancer of zeste (Drosophile) homolog 2	12.5 12.4
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	12.2
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	12.1
	409638	AW450420	Hs.21335	ESTs	11.5
70	441269 435020	AW015206	Hs.178784	ESTs	10.5
. •	422163	AW505076 AF027208	Hs.301855 Hs.112360	DiGeorge syndrome critical region gene 8 prominin (mouse)-like 1	10.5
	444969	Al203334	Hs.160628	ESTs	10.1
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	10.1 9.9
76	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	9.4
75	445101	T75202	Hs.12314	Homo sepiens mRNA; cDNA DXFZp586C1019 (f	9.2
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	9.1
	425187 449722	AW014486 BE280074	Hs.22509	ESTs	9.1
	449611	AI970394	Hs.23960 Hs.197075	cyclin B1 ESTs	8.9
80	428242	H55709	Hs.2250	leukemia inhibitory factor (cholineroic	8.9
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	8.9 8.9
	443731	AI083928	Hs.145418	ESTs	8.8
	402855			NM_001839":Homo sapiens calponin 3, acid	8.7
				·	
				22	7

	447342	AI199268	We 10333	Marina and Confession	
	410102	AW248508	Hs.19322 Hs.279727	Homo sapiens, Similar to RIKEN cONA 2010 ESTs; homologue of PEM-3 (Ciona savignyi	8.6 8.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
_	417426	NM_002291	Hs.82124	laminin, beta 1	8.4
5	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	8.3
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.1
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	8.1
	414622 430691	AI752666 C14187	Hs.76669 Hs.103538	nicotinamide N-methyltransferase	8.1
10	447726	AL137638	Hs.19368	ESTs matriin 2	8.0 8.0
	417043	NM_004369	Hs.80988	coflagen, type VI, alpha 3	7.9
	447004	AW296968	Hs.157539	ESTs	7.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.8
15	426075	AW513691	Hs.270149	ESTs. Wealthy similar to 2109260A B cell	7.8
13	419938 419508	AU076772	Hs.1279	complement component 1, r subcomponent	7.7
	411411	AW997938 AA345241	Hs.90786 Hs.55960	ATP-binding cassette, sub-tamity C (CFTR ESTs, Weakly simitar to KIAA1330 protein	7.7
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.5 7.5
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.5 7.5
20	406972	M32053		gb:Human H19 RNA gene, complete cds.	7.4
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	7.4
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.3
	409142 409902	AL136877 Al337658	Hs.50758	SMC4 (structural maintenance of chromoso	7.3
25	418113	AI272141	Hs.156351 Hs.83484	ESTs SRY (sex determining region Y)-box 4	7.3
	449961	AW265634	Hs.133100	ESTs	7.2 7.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	7.2
	424840	D79987	Hs.153479	extra spindle potes, S. cerevisiae, homo	7.2
20	428728	NM_016825	Hs.191381	hypothetical protein	7.1
30	429183	AB014604	Hs.197955	KIAA0704 protein	7.1
	439451 422106	AF086270 D84239	Hs.278554	heterochromatin-like protein 1	7.1
	406850	A1624300	Hs.111732 Hs.172928	Fc tragment of IgG binding protein collagen, type I, alpha 1	7.0
	453941	U39817	Hs.36820	Bloom syndrome	7.0 6.9
35	425234	AW152225	Hs. 165909	ESTs, Weakly similar to 138022 hypotheti	6.9
	421977	W94197	Hs.110165	ribosomal protein L26 hornolog	6.8
	411078	AJ222020	Hs.182364	CocoaCrisp	6.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.7
40	448769 418400	N66037 BE243026	Hs.38173	ESTs	6.7
40	408161	AW952912	Hs.301989 Hs.300383	KIAA0246 protein hypothetical protein MGC3032	6.6
	440210	AW674562	Hs.125296	ESTs	6.6
	437036	AI571514	Hs.133022	ESTs	6.6 6.6
4-	411968	Al207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	6.6
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	6.6
	449300	AI656959	Hs.346514	ESTs	6.5
	440052	AI633744	Hs.195648	ESTs, Wealdy similar to 138022 hypotheti	6.5
	412326 434808	R07566 AF155108	Hs.73817 Hs.256150	small inducible cytokine A3 (homotogous	6.5
50	452461	N78223	Hs.108106	Homo sapiens, Similar to RIKEN cDNA 2810 transcription factor	6.5 6.5
	408243	Y00787	Hs.624	interleukin 8	6.5
	424954	NM_000546	Hs.1848	tumor protein p53 (Li-Fraumeni syndrome)	6.4
	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
55	406478	411077443	11. 470565	Target Exon	6.4
33	427528 439710	AU077143 AF086543	Hs.179565	minichromosome maintenance deficient (S.	6.4
	458814	A1498957	Hs.170861	gb:Homo sapiens full length insert cDNA ESTs, Wealdy similar to Z195_HUMAN ZINC	6.4
	410276	AI554545	Hs.68301	angiopoletin-2	6.4 6.4
~	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	6.3
60	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	6.3
	436895	AF037335	Hs.5338	carbonic anhydrase XII	6.3
	447458 447439	AI741082 AA313565	Hs.158961 Hs.145020	ESTS	6.3
	413719	BE439580	Hs.75498	ESTs, Weakly similar to KIAA1205 protein small inducible cytokine subfamily A (Cy	6.3
65	449969	AW295142	Hs.180187	Homo sapiens cONA FLJ14337 fis, clone PL	6.3 6.2
	440704	M69241	Hs.162	insulin-like growth factor binding prote	6.2
	400419	AF084545		Target	6.2
	412140	AA219691	Hs.73625	RABS interacting, kinesin-like (rabidnes	6.2
70	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
70	424085 429469	NM_002914 M64590	Hs.139226 Hs.27	replication factor C (activator 1) 2 (40	6.2
	430630	AW269920	Hs.2621	glycine dehydrogenase (decarboxylating;	6.1
	410064	X53416	Hs.195464	cystatin A (stefin A) filamin A, alpha (actin-binding protein-	6.0 6.0
25	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
75	413627	BE182082	Hs.246973	ESTs	6.0
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.9
	421899	AJ011895	Hs.109281	Nef-associated factor 1	5.9
	407182 410286	AA312551 AI739159	Hs.230157	ESTs	5.9
80	409829	M33552	Hs.61898 Hs.56729	OKFZP586N2124 protein lymphocyte-specific protein 1	5.9
	446657	Al335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	5.9 5.8
	418097	R45137	Hs.21868	ESTs	5.8 5.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.8

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	419741	NM_007019	Hs.93002	ubiquitia corrier pentain E2 C	
	421988	AW450481	Hs.161333	ubiquitin carrier protein E2-C ESTs	5.7 5.7
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	5.7
-	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
5	434846	AW295389	Hs.119768	ESTs	5.7
	412567	A1750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	5.7
	452372	AI885742 BE614387	Hs.228474	ESTs	5.6
	443247 423198	M81933	Hs.333893 Hs.1634	c-Myc target JPO1 cell division cycle 25A	5.6
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.6 5.6
••	437034	AA742643	. 2.20.040	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	429447	AW812452	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	5.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	5.6
15	437695	AA769202	Hs.192142	ESTs	5.6
13	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	5.6
	453361 418293	AA035197 AI224483	Hs.107375 Hs.16063	ESTs hypothesical protein FLJ21877	5.5
	405348	ALLTOS	113.10000	C7001664;gi[12698061 dbj BAB21849.1 (AB	5.5 5.5
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
20	452799	A1948829	Hs.213786	ESTs	5.4
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.4
	442547 424009	AA306997	Hs.217484	ESTs, Wealdy similar to ALU1_HUMAN ALU S	5.4
25	440332	F11690 AI218517	Hs.188051	gb:HSC30D041 normalized infant brain cDN ESTs	5.4
~-	422094	AF129535	Hs.272027	F-box only protein 5	5.4 5.4
	443884	N20617	Hs.194397	leptin receptor	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
20	432731	R31178	Hs.287820	fibronectin 1	5.4
30	426108	AA622037	Hs.166468	programmed cell death 5	5.3
	407624 411048	AW157431 AK001742	Hs.248941 Hs.67991	ESTs	5.3
	412471	M63193	Hs.73946	hypothetical protein DKFZp434G0522 endothetial cell growth factor 1 (platel	5.3 5.3
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.2
35	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.2
	413786	AW613780	Hs.13500	ESTs	5.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	5.2
	428037	N47474	Hs.89230	potassium intermediate/small conductance	5.2
40	420311 416737	AW445044 AF154335	Hs.38207 Hs.79691	Human DNA sequence from clone RP4-530:15 LIM domain protein	5.1
40	445837	AI261700	Hs.145544	EST8	5.1 5.1
	425882	U83115	Hs.161002	absent in metanoma 1	5.1
	415682	AI347128	Hs.191870	ESTs	5.1
46	414053	BE391635	Hs.75725	transgelin 2	5.1
45	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	431512 432593	BE270734	Hs.2795	lactate dehydrogenase A	5.1
	433323	AW301003 AA805132	Hs.51483 Hs.159142	ESTs, Wealdy similar to hypothetical pro ESTs	5.0
	443744	AI084326	Hs.271548	ESTs, Weakly similar to 178885 serine/th	5.0 5.0
50	410434	AF051152	Hs.63668	toll-like receptor 2	5.0
	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	5.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.9
	446131	NM_000929	Hs.290	phospholipase A2, group V	4.9
55	412777 449246	AI335773 AW411209	Hs.270123 Hs.23363	ESTs	4.9
-	433244	AB040943	Hs.271285	hypothetical protein FLJ 10983 KIAA 1510 protein	4.9 4.9
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
	445118	AJ208762	Hs.345572	ESTs .	4.9
60	417404	NM_007350	Hs.82101	pleckstrin homology-tike domain, family	4.9
60	420092 412811	AA814043	Hs.88045	ESTs	4,9
	412811	H06382	Un 211001	ESTs	4.9
	438456	AW661783 AA913381	Hs.211061 Hs.20594	ESTs	4.9
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	4.9 4.9
65	431553	X78075	Hs.2799	cartilage linking protein 1	4.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.9
	411252	AB018549	Hs.69328	MD-2 protein	4.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	4.8
70	429433 403349	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
,,	402274	NM_001406		ephrin-83 C19000198*-a:I4567179bahla a D22507 11 a C00	4.8
	426044	AA502490	Hs.170290	C19000498*:gi 4567179 gb AAD23607.1 AC00 ESTs	4.8
	423600	AI633559	Hs.310359	ESTs	4.8 4.8
~-	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
75	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.8
	418054	NM_002318		tysyl oxidase-like 2	4.7
	441703 439627	AW390054	Hs.192843		4.7
_	439027 445900	8E621702 AF070526	Hs.29076 Hs.125036	hypothetical protein FLJ21841 Homo sapiens cione 24787 mRNA sequence	4.7
80	435937	AA830893	Hs.119769	ESTs	4.7 4.7
	403961			Target Exon	4.7 4.7
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	4.6
	408523	AW833259	Hs.314287	ESTs	4.6

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	403481			Target Exon	4.0
	423529	T87318	Hs.120411	ESTs	4.6 4.6
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	4.6
5	453362	H14988	Hs.107375	ESTs	4.6
J	407013 423757	U35637	Le 122624	gb:Human nebulin mRNA, partial cds	4.6
	432363	AL049337 AA534489	Hs.132571	Homo sepiens mRNA; cDNA DKFZp564P016 (fr gb:n/76g11.s1 NCI_CGAP_Co3 Homo sepiens	4.6
	408380	AF123050	Hs.44532	distriction	4.6 4.6
10	429149	AW193360	Hs.197962	ESTs. Wealty similar to (38022 hypotheti	4.6
10	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.6
	405558	44744057	44. 5454	Target Exon	4.6
	410295 450166	AA741357 AA429504	Hs.5174	nidogen (enactin) ESTs	4.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	4.6 4.5
15	420075	AF142482	Hs.203846	TEA domain family member 3	4.5
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.5
	457465	AW301344	Hs.122908	ONA replication factor	4.5
	436827 452620	H72187 AA436504	Hs.5322 Hs.119286	guanine nucleotide binding protein (G pr ESTs	4.5
20	424381	AA285249	Hs.146329	protein kinase Chk2	4.5 4.5
	444656	A1277924	Hs.145199	ESTs	4.5
	450639	AI703186	Hs.277174	ESTs	4.5
	424247 423178	X14008 AJ033140	Hs.234734	lysozyme (renal amyloidosis)	4.5
25	447072	D61594	Hs.124983 Hs.17279	Homo sepiens mRNA; cDNA DKFZp564C142 (fr tyrosylprotein suffotransferase 1	4.5
	447444	AK000318	Hs.18616	hypothetical protein FL/20311	4.5 4.4
	401454			NM_014226":Homo sapiens renal tumor anti	4.4
	420560 409205	AW207748	Hs.59115	ESTa	4.4
30	409205 451129	AI952884 BE072881	Hs.14832	ESTs, Moderately similar to unnamed prot	4.4
20	412530	AA766268	Hs.266273	gb:RC2-8T0548-200300-012-e09 BT0548 Homo hypothetical protein FLJ13346	4.4 4.4
	447752	M73700	Hs.105938	lactotransterrin	4.4
	429083	Y09397	Hs.227817	BCL2-related protein A1	4.4
35	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	4.3
33	424736 416379	AF230877 N38857	Hs.152701 Hs.203933	microtubule-interacting protein that ass	4.3
	452994	AW962597	Hs.31305	ESTs KIAA1547 protein	4.3 4.3
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.3
40	441035	A1694309	Hs.126458	ESTs	4.3
40	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.3
	418030 450811	BE207573 AI739486	Hs.83321 Hs.245497	neuromedin B ESTs	4.3
	438458	AW975186	N3.243437	gb:EST387294 MAGE resequences, MAGN Homo	4.3 4.3
4.5	442201	AW516704	Hs.208726	ESTs	4.3
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	4.3
	435677 442832	AA694142	Hs.293726	ESTs, Wealty similar to TSGA RAT TESTIS	4.3
	449318	AW206560 AW236021	Hs.253569 Hs.78531	ESTs Homo sapiens, Similar to RIKEN ¢DNA 5730	4.3
	421027	AA761198	Hs.55254	ESTs	4.2 4.2
50	414300	AJ304870	Hs.188680	ESTs	4.2
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	4.2
	444161 416908	N52543 AA333990	Hs.142940	ESTs	4.2
	418483	W26076	Hs.80424 Hs.221847	coagulation factor XIII, A1 polypeptide ESTs	4.2 4.2
55	443318	AI051603	Hs.133141	EST8	4.2
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	4.2
	416871 423678	H98716 AW983357	11- 2042	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	429643	AA455889	Hs.7847 Hs.167279	ESTs FYVE-finger-containing Rab5 effector pro	4.2
60	438875	AA827640	Hs.189059	ESTs	4.2 4.2
	428600	AW853261	Hs.242413	hypothetical protein DKFZp434K1421	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	406872 403790	AI760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.2
65	409112	BE243971	Hs.50649	NM_001334":Homo sapiens cathepsin O (CTS quinone oxidoreductase homolog	4.1
	435703	AW830133	Hs.83313	GK003 protein	4.1 4.1
	432625	AJ243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	4.1
	404407	A1970010	U. 74664	Target Exon	4.1
70	412568 422087	A1878826 X58968	Hs.74034 Hs.111301	caveolin 1, caveolae protein, 22kD	4.1
	435143	R12375	Hs.194500	matrix metalloproteinase 2 (gelatinase A ESTs	4,1 4.1
	447497	AW167254	Hs.205722	ESTs	4.1
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.1
75	427676 436608	AA394062 AA628980	Hs.300772		4.1
, ,	453331	A1240665		down syndrome critical region protein DS ESTs	4.1
	420004	AW975532	Hs.164039	ESTs, Moderately similar to 138022 hypot	4.0 4.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.0
80	426215	AW963419	Hs.155223	stanniocalcin 2	4.0
-	407603 450581	AW955705 AF081513	Hs.62604 Hs.25195	Homo sapiens, clone IMAGE:4299322, mRNA, TGF-beta 4	4.0
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	4.0 4.0
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4.0
				,	

	432058	AW665996	Hs.130729	ESTs, Wealty similar to ALU1_HUMAN ALU S	4.0
	444609	AW571659	Hs.278081	ESTs	4.0
	445666	R59960	Hs.282386	ESTs	4.0
_	437814	AI088192	Hs.135474	ESTs, Wealdy similar to DOX9_HUMAN ATP-D	4.0
5	414948	C15240	Hs.182155	ESTs	4.0
	435542	AA687376		ESTs	4.0
	422564	AI148006	Hs.222120	ESTs	4.0
	449571	AW016812	Hs.200266	ESTs	4.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.0
10	458946	AA009716	Hs.42311	ESTs	4.0
	449655	AI021987	Hs.59970	ESTs	4.0
	426649	Al914936	Hs.97152	ESTS	4.0
	457292	Al921270	Hs.281462	hypothetical protein FLJ14251	
	440435	AL042201	Hs.21273		4.0
15	456977	AK000252	Hs.169758	transcription factor NYO-sp10 hypothetical protein FiL/20245	4.0
	420649	A1866964	Hs.124704		4.0
	416406	D86961	Hs.79299	ESTs, Moderately similar to \$65657 alpha	4.0
	446291	BE397753	Hs.14623	Ipoma HMGIC fusion partner-like 2	4.0
	449256			interferon, gamma-inducible protein 30	3.9
20		AA059050	Hs.59847	ESTs	3.9
20	421637	AF035290	Hs.106300	Homo sepiens clone 23556 mRNA sequence	3.9
	456306	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.9
	438372	AI140189	Hs.123191	ESTs	3.9
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	3.9
25	415131	D61119		gb:HUM158C118 Clontech human fetal brain	3.9
23	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	424998	U\$8515	Hs.154138	chitinase 3-like 2	3.9
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.9
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	3.9
20	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.9
30	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.9
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.9
	416857	AA188775	Hs.292453	ESTs	3.9
	434784	AA649051	Hs.164007	ESTs	3.8
26	438898	AIB19863	Hs.106243	ESTs	3.8
35	408102	U46351	Hs.621	lectin, galactoside-binding, soluble, 3	3.8
	422081	AW136820	Hs.196011	ESTs .	3.8
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	3.8
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	3.8
40	406395			Target Exon	3.8
40	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	403696			C4001100":gi[5852342[gb]AAD54015.1] (AF0	3.8
	443740	R56434	Hs.21062	ESTs	3.8
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	3.8
4.5	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.8
45	444326	AI939357	Hs.270710	ESTs	3.8
	436899	AA764852	Hs.291567	ESTs	3.0
	445075	AI651827	Hs.344767	ESTs	3.8
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible.	3.8
	429163	AAB84766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
50	416114	A1695549	Hs.183868	glucuronidase, beta	3.8
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	3.8
	446839	BE091926	Hs.16244	mitotic spindle colled-coll related prot	3.8
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.8
	416664	H72780	Hs.20289	ESTs	3.8
55	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.8
	419735	AW750056	Hs.169577	Homo sapiens cONA FLJ14743 fis, clone NT	3.8
	448275	BE514434	Hs.20830	kinesin-like 2	3.7
	405141	Y14443		zinc finger protein 200	3.7
-	41,1537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.7
60	422648	D86983	Hs.118893	Melanoma associated gene	3.7
	449145	AI632122	Hs.198408	ESTs	3.7
	428060	AA420618	Hs.249483	ESTs	3.7
	404584			Target Exon	3.7
	418596	AW976721	Hs.293327	ESTa	3.7
65	458072	AJ890347	Hs.271923	Homo sapiens cONA: FLJ22785 fis, clone K	3.7
	445908	R13580	Hs.13436	Homo sepiens clone 24425 mRNA sequence	3.7
	439979	AW600291	Hs.6823	hypothetical protein FLJ 10430	3.7
	431770	BE221880	Hs.268555	5-3 exoribonuclease 2	3.7
	427809	M26380	Hs.180878	lipoprotein lipase	3.7
70	436674	AA725002	Hs.272018		3.7
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, atpha-	3.7
	434467	BE552368	Hs.231853		3.7 3.7
	448048	BE281291	Hs.170408		3.7
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7 3.7
75	402082			C18000743*:gij6678363 ref NP_033416.1 1	3.7 3.7
-	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.7
	428873	AJ701609	Hs.98908	ESTs	3.7 3.7
	437323	AA371145	Hs.194397		
	413095	AA494359	Hs.30715	potassium voltage-gated channel, isk-rei	3.7 3.7
80	425139	AW630488	Hs.25338	protesse, serine, 23	
_	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	3.7
	439574	A1459788	Hs.165190		3.7
	408829	NM_006042		heparan sulfate (glucosamine) 3-O-sulfot	3.7
	.50025				3.7

	407838	BE146411	Hs.40342	putative nuclear protein	3.7
	437748	AF234882	Hs.5814	Suppression of tumorigenicity 7	3.6
	437470 400288	AL390147 X06256	Hs.134742	hypothetical protein DKFZpS47D065	3.6
5	453438	AU6236 AI469935	Hs.149609 Hs.22792	integrin, alpha 5 (fibronectin receptor,	3.6
•	415024	AI983981	Hs.189114	ESTs ESTs	3.6
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.6 3.6
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	3.6
••	416427	BE244050	Hs.79307	Rac/Cdc42 guarine exchange factor (GEF)	3.6
10	448002	Y15227	Hs.20149	deleted in lymphocytic leukernia, 1	3.6
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) hornolog (E coli Re	3.6
	456534	X91 195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.6
	402239 450297	AMD01247	LL 20502	Target Exon	3.6
15	443715	AW901347 AJ583187	Hs.38592 Hs.9700	hypothetical protein FLJ23342	3.6
	403011	A303101	10.3700	cyclin E1 ENSP00000215330*:Probable serine/threoni	3.6
	428403	A1393048	Hs.326159	leucine rich repeat (in FUII) interactin	3.6
	425202	AW962282	Hs.152049	ESTs, Wealdy similar to 138022 hypotheti	3.6 3.6
00	409557	BE182896	Hs.211193	ESTs	3.6
20	453948	Al970797	Hs.64859	ESTs	3.6
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	442326 437640	H92962	Hs.124813	hypothetical protein MGC14817	3.6
25	424051	AA764893 AL110203	Hs.272155 Hs.138411	ESTs, Weakly similar to 138022 hypotheti	3.6
	406481	ACTIVES	NS.130411	Homo sapiens mRNA; cDNA DKFZpS86J1922 (I Target Exon	3.6
	433835	AI806185		gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Horno s	3.6
	456052	BE311901	Hs.28935	gb:601142614F1 NIH_MGC_14 Homo sapiens c	3.6 3.6
20	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.5
30	439726	AW449893	Hs.293707	ESTs, Wealdy similar to 138598 zinc fing	3.5
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	419402	268155	Hs.90291	laminin, beta 2 (laminin S)	3.5
	403108 426509	M31166	Un ODER	ENSP00000241415":Hypothetical 67.7 kDa p	3.5
35	418883	BE387036	Hs.2050 Hs.1211	pentaxin-related gene, rapidly induced b	3.5
	432188	AI362952	Hs.2928	acid phosphatase 5, tartrate resistant solute carrier family 7 (cationic emino	3.5
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.5 3.5
	427299	AA830210	Hs.214263	ESTs. Moderately similar to ALU1_HUMAN A	3.5
40	425212	AW962253	Hs.171618	ESTs	3.5
40	422938	NM_001809	Hs. 1594	centromere protein A (17kD)	3.5
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to \$65657 alpha	. 3.5
	457211 452682	AW972565 AA456193	Hs.32399 Hs.9071	ESTs. Wealdy similar to S51797 vasodilat	3.5
45	421247	BE391727	Hs.102910	progesterone membrane binding protein	3.5
	418049	AA211467	Hs.190488	general transcription factor IIH, polype Homo saptens, Similar to nuclear tocaliz	3.5
	453792	AL134539	Hs.254129	KIAA1678	3.5 3.5
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.5
50	412014	A1620650	Hs.43761	ESTs, Wealdy similar to A46010 X-linked	3.5
50	440370	AA884000	Hs.8173	hypothetical protein FLJ 10803	3.5
	407729	T40707	Hs.270862	EST ₈	3.5
	438527 455648	AI969251 BE064420	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	418630	AI351311	Hs.251946	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.5
55	432242	AW022715	Hs.162160	poly(A)-binding protein, cytoplasmic 1-I ESTs, Wealthy similar to ALU4_HUMAN ALU S	3.5
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronactin receptor,	3.5 3.4
	449932	Al675444	Hs.263024	ESTs	3.4
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	3.4
60	403849	407503		Target Exon	3.4
00	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	3.4
	451446 434589	AJ826288 AF147363	Hs.171637	hypothetical protein MGC2628	3.4
	403361	~ ·+/303		gb:Homo sapiens full length insert cONA NM_002210":Homo sapiens integrin, alpha	3.4
	420841	Al625251	Hs.94037	hypothetical protein FLJ23053	3.4
65	438206	AA780385	Hs.187885	ESTs	3.4 3.4
	425295	AA431366	Hs.37251	ESTs	3.4
	411789	AF245505	Hs.72157	Adlican	3.4
	440948	AW188311	Hs.128619	ESTs	3.4
70	439518	W76326	11- 100101	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
. 5	418821 459660	AA436002 M79082	Hs.183161	ESTs	3.4
	404209	HIT JUIGE		ESTs Target Exon	3.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	3.4
26	430694	AA810624	Ha.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4 3.4
75	425300	AW501773	Hs.270259	ESTs	3.4
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.4
	458438	AJ141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.4
	444911 421064	U06117 A1245432	Hs.250	xanihene dehydrogenase	3.4
80	441287	AW293132	Hs.101382 Hs.131373	tumor necrosis factor, alpha-induced pro	3.4
- •	446960	AW294936	Hs.156762	ESTs ESTs	3.4
	405605			C2001342:gij127814 spjP26434 NAH4_RAT SO	3.4 3.4
	433791	AA719352	Hs.112718	ESTs .	3.4

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	405238			Target Exon	3.4
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	414372 435523	AA143654 T62849	Hs.11090	gb:zo65a02.r1 Stratagene pancreas (93720 membrane-spanning 4-domains, subfamily A	3.4 3.4
5	406739	ALS66709	Hs.182426	ribosomal protein S2	3.4
-	442710	AI015631	Hs.23210	ESTs	3.4
	452526	W38537	Hs.280740	hypothetical protein MGC3040	3.4
	456060 435005	C14904 U80743	Hs.45184 Hs.306094	Horno septens cDNA FLJ12284 fis, clone MA trinucleotide repeat containing 12	3.4 3.4
10	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
••	425242	D13635	Hs.155287	KIAA0010 gene product	3.4
	436805	AA731533	Hs.270751	ESTs .	3.4
	418641 430809	BE243138 A1791150	Hs.86947 Hs.262009	a disintegrin and metafloproteinase doma ESTs, Moderately similar to I38022 hypot	3.4 3.4
15	428878	AA436884	Hs.48926	ESTs	3.3
	413774	AA131782	Hs.182314	ESTs	3.3
	400533			ENSP00000209376":PRED65 protein (Fragmen	3.3
	422448 423905	AW372922 AW579960	Hs.116774 Hs.135150	integrin, alpha 1	3.3 3.3
20	430637	BE160081	Hs.256290	lung type-I cell membrane-associated gly \$100 calcium-binding protein A11 (calgiz	3.3
	427899	AAB29286	Hs.332053	serum amyloid A1	3.3
	434206	AW136973	Hs.180479	ESTs, Wealthy similar to S69890 mittagen i	3.3
	453387 436265	AI990741 AA731331	Hs.252809 Hs.190668	ESTs ESTs	3.3 3.3
25	412971	AA889628	Hs.35125	ESTS	3.3
-+	441701	AW339828	Hs.127497	ESTs	3.3
	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.3
	434577 418216	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.3 3.3
30	436137	AA662240 Al056769	Hs.283099 Hs.133512	AF15q14 protein ESTs	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	440074	AA863045	Hs.10669	ESTs, Wealdy similar to T00050 hypotheti	3.3 3.3
35	405046 437816	AI823445	Hs.280699	C3000978:gij9280045 dbj[BAB01579.1] (AB0 ESTs	3.3 3.3
	401272			C9000559*:gil12314195jemb CAB99338.1 (A	3.3
	408896	AI610447	Hs.48778	niban protein	3.3
	432343 407881	NM_002960 AW072003	Hs.2961 Hs.40968	S100 catcium-binding protein A3	3.3 3.3
40	439978	BE139460	Hs.124673	heparan sulfate (glucosamine) 3-0-sulfot Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.3
	446134 412281	AW161234	Hs.13993	TBP-like 1 ESTs	3.3 3.3
45	436282	AI810054 R91913	Hs.14119 Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.3
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp43480425 (I	3.3
	409453 411565	AM58165 AW851728	Hs.17296	hypothetical protein MGC2376 gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3 3.3
50	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.3
	450508	NM_004460		fibroblast activation protein, alpha	3.3
	451254	AI571016	Hs.172967		3.3
	423784 433325	AK000039 AW206986	Hs.132826 Hs.143905		3.3 3.3
55	419898	299362	14.14000	pb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	3.3
	420552	AK000492	Hs.98808	hypothetical protein	3.3
	451778 427584	AI826131 BE410293	Hs.62954 Hs.179718	ESTs, Wealdy similar to zinc finger prot	3.3 3.2
	433507	AI817338	Hs.191791		3.2
60	418661	NM_001949		E2F transcription factor 3	3.2
	440933	AJ208217	Hs.142879		3.2
	426746 404120	J03626	Hs.2057	uridine monophosphate synthetase (orotat C5000537*:gi 3298595 gb AAC41376.1 (AF0	3.2 3.2
	453920	AJ133148	Hs.36602	I factor (complement)	3.2
65	437014	AA808757	Hs.222531	ESTs, Wealdy similar to S59501 interfero	3.2
	424479	AF064238	Hs.149098	1 A A	3.2
	413278 425922	BE563085 AL157466	Hs.833 Hs.162751	interferon-stimutated protein, 15 kDa Homo saplens mRNA; cDNA DKFZp761E2423 (f	3.2 3.2
	407304	AA565832	Hs.271649		3.2
70	411671	BE049094		ESTS	3.2
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
	454765	AW819629 X66839	Hs.63287	gb:RC5-ST0293-140200-014-H05 ST0293 Homo carbonic anhydrase IX	3.2 3.2
	410407 412490	AW803564	Hs.28885		3.2
75	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	3.2
	417124	BE122762	Hs.25338	ESTs	3.2
	407378	AA299264	Hs.57776		3.2
	439764 445936	T26535 BE543594	Hs.22744 Hs.61478		3.2 3.2
80	446523				3.2
	406060			Target Exon	3.2
	432250		Hs.27417 Hs.14942		3.2 3.2
	437269	~~~~	1 15. 14342	v 6013	75

	449115 425146	AW959952 AW954627	Hs.37528	ESTs, Weattly similar to AF090944 1 PRO06	3.2
	436210	A1825420	Hs.197824	gb:EST366697 MAGE resequences, MAGC Homo ESTs	3.2 3.2
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci	3.2 3.2
5	444371	BE540274	Hs.239	forkhead box M1	3.2
-	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.2
	445828	F05802	Hs.81907	ESTs .	3.2
	450810	8E207588	Hs.334360	transforming growth factor beta 1 induce	3.2
• •	439533	W76021		gb:zd64c04.r1 Soares_fetal_heart_NbHH19W	3.2
10	418079	R40058	Hs.6911	ESTs	3.2
	418781	T41160	Hs.8404	ESTs	3.2
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.2 ·
	431319	AA873350	Hs.302232	ESTs COLAT	3.2
15	445413 424947	AA151342 R77952	Hs.12677	CGI-147 protein	3.2
13	429490	AI971131	Hs.23889	ESTs, Wealth similar to atternatively sp ESTs, Wealth similar to ALU7_HUMAN ALU S	3.2
	426765	AA743603	Hs.172108	nucleoporin 88KD	3.2 3.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.2
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.1
20	439566	AF086387		gb:Home sepiens full length insert cONA	3.1
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	3.1
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.1
25	439570	179925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
25	443431	AI056847	Hs.20654	ESTs	3.1
	428289 415849	M26301 R20529	Hs.2253	complement component 2	3.1
	419652	AL157485	Hs.6806 Hs.91973	ESTs	3.1
	429500	X78565	Hs.289114	hypothetical protein hexabrachion (tenascin C, cytotactin)	3.1 3.1
30	457579	AB030816	Hs.36761	HRAS-like suppressor	3.1
	420579	AA278449	Hs.137429	ESTs	3.1
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.1
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.1
25	405183			NM_016358":Homo sapiens iroquois homeobo	3.1
35	420676	AJ434780	Hs.4248	vav 2 oncogene	3.1
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	3.1
	431176	AJ026984	Hs.293662	ESTs	3.1
	417918 437945	AA209205 T78519	Hs.163754	hypothetical protein FLJ12606	3.1
40	404632	170319		gb:yd68c08.r1 Soares fetal liver spieen NM_022490:Homo sapiens hypothetical prot	3.1
	428917	AA437337	Hs.16689	ESTs	3.1 3.1
	429940	W25215		gb:zb87a09.r1 Scares senescent fibroblas	3.1
	444016	AA448154		gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
4-	430701	A1760833	Hs.293971	ESTs	3.1
45	402229	8E262804		mitochondrial ribosomal protein \$2	3.1
	454177	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	3.1
	400090			Eos Control	3.1
	419326	W94915	Hs.42419	ESTs	3.1
50	435644 433042	AA700867 AW193534	Hs.269659 Hs.281895	ESTS	3.1
50	458810	8E407125	Hs.231510	Homo sapiens cDNA FLJ11660 fts, clone HE ESTs	3.1
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.1 3.1
	449670	F07693	Hs.85603	Homo sepiens mRNA; cDNA DKFZp434K2172 (f	3.1
	403288	·		C1001737*:gi 7511201 pirl T27904 hypothe	3.1
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.1
	432044	AW972727		gb:EST384819 MAGE resequences, MAGL Homo	3.1
	443105	X96753	Hs.9004	chondroitin sutfate proteoglycan 4 (mela	3.1
60	423789 439538	AK002084	Hs.132851	hypothetical protein FLJ11222	3.1
00	437681	AA837323 AI207958	Hs.56407 Hs.166556	ESTs Home springs Similar to TEA domain fami	3.1
	433577	AW007080	Hs.284192	Homo sapiens, Similar to TEA domain fami ESTs	3.1
	443021	AA368546	Hs.8904	lg superfamily protein	3.1 3.1
	433894	AI907682	Hs.243293	ESTs	3.1
65	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.1
	449162	AI632740	Hs.10476	ESTs .	3.1
	417893	AA290605	Hs.190002	ESTs .	3.1
70	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.0
, 0	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.0
	450756 422631	AJ733488	Hs.144062 Hs.118793		3.0
	414733	BE218919 BE514535	Hs.77171	hypothetical protein FLJ 10688 minichromosome maintenance deficient (S.	3.0
	431019	NM_005249	Hs.2714	forkhead box G18	3.0
75	434503	T96231	Hs.17762	ESTs	3.0 3.0
_	455481	AW948317		gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	427413	BE547647	Hs.177781		3.0
	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.0
٥٨	458760	AI498631	Hs.111334	ferritin, light polypeptide	3.0
80	410555	U92649	Hs_64311	a disintegrin and metalloproteinase doma	3.0
	411543	AW851248	Un 407000	gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	435375 407047	AI733610 X65965	Hs.187832		3.0
	40104	W01303		gb:H.saplens SOD-2 gene for manganese su	3.0

	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	3.0
	443338	R99575	Hs.302908	ESTs	3.0
	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.0
5	412135 418669	AW895309 U85992	Hs.87197	gb:QV4-NN0038-300300-155-e07 NN0038 Homo	3.0
,	449385	AI650471	Hs.347290	Human clone IMAGE:35527 unknown protein ESTs	3.0 3.0
	426384	AJ472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW450938	Hs.180115	ESTs	3.0
10	440388 427235	AI693520 AI126288	Hs.223000 Hs.192232	ESTs ESTs	3.0
	420116	NM_013241	Hs.95231	FH1/FH2 domain-containing protein	3.0 3.0
	419764	BE262524	Hs.931B3	vasodilator-stimulated phosphoprotein	3.0
	405673	M34996	Hs.198253	major histocompatibility comptex, class	3.0
15	445921 427695	AW015211 R88483	Hs.146181 Hs.172862	ESTs ESTs	3.0
	453324	W26592	Hs.232089	EST8	3.0 3.0
	404272			Target Exon	3.0
	428538 442786	AA446440 H50733	Hs.98643	ESTs	3.0
20	444396	T65213	Hs.256261 Hs.4257	ESTs. Moderately similar to ALUS_HUMAN A ESTs	3.0
	440483	AI200836	Hs.150386	ESTs	3.0 3.0
	429973	AJ423317	Hs.164680	ESTs	3.0
	450125 417409	AA005418 BE272506	Hs.158186 Hs.82109	ESTs	3.0
25	429569	AA454993	Hs.138343	syndecan 1 ESTs, Wealdy similar to 178885 serine/th	3.0 3.0
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.0
	427954	J03060	Hs.247551	metaxin 1	3.0
	422418 427527	AK001383 AIB09057	Hs.116385 Hs.293441	hypothetical protein FLJ10521 immunoglobulin heavy constant mu	3.0
30	416677	T83470	Hs.334840	ESTs, Moderately similar to 178885 serin	3.0 3.0
	451130	AI762250	Hs.345554	ESTs	3.0
	431431 425248	AL096711 AW957442	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	422757	A1909935	Hs.252766 Hs.65551	ESTs Homo sapiens, Similar to DNA segment, Ch	3.0
35	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	3.0 3.0
	416355	H49875	Hs.268906	ESTs	3.0
	426406 419829	AI742501 AI924228	Hs.169756 Hs.115185	complement component 1, s subcomponent	3.0
	412646	NM_006825	Hs.74368	ESTs, Moderately similar to PC4259 tem transmembrane protein (63kD), endoplasmi	3.0 2.9
40	423859	BE409301	Hs.134012	C1q-related factor	2.9
	422710 445906	AW936566	Hs.201876	ESTs	2.9
	429751	N28939 M55210	Hs.13434 Hs.214982	Homo sapiens clone 24418 mRNA sequence laminin, gamma 1 (formerly LAMB2)	2.9
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.9 2.9
45	443433	R44743	Hs.301667	ESTs	2.9
	444145 425262	BE153823 D87119	Hs.282385 Hs.155418	ESTs. Weakly similar to 2004399A chromos	2.9
	442476	AF069475	ris. 1334 10	GS3955 protein gb:AF069475 Homo sapiens astrocytoma lib	2.9 2.9
50	443361	A1792628	Hs.133273	ESTs	29
50	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	29
	415709 453385	AA649850 AW296101	Hs.278558 Hs.252806	ESTs ESTs	2.9
	442609	AL020996	Hs.8518	selenoprotein N	2.9 2.9
55	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2.9
23	414416 443502	AW409985 AI074528	Hs.76084 Hs.133949	hypothetical protein MGC2721	2.9
	444143	AW747996	Hs.160999	ESTs ESTs, Moderately similar to A56194 throm	2.9 2.9
	416308	AW291942	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxido	2.9 2.9
60	447674 408989	BE270640	Hs.19192	cyclin-dependent kinase 2	29
-	427418	AW361666 AA402587	Hs.49500 Hs.325520	KIAA0746 protein LAT1-3TM protein	2.9 2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.9 2.9
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.9
65	403290 430890	X54232	Hs.2699	C10001011*:gi 4758212tref NP_004411.1 d	2.9
	441217	AJ922183	Hs.213246	glypican 1 ESTs	2.9 2.9
	418287	AI872319	Hs.78935	methionine aminopeptidase; elF-2-associa	2.9
	443836	BE221613	Hs.140553	ESIs	2.9
70	451527 418110	AF022813 R43523	Hs.26518 Hs.217754	transmembrane 4 superfamily member 7 hypothetical protein FLJ22202	2.9
-	420886	AA805453		ESTs, Weakly similar to T29012 hypotheti	29 29
	439379	AA835002	Hs.125611	ESTs	2.9
	426197 406679	AA004410 AA070786	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.9
75	454120	AB032990	Hs.40719	gb:zm66b07.r1 Stratagene neuroepithelium hypothetical protein KIAA1164	2.9
	457244	AA581385	Hs.162473	ESTs, Wealdy similar to 138022 hypotheti	2.9 2.9
	432036	AF224266	Hs.272373	interleukin 20	2.9
	457364 437860	AW971037 AA333063	Hs.279898	gb:EST383123 MAGE resequences, MAGK Horno Horno sapiens cDNA: FLJ23165 fis, clone L	2.9
80	453544	AA831785	Hs.171914	Homo sapiens conver FLJ23165 is, clone t	2.9 2.9
	454968	AW849046		gb:IL3-CT0214-150300-085-H08 CT0214 Homo	2.9
	437528 400850	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.9
				Target Exon	2.9



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	428896	AW291932	Hs.98936	EST ₈	2.9
	426140	AF131798	Hs.343768 Hs.13291	Homo sepiens clone 25119 mRNA sequence	2.9
_	408872 414799	AI476139 AI752416	Hs.13291 Hs.77326	ESTs insulin-like growth factor binding prote	2.9 2.9
5	406646	M33600	Hs.308026	major histocompatibility complex, class	29
	416569	H64891	He 124702	gb:yr68h03.r1 Soares fetal liver spieen	2.9
	439130 451433	AA306090 AA021140	Hs.124707 Hs.269265	ESTs ESTs, Wealdy similar to A46010 X-linked	2.9
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	29 29
10	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.9
	420172	AA601122	Hs.95655	secreted and transmembrane 1	29
	442485 416505	BE092285 H66470	Hs.29724 Hs.16004	hypothetical protein FLJ13187 ESTs	29
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.9 2.9
15	420674	NM_000055	Hs.1327	butyrylcholinestergse	29
	452139 447499	AA099969 AW262580	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	28
	411373	AW262580 BE326276	Hs.147674 Hs.8861	protocadherin beta 16 ESTs	28
00	456816	AK001509	Hs.144391	hypothetical protein FLJ10647	2.8 2.8
20	414232	W85946	Hs.238246	hypothetical protein FLJ22479	2.8
	416188 447733	BE157260 AF157482	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.8
	447733 438624	AF157482 AA889055	Hs.19400 Hs.123468	MAD2 (mitotic arrest deficient, yeast, h ESTs	2.8 2.8
25	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	2.8
25	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	2.8
	42402B 421679	AF055084 AI475110	Hs.153692 Hs.203933	Homo sapiens cDNA FLJ14354 fis, clone Y7	2.8
	450651	W79000	Hs.44545	ESTs ESTs, Wealdy similar to 834087 hypotheti	2.6 2.8
20	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	28
30	432842	AW674093	Hs.334822	hypothetical protein MGC44B5	2.8
	403291 453096	AW294631	Hs.11325	Target Exon ESTs	2.8
	422545	X02761	Hs.287820	fibronectin 1	28 28
25	440296	D30829	Hs.180610	splicing factor profine/glutamine rich (2.8
35	427154	AL137262	Hs.325630	hypothetical protein MGC4289	2.8
	422282 434868	AF019225 R50032	Hs.114309 Hs.159263	epolipoprotein L collagen, type VI, alpha 2	2.8
	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sepiens	2.8 2.8
40	437437	AA226869		hypothetical protein DKFZp762L0311	28
40	427722 443623	AK000123 AA345519	Hs.180479	hypothetical protein FLJ20116	2.8
	443623 444006	BE395085	Hs.9641 Hs.10086	complement component 1, q subcomponent, type I transmembrane protein Fn14	2.8 2.8
	448432	AI783588	Hs.208575	ESTs	2.8 2.8
45	453682	T79703	-	gb:yd71e08.r1 Soares fetal liver spleen	2.8
43	447527 418557	A1702896 BE140602	Hs.42091 Hs.246645	ESTs	2.8
	409157	AA064631	rs.440043	ESTs gb:zf72c03.s1 Soares_pineal_gland_N3HPG	2.8 2.8
	457653	AJ820719	Hs.154662		2.8
50	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	2.8
50	439220 418312	AW295340 AW972468	Hs.130417 Hs.170307	ESTs, Weakly similar to Z195_HUMAN ZINC	2.8
	454581	AW809189	13.170307	Ral guanine nucleotide exchange factor R gb:MR4-ST0118-261099-012-e10 ST0118 Horno	2.8 2.8
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	2.8
55	400645 413951	ANAMEAGOA	LL 75046	Target Exon	2.8
	413951	AW051200 Al091713	Hs.75640 Hs.106597	natriuretic peptide precursor A Homo sapiens, Similar to RIKEN cDNA 1110	28
	404150		10.100381	Target Exon	2.8 2.8
	402936	******		ENSP00000217246*:DJ803K15.1 (novel prote	2.8
60	454457 439544	AW753456 W26354	LL 20004	gb:QV2-CT0261-261099-011-d11 CT0261 Homo	2.8
~	403969	1120337	Hs.28891	hypothetical protein FLI11360; artemis p ENSP0000034663:Zinc finger protein 131	2.8 2.8
	447183	Al554733	Hs.173182		2.8 2.8
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.8
65	426141 440148	C05886 AW014231	Hs.293972 Hs.90790	ESTs Homo sepiens cDNA: FLJ22930 fis, clone K	2.8
	430335	D80007	Hs.239499		2.8 2.8
	447071	AW236867	Hs.244376	ESTs	2.6 2.8
	428899	AA744610	Hs.194431		28
70	400658 403942			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM Target Exon	28
. •	420565	AI806770	Hs.30258	ESTs	2.8 2.8
	409734	8E151564	Hs.56155	hypothetical protein	2.8
	456645	AF227156	Hs.110103	RNA polymerase I transcription factor RR	2.8
75	401841 447247	AW369351	Hs.287955	NM_015113:Homo sepiens KtAA0399 protein	2.8
	450150	AI754391	Hs.23510	Homo sapiens cDNA FLJ13090 fis, clone NT Kruppel-like factor 12	2.8 2.8
	409154	U72882	Hs.50842	Interferon-induced protein 35	2.8
	410267 448224	AW978005 R48700	Hs.12600	N-ethylmalelmide-sensitive factor attach	2.8
80	410268	AA316181	Hs.20733 Hs.61635	Homo sapiens cDNA: FLJ22356 fis, clone H six transmembrane epithelial antigen of	28
	447512	AW958148	Hs.129454	ESTs	2.8 2.8
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	2.8
	415293	R49462	Hs.106541	ESTs	2.8
				220	

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	416207	NM_014745	Hs.79077	Homo sagiens, clone MGC:2908, mRNA, comp	2.8
	423337	NM_004655	Hs.127337	axin 2 (conductin, axii)	2.8
	425128	BE561929	Hs.154718	tumor protein D52-like 2	2.7
_	444491	Al151091	Hs.270714	ESTs .	2.7
5	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	2.7
	430377 417944	NM_001922 AU077196	Hs.301865 Hs.82985	dopachrome tautomerase (dopachrome delta	27 27
	444153	AK001610	Hs.10414	collagen, type V, alpha 2 hypothetical protein FLJ10748	27
	438138	R98299	Hs.177502	ESTs	2.7
10	425421	L11669	Hs.157145	tetracycline transporter-like protein	2.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.7
	451748	AK001612	Hs.26962	Homo sepiens cDNA FLJ10750 fis, clone NT	2.7
	452085 405941	AW239140	Hs.25614	ESTs, Wealdy similar to PC4396 mucin 3 T Target Exon	2.7 2.7
15	417395	BE564245	Hs.82084	Integrin beta 3 binding protein (beta3-e	2.7
	449667	AB023227	Hs.23860	KIAA1010 protein	2.7
	428808	AA436007	Hs.188780	ESTs .	2.7
	425843	BE313280	Hs.159627	death associated protein 3	2.7
20	438025 400924	AW501360	Hs.258910	ESTs Target Exon	2.7 2.7
~	412898	AJ129903	Hs.74669	vesicle-associated membrane protein 5 (m	2.7
	413834	BE296896	Hs.224179	ESTs. Weakly similar to 138022 hypotheti	2.7
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.7
25	406736 414280	A1254733	Hs.182426	ribosomal protein S2	2.7
23	434203	BE410769 BE262677	Hs.75873 Hs.283558	zyxin hypothetical protein PRO1855	2.7 2.7
	442621	AI004333	Hs.130553	ESTs, Weakly similar to ALUA_HUMAN !!!!	2.7
	414591	A1888490	Hs.55902	ESTs, Wealdy similar to ALU8_HUMAN ALU S	2.7
20	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.7
30	416784 413851	AA334592	Hs.79914	lumican Esta	2.7 2.7
	451767	AW897510 AI625014	Hs.137387 Hs.187328	ESTs ESTs	2.7
	441668	AI611973	Hs.136313	ESTs	2.7
~ ~	435664	AI032087	Hs.269819	EST8	2.7
35	435046	AA662772	Hs.174330	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.7
	439467 441329	AW292275 AI203575	Hs.158365 Hs.46821	ESTs hypothetical protein FLJ20086	2.7 2.7
	426925	NM_001196	Hs.315689	Homo sepiens cDNA: FLJ22373 fls, clone H	2.7
	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	2.7
40	449919	AI674585	Hs.200141	ESTs	2.7
	458070	AW503578	Hs.209406	ESTs. Wealthy similar to 138600 zinc fing	2.7
	444794 410781	Al419991 Al375672	Hs.145225 Hs.165028	ESTs ESTs	. 2.7 2.7
	449520	R34993	Hs.226666	ESTs, Moderately similar to 154374 gene	2.7
45	439481	AF086294	Hs.125844	ESTs	2.7
	401702			NM_001171*:Homo sapiens ATP-binding cass	2.7
	432890	NM_014442		siatic acid binding tg-like lectin 8	2.7
	435545 416422	AA587415 H60457	Hs.28107	ESTs ESTs, Moderately similar to ZN91_HUMAN Z	2.7 2.7
50	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	2.7
	420982	AW576160	Hs.100729	KIAA0692 protein	2.7
	431421	AW969118	Hs.108144	ESTs, Wealty similar to unnamed protein	2.7
	444168 419964	AW379879 AA811657	Hs.220913	gb:RC1-HT0256-081199-011-f01 HT0256 Homo ESTs	2.7 2.7
55	424480	AA341442	Hs.205299		2.7
	436314	A1983409	Hs.189226	ESTs	2.7
	405516			ENSP0000200457*:Thyroid receptor intera	2.7
	449340 457876	AW235786 AI821940	Hs.195359	hypothetical protein MGC10954 ESTs, Moderately similar to ALU8_HUMAN A	2.7 2.7
60	423799	AW026300	Hs.132906		2.7
-	422551	AW967284		gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	404592			NM_022739":Homo saplens E3 ublquitin lig	2.7
	424200 428612	AA337221 AA770001	Hs.188778	gb:EST41944 Endometrial turnor Homo sapie ESTs	2.7 2.7
65	446139	H77395	Hs.39749	ESTS	2.7
	440478	AI733047	Hs.130005		27
	429612	AF062649	Hs.252587		2.7
	422530	AW972300			2.7
70	423713 402032	AW754182		gb:RC2-C10321-131199-011-c01 C10321 Homo ENSP00000251056*:Plasma membrane calcium	2.7 2.7
, 0	424186	AI536021	Hs.288706		2.7
	402799			Target Exon	27
	423352		Hs.193570	S ESTS	2.7
75	412021			gb:RC4-OT0071-090300-011-g11 OT0071 Homo	27
, ,	458617 404170		Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr NM_000636":Homo sapiens superoxide dismu	2.7 2.7
	410886			gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	2.7
	414988	C17535		gb:C17535 Human placenta cDNA (TFujiwara	2.7
80	450325		Hs.26289		2.7
οU	458918 405760		Hs.25269	2 ESTs, Wealthy similar to 138022 hypotheti Target Exon	2.7 2.7
	406789			ribosomal protein L29	2.7
	424685			gb:EST51529 Gall bladder II Homo sepiens	2.7

	400335	Y13187	Hs.248068	Homo sapiens and gene, Intron 11	
	435065	8E064391		gb:RC4-BT0310-110300-015-b08 BT0310 Homo	27 27
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE fermity homeo	27
•	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	27
5	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	2.7
	428690 432692	AI948490 AW974944	Hs.98765 Hs.200577	ESTS	2.7
	439699	AF086534	Hs.187561	ESTs ESTs, Moderately similar to ALU1_HUMAN A	2.7
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	27 26
10	457035	AA398074	Hs.119143	ESTs, Moderately similar to KIAA1513 pro	26
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	26
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.6
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	2.6
15	422764 403431	A1767727	Hs.47522	EST8	2.6
13	439332	AW842747	Hs.300870	Target Exon	26
	412749	AA378417	Hs.74564	Homo sapiens mRNA; cDNA DKFZp547M072 (fr signal sequence receptor, beta (transloc	2.6
	409703	NM_006187	Hs.56009	2-5-ofigoadenylate synthetase 3 (100 k	26 26
••	405717			CX000838:gl]10092633 ref NP_055314.1 pu	2.6
20	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	26
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	26
	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.6
	447587 408605	AW292139	Hs.115789	ESTS	26
25	407103	AF025374 AA424881	Hs.45465 Hs.256301	T-cell, immune regulator 1	2.6
	427395	AW298741	Hs.97861	hypothetical protein MGC13170 ESTs, Moderately similar to I38022 hypot	2.6
	435113	AA665469	Hs.117136	ESTs	2.6 2.6
	419015	T79262	Hs.14463	ESTs	2.6
20	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.6
30	453707	AW003879	Hs.126522	Homo saplens, clone MGC:16722, mRNA, com	2.6
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.6
	404053 415069	AA159831	U- 20200	Target Exon	2.6
	449625	NM_014253	Hs.29286	ESTs, Weakly similar to I49836 DNA-bindi	2.6
35	438033	T26483	Hs.6059	odz (odd Oz/ten-m, Drosophila) homolog 1 EGF-conteining fibulin-like extracellula	2.6
	451593	AF151879	Hs.26706	CGI-121 protein	26 26
	435828	AA700705	Hs.13852	ESTs	26 .
	443753	AW367578	Hs.134749	ESTs	2.6
40	416097	BE397371	Hs.118964	hypothetical protein FLJ20085	2.6
40	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.6
	439755 408371	AW748482 AF161545	Hs.77873 Hs.44439	B7 homolog 3	2.6
	445658	AI469062	Hs.172660	hypothetical protein ESTs	2.6
	438166	N30158	Hs.122645	ESTs	2.6 2.6
45	449426	T92251	Hs.198882	ESTs	2.6
	422605	H16848	Hs.118666	hypothetical protein PP591	2.6
	415788	AW628686	Hs.78851	KIAA0217 protein	26
	448966 400295	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.5
50	441128	W72838 AA570256		AI905687:IL-8T095-190199-019 BT095 Homo	2.6
-	420372	AW960049	Hs.293660	ESTs, Weakly similar to T23273 hypotheti Homo sapians, clone IMAGE:3535476, mRNA,	2.6
	428977	AK001404	Hs.194698	cyclin B2	2.6 2.6
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	2.6
66	445211	BE045601	Hs.118248	ESTs, Wealthy similar to YC18_HUMAN HYPOT	2.6
55	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.6
	417838 420670	R24713 AW973577	Hs.22514	ESTs	2.6
	403267	A44313311		ESTs Target Exon	2.6
	454354	AW389896		gb:RC4-ST0173-191099-032-e12 ST0173 Homo	2.6 2.6
60	452903	AJ953425	Hs.345291	ESTs, Weakly similar to (38022 hypotheti	2.6 2.6
	427830	AA416598	Hs.98233	ESTs	2.6
	435953	AI767087	Hs.114142	ESTs	2.6
	430744	AA485229	Hs.105649	ESTs	2.6
65	413335 416370	AI613318 N90470	Hs.48442 Hs.203697	ESTs	2.6
Q 2	431865	AA521106	Hs.136375	ESTs, Weakly similar to I38022 hypotheti	2.6
	434274	AA628539	Hs.116252	ESTs, Wealdy similar to S65824 reverse t ESTs, Moderately similar to ALU1_HUMAN A	2.6 2.6
	447854	AW138454	Hs.11594	ESTs	2.6
70	412799	AJ267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	26
70	455409	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
	453055 443539	AW291436 AI076182	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.6
	434898	AW500458	Hs.134074 Hs.29956	ESTs, Moderately similar to ALUS_HUMAN A KIAA0450 protein	2.6
75	438118	AW753311	Hs.346690	ESTs	2.6
-	431786	AW452784	Hs.220718	ESTs	2.6 2.6
	421689	N87820	Hs.106826	KIAA1696 protein	2.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.6
80	424684	AW752714	Hs.5174	ribosomal protein \$17	2.6
-	439823 411962	AW665287 AA099050	Hs.124514	ESTs	2.6
	445774	A1254165	Hs.339968	gb:zk85d12.r1 Soares_pregnant_uterus_NbH ESTs	26
	400492			C10001573*:gi]7302749[gb]AAF57827.1] (AE	2.6 2.6
				1911 ase salkakan 31011.1] (VC	2.0

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	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	2.6
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.6
	440131	AI023425	Hs.222225	ESTs	26
5	438525 412247	AW368528 AF022375	Hs.100855 Hs.73793	ESTs vascular endothelial growth factor	26
•	406662	X62006	Hs.172550	polypyrimidine tract binding protein (he	2.6 2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible.	2.6
	402260 429599	AA806106	Hs.123664	NM_001436*:Homo sapiens fibrillarin (FBL	2.6
10	429562	AJ732767	Hs.158101	ESTs Homo sapiens cDNA FLJ14673 fis, clone NT	2.6 2.6
	432527	AW975028	Hs.102754	ESTs	2.6
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.6
	452732 424408	BE300078 Al754813	Hs.80449 Hs.146428	Homo sapiens, clone IMAGE:3535294, mRNA, collagen, type V, atpha 1	2.6
15	413151	H47969	Hs.141971	ESTs. Wealty similar to ALU1_HUMAN ALU S	2.6 2.6
	416244	N39535	Hs.32748	ESTs	2.6
	403104 400780			C80000641:gi[10432393]emb[CAC10283.1] (A	2.6
	433009	AA761668		NM_007325*:Homo sapiens glutamate recept gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	2.6 2.6
20	424090	X99699	Hs.139262	XIAP associated factor-1	2.6
	403212	054400	14 40000	NM_019595:Homo sapiens intersectin 2 (IT	2.6
	407855 406849	R54126 AA454809	Hs.40500 Hs.172928	similar to S. cerevisiae RER1 collagen, type I, alpha 1	2.6
	443462	AI064590	Hs.171176	ESTs	2.6 2.6
25	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrota	2.6
	450089 419571	AJ681883 AW674962	Hs.209546 Hs.91146	ESTs, Weakly similar to 2109260A B cell	26
	448140	AF146761	Hs.20450	protein kinase O2 BCM-like membrane protein precursor	26 26
20	444881	A1623288	Hs.192805	ESTs	2.6
30	420658	AW965215	Hs.130707	ESTs	2.6
	437634 426894	AW293046 AI204209	Hs.255158 Hs.143911	ESTs ESTs	2.6
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.6 2.6
35	434171	BE247688	Hs.347349	KIAA0948 protein	2.6
دد	410174 427245	AA306007 AA421022	Hs.59461 Hs.97739	DKFZP434C245 protein ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.5 2.5
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	2.5
40	452221	C21322	Hs.288057	hypothetical protein FLJ22242	2.5
70	439079 437287	AF085937 AA748180	Hs.38348 Hs.159346	ESTs hypothetical protein FLJ21369	2.5
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5 2.5
	427624	AA408245	Hs.24895	ESTs	2.5
45	435177 449433	AI018174 AI672096	Hs.42936 Hs.9012	ESTS Modely almiles to exects this binds	2.5
	447853	A1434204	Hs.164285	ESTs, Wealdy similar to \$26650 DNA-bindi ESTs, Wealdy similar to AFG1_YEAST AFG1	2.5 2.5
	416704	H77795	Hs.39785	ESTs	2.5
	401696 445677	H96577	Li. C020	Target Exon	2.5
50	413840	AI301558	Hs.6838 Hs.146381	ras homotog gene family, member E RNA binding motif protein, X chromosome	2.5 2.5
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	2.5
	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.5
	421848 421234	X15880 AA907153	Hs.108885 Hs.190060	collagen, type VI, sipha 1 ESTs	2.5
55	414598	AI094221	Hs.135150	tung type-I cell membrane-associated gly	2.5 2.5
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.5
	458199 433523	AW136417 H29882		hypothetical protein FLJ 14464	2.5
~~	429125	AA446854	Hs.271004	ESTs ESTs, Wealdy similar to I38022 hypotheti	2.5 2.5
60	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	2.5
	404748 413507	BE145360	LL 10000 4	ENSP00000238177":Similar to kynurenine 3	2.5
	418886	AA993982	Hs.190064 Hs.130858	ESTs, Weakly similar to I38022 hypotheti ESTs	2.5
<i>C</i>	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	2.5 2.5
65	452367	U71207	Hs.29279	eyes absent (Orosophila) homotog 2	2.5
	438258 459527	AW867491 AW977558	Hs.107125 Hs.291735	plasmalemma vesicle associated protein	2.5
	450543	AI394037	Hs.170296	ESTs, Weakly similar to 178885 serine/th Homo saplens cDNA: FLJ22090 fis, clone H	2.5 2.5
70	434818	AA650097	Hs.5996	ESTs	2.5 2.5
70	444534	AW271626	Hs.42294	ESTs	2.5
	452113 429115	AI859393 AA446728	Hs.289020	gb:wm11a02.x1 NCI_CGAP_Ut4 Homo sapiens Homo sapiens cDNA FLJ14098 fis, clone MA	2.5
	434012	AA621425	Hs.186256	ESTs	2.5 2.5
75	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	2.5
13	449505 419817	AI653006 AA743434	Hs.195374	ESTs	2.5
	457986	AA781745	Hs.193778 Hs.126920	ESTs Homo sapiens, clone IMAGE:4299555, mRNA,	2.5
	431454	AW975980	Hs.292918	ESTs	2.5 2.5
80	425018	BE245277	Hs.154196	E4F transcription factor 1	2.5
90	427513 441318	AI476318 AI078234	Hs.192480	ESTs SCT-	2.5
	424830	AW270580	Hs.176130 Hs.189311	ESTs ESTs, Wealdy similar to putative p150 [H	2.5
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.5 2.5
				241	
				241	

	446089	AI860021	Hs.345028	ESTs. Moderately similar to A47582 B-cel	2.5
	415983	AJ436798	Hs.117078	Homo sepiens cDNA: FLJ23028 fis, clone L	2.5
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	2.5
5	446862 448970	AV660697	Hs.282700	ESTS	25
,	459200	AW138582 Y09306	Us 20140	gb:UI-H-BI1-acw-e-06-0-UI.s1 NCI_CGAP_Su	2.5
	422627	BE336857	Hs.30148 Hs.118787	homeodomain-interacting protein kinase 3	2.5
	433388	AJ432672	Hs.288539	transforming growth factor, beta-induced hypothetical protein FLJ22191	2.5
	436222	AJ208737	Hs.122810	Homo sapiens cDNA FLJ11489 fs, clone HE	2.5
10	441255	R06350	Hs.171635	ESTs	2.5 2.5
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	2.5
	438714	AA814859	Hs.294112	ESTs	2.5
	441020	W79283	Hs.35962	ESTs	25
16	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.5
15	434267	AI206589	Hs.116243	ESTs	2.5
	446821	W03766		tropomodulin 3 (ubiquitous)	2.5
	402615			C1003844":gij6912550 ref NP_038483.1 al	2.5
	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares letal liver spleen	2.5
20	408253 444884	AW807476 Al201094	Hs.21051 Hs.148540	Homo sapiens mRNA for FLJ00012 protein,	2.5
20	440826	AW383618	Hs.346256	ESTS Madagadah almilas ta ALLIN MURAAN A	2.5
	431374	BE258532	Hs.251871	ESTs. Moderately similar to ALU2_HUMAN A CTP synthase	2.5
	458093	AJ207768	Hs.343628	sialytransferase 4B (beta-galactosidase	2.5 2.5
	422484	AA568770	Hs.123158	Homo sepiens cDNA FLJ12830 fis, clone NT	25
25	442804	AW300118	Hs.131257	ESTs	2.5
	420949	AA934063	Hs.13836	ESTs, Wealdy similar to 138022 hypotheti	2.5
	451350	AI791447		gb:ni13a05.y5 NCI_CGAP_Co4 Homo saplens	2.5
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.5
30	430426	AA478807	Hs.125173	ESTs	2.5
50	418526 406290	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.5
	442085	AA975688	Hs.159955	Target Exon	2.5
	448148	NM_016578	Hs.20509	ESTS	2.5
	432888	T86823	113.20003	HBV pX associated protein-8 gb:yd81a08.s1 Soares fetal liver spleen	2.5
35	424126	AA335635	Hs.96917	ESTs	2.5 2.5
	459727	AI906494		gb:RC-BT113-060499-024 BT113 Homo sapien	2.5
	407989	AW135208	Hs.256092	ESTs	. 25
	404571			NM_015902":Homo sapiens progestin induce	2.5
40	429139	F09092	Hs.66087	ESTs	2.5
40	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.5
	420608	BE548277	Hs.103104	ESTs	2.5
	432668 406871	AA558601 AA993857	Hs.43296	ESTs .	2.5
	443516	AA393837 AA305821	Hs.180842	ribosomal protein L13	2.5
45	445985	BE621800	Hs.9527 Hs.29444	apoptosis related protein APR-3	2.5
	424614	X54488	Hs.151242	putative small membrane protein NID67	2.5
	437267	AW511443	Hs.258110	serine (or cysteine) proteinase inhibito ESTs	2.5 2.5
	458251	AL040927	Hs.210422	ESTs	2.5 2.5
60	431198	AL047634	Hs.231913	ESTs	2.5
50	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	2.5
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-asso	2.5
	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.5
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.5
55	424662 423779	NM_002870 AW071837	Hs.151536	RAB13, member RAS oncogene family	2.5
55	405863	A1107 1037	Hs.57971	ESTs Tomat Funa	2.5
	458421	AI279978	Hs.22547	Target Exon ESTs	25
	439019	AF085902	Hs.271737	ESTs	2.5 2.5
	412577	Z22968	Hs.74076	CD163 antigen	2.5
60	404891			Target Exon	2.5
	419043	T19167	Hs.89566	ets variant gene 1	2.5
	448482	AW294078	Hs.171092	ESTs	2.5
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	2.5
65	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.5
UJ	450597 414386	AI701635 X00442	Hs.207077 Hs.75990	ESTs	2.5
	440473	BE562314		haptoglobin	2.5
	406851	AA609784	Hs.98711	Homo sapiens, clone IMAGE:3677165, mRNA,	2.5
	414821	M63835	Hs.77424	major histocompatibility complex, class Fc tragment of tgG, high affinity ta, re	25
70	417663	R07483	Hs.180461	ESTs	25
	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.5 2.5
	450683	H43540	Hs.25292	ribonuclease HI, large subunit	2.5
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spieen	25
75	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.5
13	409449	H11341	Hs.13366	Homo sapiens cDNA: FLJ23567 fis, clone L	2.5
	TADE #	40.			
	TABLE 1- Pkey:		un Ene	ant Identificance beautificance beautificance and an artist and artist artist and artist artist and artist	
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	440000	4000000 4	AA085208 AA085045
5	410886 411537	1225822_1 1248899_1	AW809324 BE144977 BE144956
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	411671	125369_1	BE049094 AA700765 H86770 AA094648 R02483 C03868 N56170
• •	411688	1254076_1	AW953440 T08189 AW857085
10	411962	126744_1	AA099050 AA099526 T47733
	412021	1272156_1	AW885592 AW885594 AW885579 AW885651
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	412799	132817_1	A1287606 AA121045 AA126521
15	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AH24991 AI693507 AI863108 AA599060 AI091148 AA598689
			R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
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	414372 414988	143909_1 1511316_1	A143654 AW753140 AA213770 AW970865 AA569075 AA492132
20	415131	1523680_1	C17535 D59244 D58878 D79090 D61119 D81508 D81734
	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	416569	1601567_1	H64891 R93444 R93458 R05590
	416871	1626761_1	H98716 N90792 N24283
25	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
23	419896 420352	1888662_1 192979_1	Z99362 Z99363 EE-258924 AMPERIUS AA DERSUI AA DERSUI AMPARIUS DAAVAA AKSEEDE DERSUI DE
	420670	195442_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AW973577 AA553821 AA279187
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	424009	234177_1	F11690 AW965370 AA333586 D30830
	424200 424686	236595_1 242486_1	AA337221 AA336756 AW966196 AA345504 AA345251 AW963243
	424947	245247_1	A77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
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	430968	326269_1	AW972830 AA527647 AA489820 AA570362
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	432363	345469_1	AA534489 AW970240 AW970323 .
45	432888	355780_1	T86823 Al821425 Al732232 AA569589 AA570737
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	433835	374758_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AI806185 AA610083 AI693089 AI693075
	434589	38929_1	AF147363 T47219 T47218
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	101 107	40703_1	BE617136 AA23844 T89946 AA247450 N55777 W38725 A7743846 A808406 AA922229 A051464 W04713 R11251 W19656 AC081849 AA489276
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	437945	44580_1	T78519 H59898 U72516
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60	439566	47387_1	W1027 AT 000032 W7200 AF086387 W77884 W7211
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	446821	69435_1	W03768 A1357775 AV660500 AV660731
	448970	791254_1	AW138582 AI638298 AI631640 AI963868 AI611082
70	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW883569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
70			N48674 AJ375997 R45432 D59344 AJ203107 F07491 R35360 R25094 AJ913631 AJ498402 T61382 AJ016320 N45526 T61415 AA331486
	450166 450375	82677_1	AA429504 R41904 AA279467 H09648 AA007236
	430375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852878 AA113758 AA826915 AA746952 A1161014 AA099554 R69067
	450506	836_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI524429 AW190535 AI446661 AI478772
75			AW022667 AA528235 AA599775 AW613820 AI433783 AW594230 AI051768 AI200109 AI680296 AA436611 AW609728 W42634 AI682584 AA405569
			A1685653 AWO
	450625	84032_1	AW970107 AAS13951 AA010408
	451129 451350	859870_1 866945_1	BE072881 BE072946 AI762181 AI791447 AI791327 AW886809
80	452113		A151447 A151327 AW8808009 A185933 BE177742
-	452203		X57522 AW295947 AI346197 AI304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R18264 T74462 AA346259
			AW502508 AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 AI819778 AA054458 AI346733

	453331	96214_1		3681 N77468 H51833 AA147247 R75732 C18450 R73999 AID95755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 498 H02668 AA035018 R75957 AIB03329 R27528 R36203 AIB09932 AIB08765 R78948 AA411449 AA976929 AI378760 AIJ78620 T48870
5	453682 454177	977454_1 1049351_1	T79703 T96 AW807321 /	307 AL079725 NW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 NW807167 AW807398 AW807320 AW807306 AW845856
	454354	1129859_1		\W389898 AW389906 AW609203 AW389873
	454457	1207274_1		W753035 AW854868 AW854862
	454581	1225710_1		AW809219 AW813574
10	454765	1233905_1	AW819629	
	454860	1237732_1		AW835537 BE160187
	454968	1247029_1		AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455104	1253737_1		E153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665
15	455409	1288355_1	AW936740	AW336609 AW336657 AW336611 AW338739 AW336734 AW336779 AW336688 AW336659 AW336738 AW336827 AW336737 AW336736 AW336833 AW336777 AW336830 AW336834 AW336829 AW338772 AW336638 AW336658 AW336638 AW336774 AW336778 AW336766
	*****	1202102.1		W936831 BW9
	455481 455646	1293182_1 1348557_1		AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324 IE064435 GE064429 BE064414 BE064400 BE064517
20	455778	1364506_1		1E088802 BE088755 BE088876 BE08B947 BE088881 BE08B952
	455899	1381547_1		E155154 BE155087 BE155247 BE155499 BE155387 BE155452
	456304	176820_1		1734077 AI820984 AA225796 AA225060 AA225 101
	457364	328154_1		AA508019 AA492345
25	457876	42814_2		67106 A1744264 AAB08846 AAB43417 AA643416 Z70715
25	458199	504856_1		A1141026 A1340960 A1091670 A1523802 AW572908 A1458860 A1924374 A1830572 A1400702 A1337539 A1968111 A1521308 A1492336
				1672594 AW665077 AA971810 AA909139 AW082128 A1335251 A1807192 AW511744 A1023232 A1536899 AW207791 A1670910 A1002047
			AW4	
	TABLÉ 14	ıc:		
30	Pkey:		ove number co	responding to an Eos probeset
	Ref.			The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
				n chromosome 22' Dunham, et al. (1999) <u>Natura</u> 402:489-495.
	Strand:			and from which exons were predicted.
35	Nt_positio	n: Indi	cates nucleotid	e positions of predicted exons.
33	Pkey	Ref	Strand	An angles
	400492	9213749	Minus	Nt_position 123881-124090
	400533	6981826	Minus	277132-277596
	400645	8117693	Minus	58471:58716
40	400658	8118459	Minus	73525-73644
	400780	8131663	Minus	118372-118619
	400850	1927150	Minus	4506-4691
	400924	7107613	Minus	30309-30498
45	401272 401454	9797373 9186923	Minus	98374-98509
43	401696	3417290	Minus Minus	114659-114832 46209-46401
	401702	1871197	Minus	68182-68325
	401841	7684597	Plus	89868-90006,91920-92085
	402032	7656761	Plus	62293-62475
50	402082	8117478	Minus	190046-190183
	402229	9965022	Minus	15739-15951,16166-16779
	402239 402260	7690131	Plus	38175-38304,42133-42266
	402274	3399665 2935596	Minus Plus	113765-113910,115653-115765,116808-116940 5604-6527
55	402604	9909420	Plus	20393-20767
	402615	9926801	Plus	131390-132157
	402799	3355547	Plus	35718-35899
	402855	9662953	Minus	59763-59909
60	402936	8894303	Plus	51655-51771
00	403011 403104	6693597 7331404	Minus Minus	3468-3623 41800-41973
	403108	8980955	Plus	93253-93667
	403212	7630897	Minus	156037-156210
	403267	7887182	Plus	116078-121885
65	403288	8081479	Plus	133763-133899,135813-135958
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403349 403361	8569773 8570313	Minus Minus	167815-168374 . 112498-112687
70	403431	7139839	Plus	56509-56860
	403481	9965004	Plus	93496-93633
	403696	3135242	Minus	143467-143534
	403790	8084957	Minus	87826-87947,89835-90002
75	403849	7708855	Plus	95043-96519
13	403942	7711825 2606076	Minus	99606-99757 1140093
	403961 403969	7596976 8569909	Minus Plus	110393-110603 31237-31375,32405-32506
	404053	3548785	Plus	51237-31373,32445-32506 61797-64205
	404120	7342152	Plus	135775-136000
80	404150	7534008	Plus	165911-165943
	404170	9930793	Plus	168836-169248
	404209	5006246	Minus	11247-11514
	404272	9885189	Plus	83207-83355,84358-84496,90519-90720,91371-91447

	404407	7329316	Minus	48154-48499
	404571	7249169	Minus	112450-112648
	404584	9857511	Plus	138551-139153
_	404592	9943965	Minus	39067-39225
5	404632	9796668	Plus	45096-45229
	404748	7263437	Plus	11446-11591
	404891	7329392	Plus	84974-85125
	405045	759682 9	Minus	4373-4528
	405141	8980911	Ptus	99861-100054
10	405183	7209940	Plus	12335-12653
	405238	7249119	Minus	51728-51836
	405348	2914717	Minus	43310-43462
	405516	9454624	Plus	112707-112876.113676-113854
	405558	1621110	Plus	4502-4644,5983-6083
15	405605	5836195	Minus	117070-117270
	405717	9588573	Plus	11275-11973
	405760	6066938	Minus	37424-38045
	405863	7657810	Plus	49410-49620
•	405941	6758796	Plus	2798-3444
20	406060	6899623	Minus	20339-20746
	406290	5686274	Plus	8711-9358
	406395	9256242	Minus	20805-20960
	406478	9857502	Plus	68314-68523,68853-68950
25	406481	9864741	Minus	91439-91579

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 15A lists about 1033 genes up-regulated in gliobtastoma compared to normal normal adult tissues. These were selected from 59680 probasets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" gliobtastoma to "average" normal tissues was greater than or equal to 3.0. The "average" gliobtastoma level was set to the 85° percentite amongst various brain tumors. The "average" normal tissues level was set to the 85° percentite amongst various non-matignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentite value amongst the various non-matignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Phey:
Unique Eos probaset Identifier number
Exacon:
Exacon:
Unique Eos probaset Identifier number
Unique number
Unique number
Unique number
Unique gene title
Ratio of GLIOBLASTOMA to NORMAL ADULT TISSUES 30

35

	Pkev	ExAcon	UnigenetD	Unigene Title	RI
40	427343	AI880044	Hs.176977	protein kinase C binding protein 2	60.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	54.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.1
	428321	AI699994	Hs.2868	peripheral myelin protein 2	49.6
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	45.4
45	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZo761C1712 (f	43.9
-	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	42.7
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.3
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	39.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
50	417183	R52089	Hs.172717	ESTA	37.6
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	36.5
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	34.3
	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	33.9
	449494	AW237014	Hs.315369	Homo saplens cDNA: FLJ23075 fls, clone L	33.9
55	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	32.7
	429276	AF058085	Hs. 198612	G protein-coupled receptor 51	32.3
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	29.0
	450133	AW969769	Hs. 105201	ESTs	27.9
	412733	AA984472	Hs.74554	KIAA0080 protein	27.6
60	425842	AL587490 ·	Hs.159623	NK-2 (Drosophila) homotog B	27.3
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	27.1
	424140	248051	Hs.141308	myelin oligodendrocyte głycoprotein	25.2
	402604		- •	Target Exon	24.3
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 safivary	24.3
65	422656	AI870435	Hs.1569	LIM homeobox protein 2	23.6
	447359	NM_012093	Hs.18268	adenylate kinase 5	23.3
	436878	BE465204	Hs.47448	ESTs	22.9
	435708	AI362949	Hs.75169	ESTs	22.9
70	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	22.7
70	439239	A1031540	Hs.235331	ESTs	22.4
	409395	U46745	Hs.336678	dystrobrevin, alpha	22.2
	425799	T08133	Hs.182906	Homo sepiens mRNA for KIAA1872 protein.	21.9
	425057	AA826434	Hs.1619	achaeta-scute complex (Orosophila) hornol	21.3
76	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	21.2
75	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	21.0
	419078	M93119	Hs.89584	insulinoma-essociated 1	21.0
	425048	H05468	Hs.164502	ESTs	20.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.3
οΛ	423853	AB011537	Hs.133466	stit (Drosophila) homolog 1	19.3
80	418110	R43523	Hs.217754	hypothetical protein FLJ22202	19.2
	447004	AW296968	Hs.157539	ESTs	18.6
	439415	F05538	Hs.4273	ESTs	18.6
	441497	R51064	Hs.23172	ESTs	18.5

	425523	AB007948	Hs.158244	KQAA0479 protein	18.3
	413597	AW302885	Hs.117183	ESTs	18.2
	433551	A1985544	Hs.12450	protocadherin 9	17.7
_	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	17.3
5	453642	AI370938	Hs.34074	dipeptidytpeptidase VI	17.3
	418338	NM_002522	Hs.84154	neuronal pentraxin I	17,1
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	16.8
	408604	D51408	Hs.21925	ESTs	16.6
10	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	16.6
10	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	16.5
	448302	AJ480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.4
	429466	M85835	Hs.12827	ESTs	16.3
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	15.9
16	448672	AI955511	Hs.225106	EST ₈	15.8
15	448743	AB032962	Hs.21896	KIAA1136 protein	15.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	441285	NM_002374	Hs.167	microtubule-associated protein 2	15.2
	431019	NM_005249	Hs.2714	forthead box G1B	14.8
20	431941	AK000106	Hs.272227	Homo sepiens cDNA FLJ20099 fis, clone CO	14.3
20	433800 416370	AI034361	Hs.135150	lung type-I cell membrane-associated gly	14.3
	439979	N90470	Hs.203697	ESTs, Wealdy similar to 138022 hypotheti	14.1
	444471	AW500291 AB020684	Hs.6823	hypothetical protein FLJ10430	14.0
	444783	AK001468	Hs.11217 Hs.62180	KIAA0877 protein	13.9
25	448595	AB014544	Hs.21572	anillin (Drosophila Scraps homolog), act	13.8
	441440	AI807981	Hs.30495	KIAA0644 gene product ESTs	13.6
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.6
	424790	AL119344	Hs.13326	ESTs, Wazikly similar to 2004399A chromos	13.5
	459516	AI049662	Hs.246858	EST	13.3
30	421264	AL039123	Hs.103042	microtubule-associated protein 18	13.2 13.2
	428342	AI739168		Homo sapiens cDNA FLJ13458 fs, clone PL	13.1
	408562	A1436323	Hs.31141	Home sapiens mRNA for KIAA1568 protein,	12.9
	412959	D87458	Hs.75090	KIAA0282 protein	12.9
~ -	439199	R40373	Hs.26299	ESTs	12.8
35	423419	R55336	Hs.23539	ESTs	12.5
	445495	BE622641	Hs.38489	ESTs, Weakly similar to 138022 hypotheti	12.4
	415849	R20529	Hs.6806	ESTs	12.4
	452372	AJ885742	Hs.228474	ESTs	12.4
40	452744	AI267652	Hs_246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	12.3
40	426344	H41821	Hs_322469	transcriptional activator of the c-los p	12.2
	415734	NM_014747	Hs.78748	KIAA0237 gene product	12.1
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	12.1
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	12.0
45	409049	AI423132	Hs.146343	ESTs	11.9
43	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.9
	427897 453941	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	11.8
	424120	U39817	Hs.35820	Bloom syndrome	11.8
	418738	T80579 AW388633	Hs.290270 Hs.6682	ESTs	11.7
50	411305	BE241596	Hs.69547	solute carrier family 7, (cationic amino	11.7
-	424945	AJ221919	FIS.08047	Myelin basic protein	11.7
	449539	W80363	Hs.58446	hypothetical protein FLJ10582 ESTs	11.6
	409638	AW450420	Hs.21335	ESTs	11.5
	441016	AW138653	Hs.25845	ESTs	11.5 11.4
55	429037	XB1895	Hs.194765	H.sapiens GENX-5624 mRNA, 3 UTR	11.3
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	11.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.2
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	11.2
40	424432	AB037821	Hs.14685B	protocadherin 10	11.1
60	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	11.1
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	11.1
	438380	T06430	Hs.6194	chondroitin sutfate proteoglycan BEHAB/b	11,1
	423678	AW963357	Hs_7847	ESTs .	10.7
65	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	10.7
05	430691	C14187	Hs.103538	ESTs .	10.7
	428728	NM_016625	Hs.191381	hypothetical protein	10.6
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	10.6
	431988 433896	AC002302	Hs.77202	protein kinase C, beta 1	10.5
70	433696	AW294729 N71831	Hs.274461	ESTs	10.5
	419249	X14767	Hs.256398 Hs.89768	Homo sapiens mRNA; cDNA OKFZp434E0528 (I	10.4
	445041	T64183	Hs.282982	gamma-aminobutyric acid (GABA) A recepto	10.3
	446782	AI553048	Hs.144006	SOLUTE CERTIES ESTS	10.3
_	451952	AL120173	Hs.301663	ESTs	10.2
75	446711	AF169692	Hs.12450	protocadherin 9	10.2
-	438054	AA776626	Hs.169309	ESTs	10.1
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	10.1
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	10.1
00	419863	AW952691	Hs.93485	Homo sepiens mRNA; cDNA OKFZp761D191 (fr	10.0
80	416857	AA188775	Hs.292453	ESTs	10.0 10.0
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.0
	419271	N34901	Hs.238532	EST8	9.9
	429927	NM_001115	Hs.2522	adenylate cyclase 6 (brain)	9.9
				• •	



	415293	R49462	Hs.106541	ESTs	9.9
	4401B4	AB002297	Hs.7022	dedicator of cyto-kinesis 3	9.8
	452526	W38537	Hs.280740	hypothetical protein MGC3040	9.8
5	427304	AA761526	Hs.163853	ESTs	9.7
J	420547 421659	AF155140 NM_014459	Hs.98738 Hs.106511	gonadotropin-regulated testicular RNA he	9.6
	426847	S78723	Hs.298623	protocadherin 17	9.6
	429656	X05608	Hs.211584	5-hydroxytryplamine (serotonin) receptor neurofilament, light polypeptide (68kD)	9.6
	447101	N72185	Hs.44189	ESTs	9.5 9.5
10	442613	AID04002	Hs.130522	Kv channel-interacting protein 1	9.5
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	445102	AW204610	Hs.22270	ESTs	9.5
	435793	AB037734	Hs.4993	KIAA1313 protein	9.5
16	437948	AA772920	Hs.303527	ESTs	9.5
15	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.4
	415170	R44386	Hs.164578	ESTs	9.3
	415486 435501	H12214	Hs.13284	ESTs. Weakly similar to 2109260A B cell	9.2
	415072	AW051819 AL110370	Hs.129908 Hs.79000	KIAA0591 protein	9.2
20	442910	Al365130	Hs.11307	growth associated protein 43 ESTs, Weakly similar to T19326 hypotheti	9.2
	438080	AA777381	Hs.291530	ESTs. Wealty similar to ALUC_HUMAN !!!!	9,1 9,1
	425187	AW014486	Hs.22509	ESTs	9.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	9.0
25	430091	AB032958	Hs.233023	KIAA1132 protein	9.0
25	427540	R12014	Hs.20976	ESTs	9.0
	447198	D61523	Hs.283435	ESTs	9.0
	449611	A1970394	Hs.197075	ESTs	8.9
	444124	R43097	Hs.6818	ESTs	8.9
30	451996 45404B	AW514021 H05626	Hs.245510	ESTs	8.8
20	412266	N59006	Hs.6921 Hs.26133	ESTs ESTs	8.8
	433597	AA708205	Hs.100343	ESTs	8.8
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.7 8.6
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	8.6
35	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	8.5
	423135	N67655	Hs.26411	ESTs	8.5
	418097	R45137	Hs.21868	ESTs	8.4
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
40	419721	NM_001650	Hs.288650	aquaporin 4	8.4
40	449300	A1656959	Hs.346514	ESTs	8.4
	436954 425 3 54	AA740151 U62027	Hs.130425	ESTs .	8.3
	424997	AL138167	Hs.155935	complement component 3a receptor 1	8.3
	442710	AI015631	Hs.96920 Hs.23210	ESTs ESTs	8.3
45	449625	NM_014253	15.23210	odz (odd Oz/ten-m, Drosophila) homolog 1	8.2
	451625	R56793	Hs.106576	elanine-glyoxylate aminotransterase 2-ti	8.2 8.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.0
	449605	AW138581	Hs.198416	ESTs	8.0
50	407886	AW969688	Hs.100826	EST ₅	8.0
50	414175	Al308876	Hs.103849	hypothetical protein DKFZp761D112	7.9
	429946	R49390	Hs.254129	KIAA1678	7.9
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	7.9
	455601 409799	AI368680 D11928	Hs.B16	SRY (sex determining region Y)-box 2	7.9
55	415279	F04237	Hs.76845 Hs.1447	phosphoserine phosphatase-like glial fibrillary acidic protein	7.8
	429918	AW873986	Hs.119383	ESTs	7.8 7.8
	449433	Al672096	Hs.9012	ESTs, Wealthy similar to \$26650 DNA-bindi	7.8
	422411	AW749443	Hs.22511	ESTs	7.7
60	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	7.7
60	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.7
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.7
	407168 448555	R45175 Al536697	Hs.117183	ESTs	7.6
	428535	AI143139	Hs.159863	ESTs	7.6
65	408947	AL080093	Hs.2288 Hs.49117	visinin-like 1 Homo saplens mRNA; cDNA DKFZp564N1662 (f	7.6
	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.6
	435624	AF218942	Hs.24889	formin 2	7.6 7.6
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	7.6
70	412068	S72043	Hs.73133	metaflothionein 3 (growth inhibitory fac	7.6
70	445568	H00918	Hs.268744	KIAA1796 protein	7.5
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	456965 458332	AW131888 AI000341	Hs.172792	ESTs. Weakly similar to hypothetical pro	7.5
75	409902	AI000341 AI337658	Hs.220491	ESTs ESTo	7.4
. •	448321	NM_005883	Hs.156351 Hs.20912	ESTs artenomatous entroseis coli libo	7.3
	420345	AW295230	Hs.25231	adenomatous polyposis coli like ESTs	7.3
	402855		2020	NM_001839°:Homo saplens calponin 3, acid	7.3 7.2
00	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.2
80	425741	AF052152	Hs.159412	Homo sepiens clone 24628 mRNA sequence	7.2
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	7.2
	415651	AI207162	Hs.3815	stathmin-like-protein RB3	7.2
	412709	AL022327	Hs.7451B	KIAA0027 protein	7,1

	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	7.1
	445745	AB007924	Hs.13245	KIAAD455 gene product	7.1
	439451	AF085270	Hs.278554	heterochromatin-like protein 1	7,1
5	418030 400292	BE207573 AA250737	Hs.83321	neuromedin 8	7.1
,	400292	AL079409	Hs.72472 Hs.38176	BMP-R1B	7.1
	440435	AL042201	Hs.21273	KIAA0606 protein; SCN Circadian Oscillat transcription factor NYD-sp10	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	7.0
10	440152	AB002376	Hs.7006	KIAA0378 protein	7.0 7.0
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.0
	454293	H49739	Hs.134013	ESTs. Moderately similar to HK61_HUMAN H	7.0
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.0
15	426814	AF036943	Hs.172619	myelin transcription factor 1-Bus	6.9
13	416836	D54745	Hs.80247	cholecystokinin	6.9
	447350 440074	Al375572 AA863045	Hs. 172634	ESTs	6.9
	436039	AW023323	Hs.10669 Hs.121070	ESTs, Weakly similar to T00050 hypotheti ESTs	6.9
	444396	T65213	Hs.4257	ESTs	6.9
20	425234	AW152225	Hs.165909	ESTs, Wealdy similar to 138022 hypotheti	6.9
	438330	AW450572	Hs.257316	ESTs	6.9 6.8
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	6.B
	421141	AW117261	Hs.125914	ESTs	6.7
25	412788	AA120960	Hs.198416	ESTs	6.7
23	411078	AJ222020	Hs.182364	CocoaCrisp	6.7
	443455	A8001025	Hs.9349	ryanodine receptor 3	6.7
	448769 441523	N66037 AW514263	Hs.38173	ESTS	6.7
	414214	D49958	Hs.301771	ESTs, Weatdy similar to ALUF_HUMAN !!!!	6.7
30	439845	AL355743	Hs.75819 Hs.56663	glycoprotein M6A	6.6
••	437036	AI571514	Hs.133022	Homo saplens EST from clone 41214, full ESTs	6.6
	429239	AA448419	Hs.45209	ESTs	6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6 6.6
36	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.5
35	452834	A1638627	Hs.105685	KIAA1688 protein	6.5
	441916	AA993571	Hs.129075	ESTS	6.5
	451516	AI800515	Hs.12024	ESTs	6.5
	434808 452461	AF155108	Hs.256150	Homo saplens, Similar to RIKEN cDNA 2810	6.5
40	450375	N78223 AA009647	Hs.108106	transcription factor	6.5
••	434811	AW971205	Hs.114280	a disintegrin and metalloproteinase doma ESTs	6.4
	424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	6.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.4 6.3
4.0	414245	BE148072	Hs.75850	WAS protein family, member 1	6.3
45	433447	U29195	Hs.3281	neuronal pentraxin II	6.3
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	6.3
	426919	AL041228		ELAV (embryonic tethal, abnormal vision,	6.3
	411411 415669	AA345241	Hs.55950	ESTs, Wealdy similar to KIAA1330 protein	6.3
50	449048	NM_005025 Z45051	Hs.78589 Hs.22920	serine (or cysteine) proteinase inhibito	6.2
	433929	Al375499	Hs.27379	similar to S68401 (cattle) glucose induc ESTs	6.2
	423346	AI267677	Hs.127416	synaptojanin 1	6.2
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.2 6.2
	412140	AA219691	Hs.73825	RAB6 Interacting, kinesin-like (rabkines	6.2
55	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
	420608	BE548277	Hs.103104	ESTs .	6.2
	424085	NM_002914	Ha.139226	replication factor C (activator 1) 2 (40	6.2
	422175 428845	N79885 AL157579	Hs.6382 Hs.153610	ESTs. Highly similar to T00391 hypotheti	6.1
60	439274	AF086092	Hs.48372	KIAA0751 gene product ESTs	6.1
	447499	AW262580	Hs.147674	protocadherin beta 16	6.1
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1 6.1
	453924	R49295	Hs.24886	ESTs	6.1
45	449340	AW235786	Hs.195359	hypothetical protein MGC10954	6.1
65	420077	AW512260	Hs.87767	ESTs	6.1
	431721	AB032996	Hs.268044	KIAA1170 protein	6.1
	433701	AW445023	Hs.15155	EST8	6.1
	430968 429469	AW972830 M64590	11- 07	gb:EST384925 MAGE resequences, MAGL Homo	6.1
70	456723	Z43902	Hs.27 Hs.4748	glycine dehydrogenase (decarboxylating;	6.1
	448681	AL109781	Hs.21754	adenylate cyclase activating polypeptide Homo sapiens mRNA full length insert cDN	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	6.0 6.0
76	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
75	448243	AW369771	Hs.52620	integrin, beta 8	6.0
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.0
	419704	AA429104	Hs.45057	ESTS	6.0
	436936 428409	AL134451 AW117207	Hs.197478	ESTs .	6.0
80	433244	AB040943	Hs.98523	ESTs	6.0
	439772	AL365406	Hs.271285 Hs.10268	KIAA1510 protein	6.0
	408096	BE250162	Hs.83765	Homo sapiens mRNA full length insert cDN dihydrofolate reductase	6.0
	419929	U90268	Hs.93810	cerebral cavernous mationmations 1	6.0 6.0
				vervirus imanui (MAN)	₽0

	100211		15- 440440		
	422544 413627	AB018259 BE182082	Hs.118140 Hs.246973	KIAA0716 gene product ESTs	6.0
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	6.0 6.0
_	410366	AI267589	Hs.302689	hypothetical protein	6.0
5	429183	AB014604	Hs.197955	KIAA0704 protein	5.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.9
	441102 448533	AA973905 AL119710	Hs.21365	intermediate filament protein syncollin	5.9
	407182	AA312551	Hs.230157	nucleosome assembly protein 1-like 3 ESTs	5.9 5.9
10	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.9
	433523	H29882		ESTs	5.9
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.9
	424343 420156	AW956360 AW449258	Hs.4748 Hs.6187	adenylate cyclase activating polypeptide	5.9
15	422864	AA318323	Hs.12827	eSTs gb:EST20390 Retina II Homo sapiens cDNA	5.9 5.8
	445727	AB011095	Hs.16032	KIAA0523 protein	5.8
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (I	5.8
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	5.8
20	425782 419629	U66468 AB020695	Hs.159525 Hs.91662	cell growth regulatory with EF-hand doma	5.8
~	452279	AA286844	Hs.61260	KIAA0888 protein hypothetical protein FLJ13164	5.8 5.8
	407608	AA663559	Hs.279789	histone deacetylase 3	5.8
	414737	AI160386	Hs.125087	ESTs	5.8
25	432154	AI701523	Hs_112577	ESTs	5.8
23	410099 411379	AA081630 Al816344	Hs.12554	KIAA0036 gene product ESTs, Weakly similar to NPL4_HUMAN NUCLE	\$.8 5.8
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.7
	424560	AA158727	Hs.150555	protein predicted by clone 23733	5.7
30	419498	AL036591	Hs.20887	hypothetical protein FLI 10392	5.7
30	436643 416111	AA757626 AA033813	Hs.10941 Hs.79018	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.7
	419088	AI538323	Hs.52620	chromatin assembly factor 1, subunit A (integrin, beta 8	5.7 5.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
26	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.7
35	451752	AB032997	Hs.26966	KIAA1171 protein	5.7
	413492 414683	D87470 S78296	Hs.75400 Hs.76888	KIAA0280 protein hypothetical protein MGC12702	5.7
	418079	R40058	Hs.6911	ESTs	5.6 5.6
40	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.6
40	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sepiens	5.6
	419544	AI909154	14- 200424	gb:QV-BT200-010499-007 BT200 Homo sepien	5.6
	452785 408081	AL359942 AW451597	Hs.296434 Hs.167409	erythroid differentiation and denucleati ESTs	. 5.6 5.6
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	5.6
45	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	5.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	5.6
	433556 448299	W56321 AA497044	Hs.111460 Hs.20887	calcium/calmodulin-dependent protein kin	5.5
	425154	NM_001851	Hs.154850	hypothetical protein FLJ 10392 collagen, type IX, alpha 1	5.5 5.5
50	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 (H	5.5
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	5.5
	453128 453220	AW026516 AB033089	Hs.31791	acylphosphatase 2, muscle type	5.5
	440866	AB033089 AI703103	Hs.32452 Hs.271360	Homo sapiens mRNA for KIAA1263 protein, hypothetical protein MGC16275	5.5 5.4
55	428976	AL037824	Hs.194695	ras homolog gene family, member I	5.4
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.4
	452799	AJ948829	Hs.213786	ESTs	5.4
	429038 445255	AL023513 NM_014841	Hs.194766 Hs.12477	seizure related gene 6 (mouse)-like synaptosomal-associated protein, 91 kDa	5.4
60	424332	AA338919	Hs.101615	ESTs	5.4 5.4
	440210	AW674562	Hs.125296	ESTS	5.4
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.4
	448935 452786	AL078596 R61362	Hs.22591 Hs.106642	nuclear receptor subfamily 2, group E, m ESTs, Weakly similar to T09052 hypotheti	5.4
65	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	5.4 5.4
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	5.4
	448507	AL133109	Hs.21333	Homo saplens mRNA; cDNA DKFZpS66N1047 (f	5.4
	419683 407728	AA248897 AW071502	Hs.48784	ESTs	5.4
70	453313	BE005771	Hs.175931 Hs.153746	ESTs hypothetical protein FLJ22490	5.4 5.4
	422094	AF 129535	Hs.272027	F-box only protein 5	5.4 5.4
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	5.4
	434792	AA649253	Hs.132458		5.4
75	412190 425588	R16180 F07396	Hs.274461 Hs.46627	ESTs ESTs	5.3
. •	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	5.3 5.3
	429698	A1685086	Hs_26339	ESTs, Weakly similar to S21348 probable	5.3 5.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	5.3
80	446997 427302	AA383439 AA400540	Hs.16758 Hs.135282	Spir-1 protein	5.3
- •	439607	BE540565	Hs.159460		5.3 5.3
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.3 5.3
	410037	AB020725	Hs.58009	KIAA0918 protein	5.3

	451407	AA131376	Hs.343809	fibroblast growth factor 128	5.3
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.3
	428784 418512	Y12851 AW498974	Hs.193470	purinergic receptor P2X, ligand-gated io	5.3
5	435538	AB011540	Hs.4930	diacylglycerol kinase, zeta (104kD)	5.3
_	420285	AA258124	Hs.293878	tow density lipoprotein receptor-related ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	5.2 5.2
	404819			NM_002688":Homo sapiens peanut (Orosophi	5.2 5.2
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
10	405348			C7001664:gi[12698061 dbj[BAB21849.1] (AB	5.2
	431552	AJ815863	Hs.259873	axonal transport of synaptic vesicles	5.2
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.2
	427250	R35941	Hs.25418	ESTs	5.2
15	428037	N47474	Hs.69230	potassium intermediate/small conductance	5.2
IJ	445740 430130	T78281 AL137311	Hs.13226	Homo sepiens clone 25181 mRNA sequence	5.2
	423869	BE409301	Hs.234074 Hs.134012	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	416220	N49776	Hs.170994	C1q-related factor hypothetical protein MGC10946	5.2
	457005	AJ007421	Hs.172597	sel (Drosophila)-like 3	5.2 5.1
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.1
	410631	AA086469	Hs.47171	ESTs	5.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity ta, re	5.1
25	420133	AA426117	Hs.155543	ESTs	5.1
23	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	414922 414727	D00723 BE466904	Hs.77531	glycine cleavage system protein H (amino	5.1
	441869	NM_003947	Hs.190162 Hs.8004	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	5.1
	437387	Al198874	Hs.28847	huntingtin-associated protein interactin AD026 protein	5.1
30	400533	7-1000/4	113.20017	ENSP00000209376":PRED65 protein (Fragmen	5.0 5.0
	430979	AI479755	Hs.129010	ESTs	5.0 5.0
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.0
	444600	R41398	Hs.6996	ESTs	5.0
25	453785	A1368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	5.0
35	428878	AA436884	Hs.48926	ESTs	5.0
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.0
	440471 410434	AA886146	Hs.307944	ESTs .	5.0
	441390	AF051152 Al692560	Hs.63668 Hs.131175	toll-like receptor 2	5.0
40	448765	R15337	Hs.21958	ESTs Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.9
	422263	AA307639	Hs.129908	KIAA0591 protein	4.9
	431117	AF003522	Hs.250500	della (Drosophila)-like 1	4.9 4.9
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
45	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.9
	420092	AA814043	Hs.88045	ESTs	4.9
	449571	AW016812	Hs.200266	ESTs	4.9
	412811 409100	H06382 H98216	11- 40045	ESTs	4.9 ·
50	403142	r190210	Hs.42245	ESTs, Moderately similar to 138022 hypot	4.9
-0	414300	AI304870	Hs.188680	NM_002706*:Horno sapiens protein phosphat ESTs	4.9
	436607	AW661783	Hs.211061	ESTs	4.9 4.9
	431553	X78075	Hs.2799	cartilage linking protein 1	4.9
	449328	AI962493	Hs.345303	ESTs	4.9
55	420805	L10333	Hs.99947	reticulon 1	4.9
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	4.9
	452898	AA814497	Hs.78792	ESTs	4.9
	427958 432328	AA418000	Hs.98280 Hs.195471	potassium intermediate/small conductance	4.9
60	408453	AI572739 AI369838	Hs.1954/1 Hs.45127	6-phosphofructo-2-kinase/fructose-2,6-bi	4.9
••	428841	Al418430	Hs.104935	chondroitin sulfate proteoglycan 5 (neur ESTs	4.8
	416439	AA180363	Hs.118769	ESTs	4.8 4.8
	447458	AI741082	Hs.158961	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
65	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	4.8
	436511	AA721252	Hs.291502	ESTs	4.8
	443392	AI055821	Hs.293420	ESTs	4.8
	423600	AI633559	Hs.310359	ESTs	4.8
70	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
, ,	414706 407385	AW340125	Hs.76989	KIAA0097 gene product	4.B
	439340	AA610150 AB032436	Hs.272072 Hs.6535	ESTs, Weakly similar to 138022 hypotheti brain-specific Na-dependent inorganic ph	4.8
	427624	AA406245	Hs.24895	ESTs	4.7
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4,7 4.7
75	408670	AF160967	Hs.45784	potassium large conductance calcium-acti	4.7
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	4.7
	411555	AF113537	Hs.70669	HMP19 protein	4.7
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.7
80	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALUB_HUMAN A	4.7
-	445900 426457	AF070526 AW894667	Hs.125038	Homo sapiens clone 24787 mRNA sequence	4.7
	459527	AVV094007 AW977556	Hs.169965	chimerin (chimaerin) 1	4.7
	453096	AW294631	Hs.291735 Hs.11325	ESTs, Weakly similar to 178885 serine/th ESTs	4,7
					4.7

	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7
	428001 410276	H97428 A1554545	Hs.219907 Hs.68301	ESTs, Moderately similar to Transforming	4.7
	421637	AF035290	Hs.106300	angiopoietin-2 Homo sapiens clone 23556 mRNA sequence	4.7
5	421633	AF121860	Hs.106260	sorting nexts 10	4.7 4.7
	440052	AI633744	Hs.195648	ESTs, Wealdy similar to 138022 hypotheti	4.7
	439566	AF086387		gh:Homo sapiens full length insert cONA	4.7
	432890	NM_014442	Hs.279751	siafic acid binding tg-like fectin 8	4.6
10	402145	*******		Target Exon	4.6
10	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	4.6
	458760 453362	AJ498631 H14988	Hs.111334 Hs.107375	ferritin, light polypeptide	4.6
	436734	AI937612	Hs.273758	ESTs hypothetical protein FLJ23112	4.6
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fs, clone H	4.6 4.6
15	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.6
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	4.6
	423770	AW976766	Hs.132776	Homo saplens cDNA FLJ 10077 fis, clone HE	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	4.6
20	429149 437762	AW193360 T78028	Hs.197962	ESTs, Wealdy similar to I38022 hypotheti	4.6
20	439249	AF086060	Hs.154679 Hs.170053	Synaptotagmin I	4.6
	416426	AA180256	Hs.210473	G-protein coupled receptor 88 Horno sapiens cDNA FLJ14872 fis, clone PL	4.6 4.6
	425258	BE297611	Hs.155392	collapsin response mediator protein 1	4.6
25	415257	F03016	Hs.27513	ESTs	4.6
25	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.6
	458814	Al498957	Hs.170861	ESTs. Weakly similar to Z195_HUMAN ZINC	4.6
	451320 424998	AW118072 U58515	Hs.154138	diacylglycerol kinase, zeta (104kD)	4.5
	422709	AA315331	Hs.153485	chitinase 3-like 2 ESTs	4.5
30	420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.5 4.5
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.5
	457465	AW301344	Hs.122908	DNA replication factor	4.5
	427712	AI368024	Hs_283696	ESTs	4.5
35	444656	AI277924	Hs.145199	ESTs	4.5
"	413409 429399	AI638418 AA452244	Hs.1440 Hs.16727	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep ESTs	4.5
	450639	AI703186	Hs.277174	ESTs	4.5 4.5
	452106	AI141031	Hs.21342	ESTs	4.5
40	424240	AB023185	Hs.143535	catcium/calmodulin-dependent protein kin	4.5
40	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	4.5
	446657	Al335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.5
	428189 423178	AA424030 Al033140	Hs.46627 Hs.124983	ESTS	4.5
	445133	AW157646	Hs.198689	Homo sapiens mRNA; cDNA DKFZp564C142 (fr ESTs	4.5 4.5
45	418771	AA807881	Hs.25329	ESTs	4.4
	438456	AA913381	Hs.20594	ESTs	4.4
	410386	W25187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	4.4
	413834	BE295896	Hs.224179	ESTs. Weakly similar to 138022 hypotheti	4,4
50	419103 420560	Z40229 AW207748	Hs.96423 Hs.59115	hypothetical protein FLJ23033	4.4
-	439662	H97552	Hs.269060	ESTs ESTs	4.4 4.4
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445034	AW293376	Hs.143659	ESTs	4.4
55	402605			Target Exon	4.4
55	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	4.4
	457561 430676	AA331517 AF084866	Hs.286055	chilmerin (chimaerin) 2	4.4
	439570	179925	Hs.269165	gb:Homo sapiens envelope protein RtC-3 (ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.4
	452752	AW044058	Hs.33578	KIAA0820 protein	4.4 4.4
60	439108	AW163034	Hs.6467	synaptogyrin 3	4.4
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
	446544	AI631932	Hs.7047	ESTs, Wealdy similar to Unknown (H.sapie	4.4
	412530 420871	AA766268 AA702972	Hs.266273	hypothetical protein FLJ13346	4.4
65	408622	AA056060	Hs.65300 Hs.202577	ESTS	4.4
	429269	AA449013	Hs.99203	Homo sepiens cDNA FLJ12166 fis, clone MA ESTs	4.4 4.3
	427463	AA442224	Hs.97900	ESTs	4.3
	425402	AI215881	Hs.24970	ESTs. Wealty similar to 834323 GTP-bindi	4.3
70	412046	Y07847	Hs.73088	RAS-related on chromsome 22	4.3
70	427194	AA399018	Hs.250835	ESTs	4.3
	437834 409172	AA769294 299399	Hs.283854 Hs.122593	gb:rz36g03.s1 NCI_CGAP_GC81 Homo saplens	4.3
	409953	AA332277	Hs.57691	ESTs cadherin 18, type 2	4.3
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	4.3 4.3
75	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.3
	446936	H10207	Hs.47314	ESTs	4.3
	433932 424800	AW954599 AL035588	Hs.169330	neuronal protein	4.3
80	421988	AW450481	Hs.153203 Hs.161333	MyoD family inhibitor ESTs	4.3
	442832	AW206560	Hs.253569	ESTs	4.3 4.3
	416586	D44843	Hs.14144	secreted modular calcium-binding protein	4.2
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	4.2

	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.2
	449318 438624	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.2
	430024 421027	AA889055 AA761198	Hs.123468 Hs.55254	ESTs ESTs	4.2
5	417632	R20855	Hs.5422	glycoprotein M6B	4.2 4.2
-	419412	AW161058	Hs.90297	synuclein, beta	4.2
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.2
	450813	AI739625	Hs.203376	ESTs	4.2
10	412505 440168	AA974491	Hs.21734	ESTs	4.2
10	441707	AA868507 R42637	Hs.126141 Hs.21963	ESTs	4.2
	438703	AI803373	Hs.31599	hypothetical protein DKFZp761B0514 ESTs	4.2 4.2
	444127	N63620	Hs.13281	ESTs	4.2
1.0	447397	BE247676	Hs.18442	E-1 enzyme	4.2
15	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.2
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	4.2
	416871 408838	H98716 Al669535	Hs.40369	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	425287	R88249	Hs.155524	ESTs peanut (Drosophila)-like 2	4.2 4.2
20	404584			Target Exon	4.2
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	4.2
	409091	AW970386	Hs.269423	ESTs	4.2
	437117	AL049256	Hs.122593	ESTs	4.2
25	429643 439231	AA455889 AW581935	Hs.167279	FYVE-linger-containing Rab5 effector pro	4.2
23	408177	AI241733	Hs.141480 Hs.43871	Homo sapiens mRNA; cDNA DKFZp434N079 (fr ESTs	4.2
	438875	AA827640	Hs.189059	ESTS	4.2 4.2
	447877	AJ435184	Hs.164252	ESTs	4.2
20	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	4.2
30	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.2
	449714 427315	AB033015 AA179949	Hs.23941	KIAA1189 protein	4.2
	404541	PA 11 3343	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.2
	449969	AW295142	Hs.180187	NM_030795:Homo sapiens stathmin-like 4 (Homo sapiens cDNA FLJ14337 fis, clone PL	4.1 4.1
35	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	422253	W81526	Hs.118329	ESTs. Moderately similar to GAD_HUMAN GA	4.1
	440483	AI200836	Hs.150386	ESTs	4.1
	429421 432882	AL031658 NM_013257	U- 22000	Human DNA sequence from clone RP1-310O13	4.1
40	432002 424001	W87883	Hs.279696 Hs.137476	serum/glucocorticoid regulated kinase-li paternally expressed 10	4.1
	422170	Al791949	Hs.112432	anti-Mullerian hormone	4.1 4.1
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	4.1
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4.1
45	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	4.1
43	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	4.1
	415796 446619	R87548 AU076643	Hs.78854 Hs.313	ATPase, Na? transporting, beta 2 polypep	4.1
	457211	AW972565	Hs.32399	secreted phosphoprotein 1 (osteopontin, ESTs, Weakly similar to S51797 vasodilat	4.1 4.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
50	412777	Al335773	Hs.270123	ESTs	4,1
	445225	AJ216555	Hs.202398	ESTs	4.1
	408926 417873	AF217525	Hs.49002	Down syndrome cell adhesion molecule	4.1
	443301	BE266659 AJ733614	Hs.293659 Hs.220587	Homo sapiens, Similar to RIKEN cDNA A430 ESTs, Moderately similar to ALUS_HUMAN A	4.1
55	429281	AA830856	Hs.29808	Homo saplens cDNA: FLJ21122 fis, clone C	4.1 4.1
	448966	AW372914	Hs.66149	phospholnositol 3-phosphate-binding prot	4.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.1
	417355	D13168	Hs.82002	endothelin receptor type B	4.1
60	410359 426529	R38824 AF090100	Hs.106313 Hs.170241	ESTs	4.1
••	433323	AA805132	Hs.159142	Homo sapiens clone IMAGE 23915 ESTs	4.1
	434933	R91095	Hs.4276	KIAA1701 protein	4.1 4.1
	453331	A1240665		ESTs	4.1
45	422661	NM_014700	Hs.119004	KIAA0665 gene product	4.1
65	424726 416805	AK001007 F13271	Hs.138760	Homo sapiens cDNA FU10145 fis, clone HE	4.0
	441797	A1936933	Hs.79981	Human clone 23560 mRNA sequence	4.0
	424282	R76421	Hs.214635 Hs.135694	EST8 ESTs	4.0
	407792	AI077715	Hs.39384	putative secreted ligand homologous to I	4.0 4.0
70	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	4.0
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.0
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
75	444001 410768	Al095087 AF038185	Hs.152299 Hs.66187	ESTs, Moderately similar to S65657 alpha	4.0
	426413	AA377823	19.00107	Homo sapiens clone 23700 mRNA sequence gb:EST90805 Synovial sarcoma Homo sapien	4.0
	450581	AF081513	Hs.25195	TGF-beta 4	4.0 4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
80	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
90	432058	AW665996	Hs.130729		4.0
	439774 445668	AL360257 R59960	Hs.213493 Hs.282386		4.0
	450582	AJ339732	15.404300	G-rich RNA sequence binding factor 1	4.0
				A	4.0

	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
	449277 440553	AA001064 AA889416	Hs.43670 Hs.344043	ESTs Homo sapiens cDNA FL114459 fls, clone HE	4.0 4.0
5	445888	AF070564	Hs.13415	Homo sepiens clone 24571 mRNA sequence	4.0
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.0
	407198 422564	H91679 Al148006	Hs.222120	gb:yv04a07.s1 Soares fatal liver spleen ESTs	4.0
	443992	AW022228	Hs.322922	ESTs	4.0 4.0
10	435542	AA687376	-	ESTs	4.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.0
	437748 439285	AF234882 AL133916	Hs.5814	suppression of turnorigenicity 7 hypothetical protein FLJ20093	4.0 4.0
	449655	AI021987	Hs.59970	ESTs	4.0
15	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.0
	412659 423905	AW753865 AW579960	Hs.74376 Hs.135150	olfactomedin related ER localized protel king type-I cell membrane-associated gly	4.0
	432683	AW995441	Hs.10475	ESTs	4.0 4.0
20	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.0
20	420649 450927	AJ866964 AJ807804	Hs.124704 Hs.134342 .	ESTs, Moderately similar to S65657 alpha	4.0
	448985	AA324885	Hs.22777	TASP for tastis-specific adriamycin sens carbonic anhydrase XI	4.0 4.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.0
25	412754 416340	AW160375 N31772	Hs.74565 Hs.79226	emyloid beta (A4) precursor-like protein	3.9
	428862	NM_000345	Hs.2316	fasciculation and etongation protein zet SRY (sex determining region Y)-box 9 (ca	3.9 3.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	3.9
	419687 453438	A1638859 A1469935	Hs.227699 Hs.22792	ESTs, Wealthy similar to T2D3_HUMAN TRANS	3.9
30	410082	AA081594	Hs.158311	ESTs Musashi (Drosophila) homolog 1	3.9 3.9
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	3.9
	412326 411666	R07566 AF106564	Hs.73817 Hs.71346	small inducible cytokine A3 (homologous	3.9
	439935	S75105	Hs.8358	neurofilament 3 (150kD medium) glutamate receptor, ionotropic, kainate	3.9 3.9
35	459278	AW294659	Hs.34054	Home sepiens cDNA: FLJ22488 fis, clone H	3.9
	432809 450568	AA565509 AL050078	Hs.131703	ESTs	39
	413951	AW051200	Hs.25159 Hs.75640	Homo sapiens cDNA FLJ10784 fis, clone NT natriuretic peptide precursor A	39 39
40	435743	T66861	Hs.12962	ESTs	3.9
40	447937 417576	AL109716 AA339449	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	448526	AB028945	Hs.82285 Hs.21361	phosphoribosylglycinamide formyttransfer KIAA1023 protein	3.9 3.9
	445890	AF055019	Hs.21906	Homo sapiens clone 24570 mRNA sequence	3.9
45	425241 417333	AA324624	Hs.155247	aldolase C, tructose-bisphosphate	3.8
7.5	435832	AL157545 AA425688	Hs.173179 Hs.41641	bromodomain and PHD finger containing, 3 Bruno (Drosophila) -fike 4, RNA binding	3.8 3.8
	410592	R94088	Hs.43569	ESTs	3.8
	443361 403596	AJ792628	Hs.133273	ESTs CAMMANATION CONTROL OF AN ARCON CONTROL OF A CAMMANATION CONTROL O	3.8
50	437756	AA767537	Hs.197096	C40011007:gi 5852342 gb AAD54015.1 (AF0 ESTs	3.8 3.8
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	414998 425652	NM_002543 AB021742	Hs.77729 Hs.322431	oxidised low density lipoprotein (lectin	3.8
	437449	AL390153	Hs.208339	naurogenic differentiation 2 Homo sapiens mRNA; cDNA DKFZp762G113 (fr	3.8 3.8
55	421040	AA715026	Hs.135280	ESTs	3.8
	454171 443740	AW854832 R56434	Hs.21062	gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.8
	441558	AI611973	Hs.136313	ESTs ESTs	3.8 3.8
60	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.8
60	457183 438142	H91882 T90309	Hs.118569 Hs.269651	DvI-binding protein IDAX (inhibition of	3.8
	408875	NM_015434	Hs.48604	ESTs DKFZP434B168 protein	3.8 3.8
	436899	AA764852	Hs.291567	ESTs	3.8
65	456497 416892	AW967956 L24498	Hs.123648 Hs.80409	ESTs. Weakly similar to AF108460 1 ubinu	3.8
00	413199	M62843	Hs.75236	growth arrest and DNA-damage-inducible, ELAV (embryonic lethal, abnormal vision,	3.B 3.8
	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
	454117 438944	BE410100 AA302517	Hs.40368 Hs.92732	adaptor-related protein complex 1, sigma	3.8
70	436944	AI869975	Hs.4775	KIAA1444 protein junctophilin 3	3.8 3.8
	424330	AW073953	Hs.333396		3.8
	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	3.8
	449444 411252	AW818436 AB018549	Hs.23590 Hs.69328	solute carrier family 16 (monocarboxylic MD-2 protein	3.8
75	448275	BE514434	Hs.20830	kinesin-like 2	3.7 3.7
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.7
	400777 419586	AI088485	Hs.144759	NM_007325*:Homo sapiens glutamate recept ESTs, Wealdy similar to I38022 hypotheti	3.7
00	458072	AI890347	Hs.271923		3.7 3.7
80	445908	R13580	Hs.13438	Homo sapiens clone 24425 mRNA sequence	3.7
	448451 430183	AW015994 BE010038	Hs.345433	gb:UI-H-BI0p-abh-g-09-0-UI.s1 NCI_CGAP_\$ gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.7
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	3.7 3.7
			-	252	w.,

	458912	AJ911066		ESTs	3.7
	428110	AI312485	Hs.138294	ESTs, Moderately similar to Z195_HUMAN Z	3.7
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.7
5	442326 422798	H92962 R92347	Hs.124813 Hs.34574	hypothetical protein MGC14817 ESTs, Wealdy similar to ALUT HUMAN ALU S	3.7
•	428873	Al701609	Hs.98908	ESTs	3.7 3.7
	438208	ALD41224	Hs.65379	ESTs .	3.7
	414040	N58513	Hs.32171	ESTs	3.7
10	407846 408829	AA426202 NM_006042	Hs.40403	Cbp/p300-interacting transactivator, wit	3.7
10	425010	T16837	Hs.48384 Hs.4241	heparen sutfate (glucosamine) 3-O-suffot ESTs	3.7 3.7
	427209	H06509	Hs.92423	KIAA1566 protein	3.7
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.6
15	410126	BE169274		KIAA0036 gene product	3.6
15	426646 418329	AA382787 AW247430	Hs.122713 Hs.84152	ESTs cystathionine-beta-synthase	3.6
	419390	AJ701162	Hs.90207	hypothetical protein MGC11138	3.6 3.6
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.6
20	431725	X65724	Hs.2839	Nome disease (pseudoglioma)	3.6
20	448425 423611	AI500359 AB011163	Hs.346112 Hs.129908	ESTs	3.6
	438831	BE263273	Hs.6439	KIAA0591 protein synapsin II	3.6 3.6
	419235	AW470411	Hs.288433	neurotrimin	3.6
25	451027	AW519204	Hs.40808	ESTs	3.6
25	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	424947 404150	R77952		ESTs, Wealtly similar to atternatively sp Target Exon	3.6
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6 3.6
20	443715	AI583187	Hs.9700	cyclin E1	3.6
30	435910	AI084152	Hs.21782	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.6
	418064	8E387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	432488 431342	AA551010 AW971018	Hs.216640 Hs.21659	ESTs ESTs	3.6 3.6
	437916	8E566249	Hs.20999	hypothetical protein FLJ23142	3.6
35	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.6
	448448	NM_014954	Hs.21239	KIAA0985 protein	3.6
	447818 445105	W79940 AF238869	Hs.21906 Hs.283955	Homo sapiens clone 24670 mRNA sequence	3.6
	409557	BE182896	Hs.211193	Homo sapiens clone GLSH-2 similar to gli ESTs	3.6 3.6
40	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	3.6
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	412799 435040	AI267606 AI932350	Hs.152825	gb:aq91h03.x1 Stanley Frontal SB pool 1 ESTs	3.6
45	434149	Z43829	Hs.244624	hypothetical protein MGCS469	3.6 3.6
	415709	AA649850	Hs.278558	ESTs	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	437640 445953	AA764893 Al612775	Hs.272155 Hs.145710	ESTs, Wealdy similar to I38022 hypotheti ESTs	3.6
50	449256	AA059050	Hs.59847	ESTs	3.6 3.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.6
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	3.6
	417675 423641	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.6
55	443912	AL137256 R37257	Hs.130489 Hs.184780	ATPase, aminophospholipid transporter-li ESTs	3.6 3.6
	424572	M19650		2,3-cyclic nucleotide 3' phosphodieste	3.5
	424899	AL119387	Hs.119062	ESTs	3.5
	439726 416490	AW449893	Hs.293707	ESTs. Wealdy similar to 138598 zinc fing	3.5
60	458809	AF090116 AW972512	Hs.79348 Hs.20985	regulator of G-protein signatting 7 sin3-associated polypeptide, 30kD	3.5
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.5 3.5
	407624	AW157431	Hs.248941	ESTS	3.5
	419038	AW134924	Hs.190325	ESTs	3.5
65	451489 428242	NM_005503 H55709	Hs.26468 Hs.2250	amyloid beta (A4) precursor protein-bind	3.5
	411048	AK001742	Hs.67991	leukemia Inhibitory factor (cholinergic hypothetical protein DKFZp434G0522	3.5 3.5
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.5
	424340	AA339036	Hs.7033	ESTs	3.5
70	425790 432188	AW136286 Al362952	Hs.288446 Hs.2928		3.5
. •	453898	AW293483	Hs.255205	solute carrier family 7 (cationic amino KIAA1853 protein	3.5 3.5
	434784	AA649051	Hs.164007		3.5 3.5
	452449	AW068658	Hs.20943	ESTs	3.5
75	425212	AW962253	Hs.171618		3.5
	407253 418049	AA411175 AA211467	Hs.141939 Hs.190488		3.5
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	3.5 3.5
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.5
80	439450	R51613	Hs.125304	ESTS	3.5
30	435545 445729	AA687415 H21066	Hs.28107	ESTS	3.5
	448999	H21066 AF179274	Hs.13223 Hs.22791	Homo sapiens mRNA full length insert cDN transmembrane protein with EGF-like and	3.5 3.5
	412590	AL134388	Hs.135033		3.5 3.5
				• • • • • • • • • • • • • • • • • • • •	
				254	
					•

	420507			•	
	438527 441111	AI969251 AI806867	Hs.115325 Hs.126594	RAB7, member RAS oncogene family-like 1	3.5
	418630	AI351311	Hs.251946	ESTs poly(A)-binding protein, cytoplasmic 1-l	3.5
_	439920	H05430	Hs.288433	venopium	3.5 3.5
5	421268	AI126821	Hs.30514	ESTs	3.5
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cONA DKFZp761L1212 (f	3.5
	412719	AW016610	Hs.816	EST8	3.5
	435092	AL137310	Hs.4749	Homo sepiens mRNA; cDNA DKFZp761E13121 (3.5
10	414178	AW957372	Hs.46791	ESTs, Wealdy similar to I38022 hypotheti	3.5
10	437252	AI433833	Hs. 164159	ESTs, Weatry similar to ALU1_HUMAN ALU S	3.5
	452108 421183	AW135982 AL135740	Hs.203013 Hs.102447	hypothetical protein FLJ 12748	3.4
	441834	AL138034	Hs.7979	TSC-22-like KIAA0736 gene product	3.4
	413812	AW188687	Hs.44748	ESTs	3.4 3.4
15	449932	AI675444	Hs.263024	ESTs	3.4
	447067	R42098	Hs.21964	ESTs	3.4
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.4
	447028	AJ973128	Hs.167257	brain link protein-1	3.4
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.4
20	418358 417084	L02840 H08370	Hs.84244	potassium voltage-gated channel, Shab-re	3.4
	444534	AW271626	Hs.33067 Hs.42294	ESTs ESTs	3.4 3.4
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4
	435637	AI783529	Hs.26766	ESTs	3.4
25	412820	BE001238		gb:CM3:8N0075-240200-101-d11 BN0075 Homo	3.4
	428138	AA773842	Hs.293799	ESTs	3.4
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.4
	453305 459660	R39224	Hs.267997	EHM2 gene	3.4
30	418821	M79082 AA436002	Hs.183161	ESTS ESTS	3.4
	439518	W76326	15.103101	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4 3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	437085	AA743935	Hs.202329	ESTs	3.4
26	419852	AW\$03756	Hs.286184	hypothetical protein dJ551D2.5	3.4
35	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4
	441287	AW293132	Hs.131373	EST6	3.4
	425870 443672	R13406 AA323362	Hs.56782	ESTs	3.4
	448044	AI458682	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.4
40	405238	700002		gbtk13e01.x1 NCI_CGAP_Lu24 Homo sapiens Target Exon	3.4 3.4
•	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	3.4
	453590	AF150278	Hs.33578	KIAA0820 protein	3.4
	450756	A1733488	Hs.144062	ESTs	3.4
45	404283			ENSP00000244751*:Copine-like protein KIA	3.4
43	423257	AW161039	Hs.125878	synapsin (II)	3.4
	432149 412986	AW614326 X81120	Hs.133483 Hs.75110	ESTs, Wealdy similar to T34549 probable	3.4
	422809	AK001379	Hs.121028	cannabinoid receptor 1 (brain) hypothetical protein FLJ 10549	3.4 3.4
	420050	AL118615	Hs.94653	neurochondrin	3.4
50	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	3.4
	408601	U47928	Hs.86122	protein A	3.4
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	3.4
	449919 426380	AI674685 AI291267	Hs.200141	ESTs	3.4
55	408554	AAB36381	Hs.149990 Hs.315111	ESTs nuclear receptor co-repressor/HDAC3 comp	3.4 3.3
	443257	AI334040	Hs.11614	HSPC065 protein	3.3
	432731	R31178	Hs.287820	fibronectin 1	3.3
	421679	AJ475110	Hs.203933	ESTs .	3.3
60	453169	AB037815	Hs.32156	KIAA1394 protein	3.3
00	437397 443310	AA349847 BE552018	Hs.4221	hypothetical protein DKFZp761H039 ESTs	3.3
	423169	BE047009	Hs.133152 Hs.21837		3.3
	433657	AI244368	Hs.8124	ESTs, Wealtly similar to KIAA0927 protein PH domain containing protein in retine 1	3.3 3.3
	408449	NM_004408	Hs.166161	dynamin 1	3.3
65	417402	8E503227	Hs.134759	EST\$	3.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.3
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.3
	455646 450337	BE064420 A1693256	Ha 202103	gb:RC4-BT0311-241199-012-c08 BT0311 Hama	3.3
70	423420	AI553250 AI571364	Hs.202427 Hs.128382	ESTs Homo sapiens mRNA; cDNA DKFZp761I1224 (f	3.3
	433236	NM_004296	Hs.3221	regulator of G-protein signalling 6	3.3 3.3
	417868	AI078534	Hs.122592	ESTs	3.3
	438207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
75	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	3.3
13	449249	T\$2285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	418216 456060	AA662240 C14904	Hs.283099		3.3
	449145	AJ532122	Hs.45184 Hs.198408	Homo sapiens cONA FLJ12284 fis, clone MA ESTs	3.3
^^	415101	R45531	Hs.144534		3.3 3.3
80	401272			C9000559*:gij12314195jembjCAB99338.1j (A	3.3
	420297	A1628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.3
	443761	AI525743	Hs.345187	ESTs	3.3

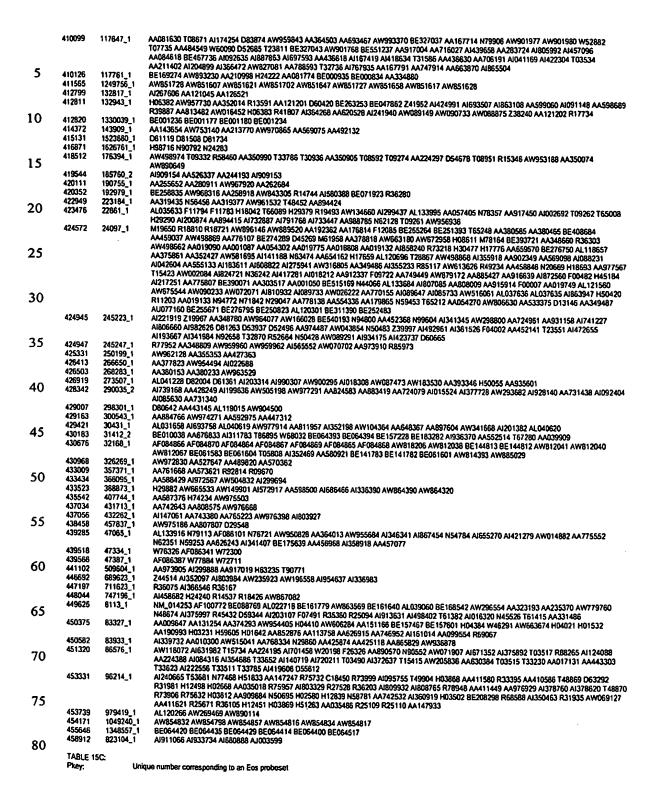
	422212	4 D0000FF	LL 475700	MIA A STOP masters	22
	427317 426920	AB028955 AA393351	Hs.175780 Hs.132121	KIAA1032 protein ESTs	3.3 3.3
•	433894	A1907682	Hs.243293	ESTs	3.3
_	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.3
5	419647	AA348947	Hs.91816	hypothetical protein	3.3
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	407881 428670	AW072003 AA431682	Hs.40968 Hs.134832	heparan sulfate (glucosamine) 3-0-sulfot ESTs	3.3 3.3
	435375	AJ733610	Hs.187832	ESTS	33
10	419043	T19167	Hs.89566	ets variant gene 1	3.3
	403341	•		Target Exon	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	439627 456209	BE621702 W60633	Hs.29076 Hs.297792	hypothetical protein FLJ21841 ESTs	3.3 3.3
15	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	418203	X54942	Hs.83758	COC28 protein kinase 2	3.3
	451254	AJ571016	Hs.172967	ESTs	3.3
20	435056 433842	AW023337 AI652156	Hs.5422 Hs.26346	glycoprotein M6B ESTs	3.3 3.3
20	433325	AW206986	Hs.143905	ESTS	3.3
	451066	AI758660	Hs.206132	ESTs	3.3
	436114	AA77B232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.3
25	421688	AB011156	Hs.106794	KIAA0584 protein	3.3
25	429228 450325	A1553633 A1935962	Hs.326447 Hs.26289	ESTs .	3.3 3.3
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.3
	451778	AJ826131	Hs.62954	ESTs. Wealty similar to zinc finger prot	3.3
20	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.2
30	450475	AW805634	Hs.205015	ESTs .	3.2
	418661 436480	NM_001949 AJ271643	Hs.1189 Hs.87469	E2F transcription factor 3 putative acid-sensing ion channel	3.2 3.2
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.2
	415131	D61119	***************************************	gb:HUM158C11B Clontech human fetal brain	3.2
35	409248	AB033035	Hs.51965	KIAA1209 protein	3.2
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434834 450358	AF156774 AB010098	Hs.324020 Hs.24907	1-acylglycerol-3-phosphate O-acyltransfe	3.2 3.2
	438461	AW075485	Hs.286049	coronin, actin-binding protein, 2B phosphoserine aminotransferase	3.2
40	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	3.2
	407304	AA565832	Hs.271649	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.2
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.2
	435071 420352	D60683 B£258835	Hs.35495	ESTs gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2 3.2
45	412193	AI684467	Hs.144057	ESTs	3.2
	442320	AI287817	Hs.129636	ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.2
	414528	AA148950	Hs.188836	EST8	3.2 3.2
50	439764 410425	T26535 BE278367	Hs.22744 Hs.63510	hypothetical protein MGC13105 KIAA0141 gene product	3.2
50	429876	AB028977	Hs.225974	KIAA1054 protein	3.2
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.2
	439039	A1656707	Hs.48713	ESTs	3.2
55	447925 447714	AW292271 AW296313	Hs.250718 Hs.255537		3.2 3.2
55	434574	A1424458	Hs.33470	ESTs	3.2
	437269	AA334384	Hs.149420		3.2
	416845	H95279	Hs.293788		3.2
60	452234	AW084176 R24595	Hs.223298		3.2 3.2
UU	440274 437698	R61837	Hs.7122 Hs.7990	scrapie responsive protein 1 ESTs, Moderately similar to 184505 calci	3.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.2
	445828	F05802	Hs.81907	ESTs	3.2
65	423779	AW071837	Hs.57971	ESTs .	3.2
03	403790	AL134539	Hs.254129	NM_001334*:Homo sapiens cathepsin O (CTS	3.2 3.2
	453792 428167	AA770021	Hs. 16332	KIAA1678 ESTs	3.2
	445413		Hs.12677	CGI-147 protein	3.2
70	415314	N88802	Hs.5422	glycoprotein MGB	3.2
70	425115		Hs.123956		3.2
	432625		Hs.94830 Hs.73853	ESTs, Moderately similar to T03094 A-kin	3.2 3.1
	412420 422772		Hs.12022	bone morphogenetic protein 2 B KIAA0749 protein	3.1
	437414				3.1
75	427961	AW293165	Hs.14313	4 ESTs	3.1
	435256		Hs.13872		3.1
	428966 413995		Hs.19468 Hs.75671		3.1 3.1
	443431		Hs.20654		3.1
80	414217	AI309298	Hs.27989	8 Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	419617	AL008583	Hs.91622		3.1
	444326 436315		Hs.27071 Hs.27935		3.1 3.1
	+30313	دا بہودیں	14.47 333	(Illustrations business transmission)	J. I

	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DXFZp43480650 (f	3.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.1
_	432682	Al376400	Hs.159588	ESTs	3.1
5	450661	AW952160	Hs.83849	ESTs	3.1
	417636	R08916	Hs.191212	ESTs	3.1
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.1
	454032	W31790	Hs.194293 Hs.34650	ESTs, Weakly similar to I54374 gene NF2	3.1
10	443150 404532	AI034467	15.34000	ESTs NM_022490:Homo sepiens hypothetical prot	3.1
	425537	AB007913	Hs.158291	KIAA0444 protein	3.1 3.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.1
	400090			Eos Control	3.1
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.1
15	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	3.1
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.1
	433560 453042	AI925195 AW193534	Hs.130891	hypothetical protein MGC4400	3.1
	449722	BE280074	Hs.281895 Hs.23960	Homo sapiens cDNA FLJ11660 fts, clone HE cyclin B1	3.1 3.1
20	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
_	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.1
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.1
25	405605	41000405		C2001342gi 127814 sp P26434 NAH4_RAT SO	3.1
23	417565 439538	A1203405 AA837323	Hs.47831 Hs.56407	ESTs ESTs	3.1
	414117	W88559	Hs.1787	proteofipid protein 1 (Palizaeus-Merzbac	3.1 3.1
	430818	AJ311928	Hs.348156	gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	3.1
	408508	AI806109	Hs.135736	KIAA1580 protein	3.1
30	414884	R54418	Hs.183745	hypothetical protein FLI 13456	3.1
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.1
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
	417169 450202	R13550 AW969756	Hs.248773 Hs.34145	ESTs ESTs, Wealdy skraller to 849647 GTP-bindi	3.1
35	428060	AA420616	Hs.249483	ESTS	3.1 3.1
	430526	AF181852	Hs.242407	G protein-coupled receptor, family C, gr	3.1
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.1
	429163	AA884766		gb:arn20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
40	428180 422631	A1129767	Hs.182874 Hs.118793	guanine nucleotide binding protein (G pr	3.0
70	433290	BE218919 R20077	Hs.302185	hypothetical protein FLJ10688 Homo sapiens clone 23618 mRNA sequence	3.0 3.0
	412507	L36645	Hs.73964	EphA4	3.0
	415827	H17462	Hs.23079	ESTs .	3.0
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	3.0
45	457358 441732	AI479755 AW298818	Hs.129010	ESTs	3.0
	459318	NM_000038	Hs.127341	ESTs gb:Homo sapiens adenomatosis polyposis c	3.0 3.0
	426384	A1472078	Hs 303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW450938	Hs. 180115	ESTs	3.0
50	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.0
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	3.0
	459080	AW192083	Hs.290855	ESTs	3.0
	412783 432593	BE276738 AW301003	Hs.74578 Hs.51483	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep ESTs, Weakly similar to hypothetical pro	3.0
55	443753	AW367578	Hs.134749	ESTs	3.0 3.0
_	445921	AW015211	Hs.146181	ESTs	3.0
	427695	R88483	Hs.172862		3.0
	438283	AI458931	Hs.37282	ESTs	3.0
60	453324	W26592	Hs.232089		3.0
OU	421094 433434	AW978202 AA\$88429	Hs.289064		3.0
	452850	H23230	Hs.22481	gb:no22b03.s1 NCI_CGAP_Pr22 Homo septens ESTs, Moderately similar to A46010 X-lin	3.0 3.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.0
	429569	AA454993	Hs.138343		3.0
65	428600	AW863261	Hs.242413		3.0
	443833	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.0
	433229 429046	AB040925	Hs.91625	KIAA1492 protein	3.0
	431431	X57436 AL096711	Hs.194772 Hs.252953		3.0
70	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.0 3.0
_	423165	AI937547	Hs.124915		3.0
	440261	M81886	Hs.7117	glutamete receptor, ionotropic, AMPA 1	3.0
	441364	AW450466	Hs.126830	ESTs, Wealthy similar to YD38_YEAST HYPOT	3.0
75	437058	A1147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.0
, ,	429168 453739	AA984682 AL120266	Hs.146589	ESTs, Weakly similar to JC5238 galactosy ESTs	3.0
		,		20.3	3.0
	TABLE 1	158:			

TABLE 158: Pkey: CAT number: Accession: Unique Eos probeset identifier number Gene cluster number Genbank accession numbers 80

Pkey CAT Number Accession





	Ref:	Sequ	ience source. T	he 7 digit numbers in this column are Genhank Identi	fier (GI) numbers.	*Dunham, et al.* refers to the publication entitled *The DNA
				thromosome 22" Dunham, et al. (1999) Nature 402:4		perment of all 1000 as and beamstand change the dist
	Strand:			from which exons were predicted.		
-	Nt_position	: Indic	ates nucleotide	positions of predicted exons.		
5		_				
	Pkey	Ref	Strand	Nt_position		
	400533	6981826	Minus	277132-277595		
	400777	8131663	Plus	70745-71121		
10	401272	9797373	Minus	98374-98509		
10	402145	8018280	Plus	113086-114800		
	402604	9909420	Plus	20393-20767		
	402605	9909420	Minus	47680-47973		
	402855	9662953	Minus	59763-59909		
15	403142	9444521	Plus	89286-90131		
13	403341	8569175	Phrs	30699-30910		
	403696	3135242	Minus	143467-143634		
	403790	8084957	Minus	87826-87947,89835-90002		
	404150 404283	7534008	Plus	165811-165943		
20		2276311	Minus	99460-99564		
20	404541 404584	8318559	Plus	103456-103664		
	404564	9857511 9796668	Plus	138651-139153		
	404819	4678240	Plus	45096-45229	NOC 42420 42207	17000 17500 10001 10057 10440 10570
	405238	7249119	Plus Minus	16223-16319,16427-16513,16736-16859,16941-17	U/ 5, 1/ 1/U-1/20/.	17303-17329,10201-16327,16443-18378
25	405239	7249119	Plus	51728-51836 144345-144464,144690-144836,151750-151883,15	2402 452404	
23	405348	2914717	Minus	43310-43462	2401-132404	
	405605	5836195	Minus	117070-117270		
	405819	4007557	Plus	2830-2967		
	400013	4001001	rius	2030-2507		
30						•
	TABLE 16	A: ABOUT 85	GENES UP-RI	GULATED IN GLIOBLASTOMA MULTIFORMA CO	MPARED TO NOR	IMAL CENTRAL NERVOLIS SYSTEM
	Table 16A	fists about 859	oenes un-recul	ated in clinhlastoma multiforma (GRM) compared to	normal central neo	rous system (CNS). These were selected from 59680 probesets on
						ater than or equal to 3.0. The "average" GBM level was set to the
	85th percer	ntile amonast v	arious GBM turn	iors. The "average" normal CNS tissue level was set	to the 85° percen	tile amongst vrious CNS tissues. In order to remove gene-specific
35						was subtracted from both the numerator and the denominator before
		ras evaluated.	•		. •	
	Pkey:	Uni	que Eos probes	at identifier number		
	ExAccn:		emplar Accession	number, Genbank accession number		
40	Unigenet		gene number			
40	Unigene T		gene gene title			
	R1:	Rai	to of GLIOBLAS	TOMA MULTIFORMA to CNS		
	Pkey	ExAcon	UnigeneID	Unigene Title		R1
45	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,		47.2
42	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl		44.9
	423961	013666	Hs.136348	periostin (OSF-2os)		33.3
	433001 449539	AF217513	Hs.279905	cione HQ0310 PRO0310p1		25.9
	417308	W80383	Hs.58446	ESTs		25.8
50	424800	H60720 AL035588	Hs.81892	KIAA0101 gene product		23.3
50	414825	X06370	Hs.153203 Hs.77432	MyoD family inhibitor		23.0
	431941	AK000106	Hs.272227	epidermal growth factor receptor (avian Homo sapiens cDNA FLJ20099 fis, clone CO		19.6 18.7
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11		17.8
	444190	AIB7891B	Hs.10526	cysteine and glycine-rich protein 2		17.8
55	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matritysin,		17.7
	417130	AW276858		S100 calcium-binding protein A4 (calcium		17.5
	414217	AI309298	Hs.279898	Homo sepiens cDNA: FLJ23165 fis, clone L		17.0
	428242	H55709	Hs.2250	laukernia inhibitory factor (cholinergic		15.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)		15.6
60	424835	AA420687	Hs.115455	Homo sepiens cDNA FLJ14259 fis, clone PL		15.2
	408243	Y00787	Hs.624	Interleukin 8		14,7
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	1	14.7
	434078	AW880709		chromosome 8 open reading frame 4		14.6
	409799	D11928	Hs.76845	phosphoserine phosphatase-like		14.2
65	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2		14.2
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468		14.1
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1		14.0
	444969	AJ203334	Hs.16062B			13.5
70	430691	C14187	Hs.103538			12.9
70	426075	AW513691				12.4
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f		12,1
	441269	AW015206				11.9
	417426	NM_00229		laminin, beta 1		11.9
75	430132	AA204686				11.8
13	422163	AF027208				11.3
	411411	AA345241		ESTs, Weakly similar to KIAA1330 protein		11.3
	449722	BE280074		cyclin B1		11.2
	436291	BE568452				11.0
80	435020	AW505076				10.9
50	412140 419239	AA219691		RAB6 interacting, kinesin-like (rabkines		10.9
	417043	AA468183 NM_00436		Homo sapiens cONA: FLJ23241 fis, clone C collagen, type VI, atcha 3		10.6
	413929	BE501689		collagen, type VI, arpha 3 collagen, type IV, afpha 2		10.6
	713323	DE301009	Hs.75617	7 77 7		10.6
				25	Λ	

	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	10.6
	409142 406972	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	10.4
	412986	M32053 X81120	Hs.75110	gb:Human H19 RNA gene, complete cds. cannabinoid receptor 1 (brain)	10,4 10.3
5	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	10.3
	449611	A1970394	Hs.197075	ESTs	10.1
	427581 431512	NM_014788	Hs.179703 Hs.2795	KIAA0129 gene product	10.1
	429183	BE270734 AB014604	Hs.197955	lactate dehydrogenase A KIAA0704 protein	9.9 9.8
10	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	9.7
	424840	D79987	Hs.153479	extra spindle poles, S. carevisiae, homo	9.7
	433800 433647	AI034361 AA603367	Hs.135150	lung type-1 cell membrane-associated gly	9.7
	414622	A1752666	Hs.222294 Hs.76669	ESTs nicotinamide N-methyttransferase	9.7 9.5
15	413719	BE439580	Hs.75498	small inducible cytokine subternily A (Cy	9.3
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	9.3
	409902 450375	A1337658	Hs.156351	ESTs	9.3
	445873	AA009647 AA250970	Hs.251946	a disintegrin and metalloproteinase doma poly(A)-binding protein, cytoplasmic 1-l	9.2 9.1
20	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	9.1
	452461	N78223	Hs.108106	transcription factor	9.1
	434846 422158	AW295389 L10343	Hs.119768 Hs.112341	ESTS	9.1
	425187	AW014485	Hs.22509	protesse inhibitor 3, skin-derived (SKAL ESTs	9.0 9.0
25	443247	BE614387	Hs.333893	c-Myc target JPO1	8.7
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	8.7
	410276 402855	A1554545	Hs.68301	angiopoletin-2 NM_001839*:Homo sapiens calponin 3, acid	8.6
	439710	AF086543		gb:Homo sapiens full length insert cDNA	8.6 8.6
30	411968	AJ207410	Hs.69280	Horno sapiens, clone IMAGE:3636299, mRNA,	8.6
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	8.6
	436895 418203	AF037335 X54942	Hs.5338 Hs.83758	carbonic anhydrase XII CDC28 protein kinase 2	8.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	B.6 8.5
35	425234	AW152225	Hs. 165909	ESTs. Wealdy similar to I38022 hypotheti	8.5
	449961	AW265634	Hs.133100	ESTs	8.5
	449444 417061	AW818436 Al675944	Hs.23590 Hs.188691	solute carrier family 16 (monocarboxytic Homo sapiens cDNA FLJ12033 fis, clone HE	8.4 8.3
4.0	453884	AA355925	Hs.36232	KIAA0186 gene product	8.3
40	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.2
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	8.1
	411078 406850	A1222020 A1624300	Hs.182364 Hs.172928	CocoaCrisp collagen, type 1, alpha 1	8.1 8.0
	447726	AL137638	Hs.19368	matriin 2	8.0
45	439999	AA115811	Hs.6838	ras homotog gene family, member E	8.0
	416658 439451	U03272 AF086270	Hs.79432	fibrillin 2 (congenital contractural ara	7.9
	458814	AI498957	Hs.278554 Hs.170861	heterochromatin-like protein 1 ESTs, Weakly similar to Z195_HUMAN ZINC	7.9 7.9
50	447004	AW296968	Hs.157539	ESTs	7.9
50	436140	W87355	Hs.269587	ESTs	7.9
	436607 422809	AW661783 AK001379	Hs.211061 Hs.121028	ESTs hypothetical protein FLI10549	7.8
	440052	AJ533744	Hs. 195648	ESTs, Weakly similar to I38022 hypotheti	7.7 7.7
E E	422106	D84239	Hs.111732	Fc tragment of IgG binding protein	7,7
55	418113 410286	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.7
	424687	AI739159 J05070	Hs.61898 Hs.151738	DKFZP586N2124 protein matrix metafloproteinase 9 (gelatinase B	7.7 7.6
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.6
60	421988	AW450481	Hs.161333	ESTs	7.6
UU	452620 453941	AA436504 U39817	Hs.119286 Hs.36820	ESTs Bloom syndroms	7.6
	416737	AF154335	Hs.79691	LIM domain protein	7.5 7.5
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	7.5
65	418400	BE243026	Hs.301989	KIAA0246 protein	7.5
UJ	437036 421899	AI571514 AJ011895	Hs.133022 Hs.109281	ESTs Nef-associated factor 1	7.5 7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	7.4
70	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.3
, 0	448935 415079	AL078596 R43179	Hs.22591 Hs.22895	nuclear receptor subfamily 2, group E, m hypothetical protein FLJ23548	7.3 7.3
	449571	AW016812	Hs.200266		7.3
	427899	AA829286	Hs.332053	serum amyloid A1	7.3
75	447458 430630	A1741082 AW269920	Hs.158961		7.3
	411252	AB018549	Hs.2621 Hs.69328	cystatin A (stefin A) MD-2 protein	7.2 7.2
	432731	R31178	Hs.287820		7.2 7.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	7.2
80	407881 428728	AW072003 NM_016625	Hs.40968 Hs.191381	heparan suffate (glucosamine) 3-O-suffot	7.2
	416111	AA033813	Hs.79018	hypothetical protein chromatin assembly factor 1, subunit A (7.1 7.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	7.1
	410434	AF051152	Hs.63668	toll-like receptor 2	7.1

	400040	1156207	11-04000		
	420018 418293	U56387 A1224483	Hs.94376	proprotein convertase subtilisin/kexin t	7.1
	424954	NM_000546	Hs.16063 Hs.1846	hypothetical protein FLJ21877	7.1
	445900	AF070526	Hs.125036	tumor protein p53 (Li-Fraumeni syndrome) Homo saptens clone 24787 mRNA sequence	7.0
5	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	7.0 7.0
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	7.0
	434808	AF155108	Hs.256150	Horno sapiens, Similar to RIKEN cDNA 2810	6.9
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	6.9
10	424381	AA285249	Hs.146329	protein kinase Chk2	6.9
10	410064	X53416	Hs.195464	Marrin A, alpha (actin-binding protein-	6.9
	415682 421977	AI347128	Hs.191870	ESTs	6.9
	429447	W94197 AW812452	Hs.110165 Hs.83286	ribosomal protein L26 homolog	6.8
	423198	M81933	Hs.1634	ESTs, Wealthy similar to \$14747 aphingomy cell division cycle 25A	6.8 6.8
15	413627	BE182082	Hs.246973	ESTs	6.8
	412777	AJ335773	Hs.270123	ESTs	6.8
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	6.8
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	6.8
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothes	6.7
20	446131 441703	NM_000929 AW390054	Hs.290	phospholipase A2, group V	6.7
	420311	AW445044	Hs.192843 Hs.38207	leucine zipper protein FKSG14	6.7
	425202	AW962282	Hs.152049	Human DNA sequence from clone RP4-530115 ESTs, Weakly similar to 138022 hypotheti	6.7 6.7
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	6.7
25	440704	M69241	Hs.162	Insufin-like growth factor binding prote	6.7
	407182	AA312551	Hs.230157	ESTs	6.7
	445837	AI261700	Hs.145544	ESTs	6.6
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	6.6
30	431211 447439	M86849 AA313565	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.6
50	407235	D20569	Hs.145020 Hs.169407	ESTs. Wealdy similar to KIAA1205 protein SAC2 (suppressor of actin mutations 2, y	6.5
	450506	NM_004460	13.103701	fibroblast activation protein, alpha	6.5 6.5
	432593	AW301003	Hs.51483	ESTs. Wealdy similar to hypothetical pro	6.5
20	418054	NM_002318	Hs.83354	tysyl oxidase like 2	6.5
35	452799	AJ948829	Hs.213786	ESTs	6.5
	446657	Al335191	Hs.260702	ESTs, Wealthy similar to 2109260A B cell	6.4
	424247 443884	X14008 N20617	Hs.234734	lysozyme (renal amyloidosis)	6.4
	420560	AW207748	Hs.194397 Hs.59115	leptin receptor ESTs	6.4
40	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	6.4
. •	420649	A1866964	Hs.124704	ESTs. Moderately similar to S65657 alpha	6.3 6.3
	457465	AW301344	Hs.122908	DNA replication factor	6.3
	440332	AJ218517	Hs.188051	ESTs	6.3
45	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	6.3
43	413063	AL035737	Hs.75184	chilinase 3-like 1 (cartilage glycoprote	6.2
	448275 440286	BE514434 U29589	Hs.20830 Hs.7138	kinesin-like 2	6.2
	439518	W76326	ns./ 130	cholinergic receptor, muscarinic 3 gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	6.2
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	6.1 6.1
50	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	6.1
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	6.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homotog 4	6.0
55	413786 410555	AW613780 U92649	Hs.13500 Hs.64311	ESTs	6.0
	400419	AF084545	113.04311	a disintegrin and metalloproteinase doma Target	5.9
	408380	AF123050	Hs.44532	diubiquitin	5.9 5.9
	426108	AA522037	Hs.166468	programmed cell death 5	5.9
40	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.9
60	437695	AA769202	Hs.192142	ESTs	5.8
	409463 411048	AI458165 AKOO1742	Hs.17296	hypothetical protein MGC2376	5.8
	443731	AI083928	Hs.67991 Hs.145418	hypothelical protein DKFZp434G0522 ESTs	5.8
	405558			Target Exon	5.8 5.8
65	422094	AF129535	Hs.272027	F-box only protein 5	5.8 5.8
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	5.8
	425882	U83115	Hs.161002	absent in melanoma 1	5.8
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	5.8
70	429149 436827	AW193360 H72187	Hs.197952	ESTs, Weakly similar to 138022 hypotheti	5.8
	425905	AB032959	Hs.5322 Hs.318584	guanine nucleotide binding protein (G pr novel C3HC4 type Zinc finger (ring finge	5.7
	414053	BE391635	Hs.75725	transgelin 2	5.7 5.7
	436805	AA731533	Hs.270751	ESTs	5.7
75	442201	AW516704	Hs.208726	ESTs	5.7
75	453361	AA035197	Hs.107375	ESTs	5.6
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.6
	426490 423081	NM_001621 AF262992	Hs.170087	aryl hydrocarbon receptor	5.6
_	407013	U35637	Hs.123159	sperm associated antigen 4	5.6
80	406478			gb:Human nebulin mRNA, partial cds Target Exon	5.5
_	435937	AAB30893	Hs.119769	ESTs	5.5 5.5
	453362	H14988	Hs.107375	ESTs	5.5 5.5
	449969	AW295142	Hs.180187	Homo sapiens cONA FLJ14337 ffs, clone PL	5.5



	440043		11- 042404		
	442547 443883	AA306997 AA114212	Hs.217484 Hs.9930	ESTs, Weatly similar to ALU1_HUMAN ALU S	5.5
	429643	AA455889	Hs.167279	serine (or cysteine) proteinase inhibito	5.5
	407862	BE548267	Hs.337986	FYVE-finger-containing Rab5 effector pro Homo sapiens cDNA FLJ10934 ffs, clone OV	5.5 5.4
5	407624	AW157431	Hs.248941	ESTs	5.4 5.4
	448769	N66037	Hs.38173	ESTs	5.4
	417124	BE122762	Hs.25338	EST8	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
10	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	5.3
10	418596	AW976721	Hs.293327	ESTs	5.3
	410295 433323	AA741357 AA805132	Hs.5174 Hs.159142	midogen (enactin)	5.3
	412326	R07566	Hs.73817	ESTS small induction autobing A3 themselves	5.3
	418630	AI351311	Hs.251946	small inducible cytoltine A3 (homologous poly(A)-binding protein, cytoplasmic 1-l	5.3 5.3
15	420075	AF142482	Hs.203846	TEA domain family member 3	5.2
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	5.2
	407729	T40707	Hs.270862	ESTs	5.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	5.2
20	414372	AA143654	11. 444466	gb:zo65a02.r1 Stratagene pancreas (93720	5.2
20	433556 424998	W56321 U58515	Hs.111460	calcium/calmodufin-dependent protein kin chitinase 3-like 2	5.2
	407603	AW955705	Hs.154138 Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	5.2 5.2
	445118	AI208762	Hs.345572	ESTs	5.2
	408523	AW833259	Hs.314287	ESTs	5.2
25	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	5.2
	449300	AI656959	Hs.346514	ESTs	5.2
	429732	U2015B	Hs.2488	lymphocyte cytosofic protein 2 (SH2 doma	5.2
	423757 439570	AL049337 T79925	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	5.1
30	415323	BE269352	Hs.269165 Hs.949	ESTs, Weatly similar to ALU1_HUMAN ALU S	5.1
-	443604	C03577	Hs.9615	neutrophil cytosotic factor 2 (65kD, chr myosin regulatory light chain 2, smooth	5.1 5.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	5.1
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.1
25	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	5.0
35	424009	F11690		gb:HSC30D041 normalized infant brain cDN	5.0
	418283 429469	S79895	Hs.83942	cathepsin K (pycnodysostosis)	5.0
	417404	M54590 NM_007350	Hs.27 Hs.82101	glycine dehydrogenase (decarboxylating;	5.0
	408829	NM_006042	Hs.48384	pleckstrin homotogy-like domain, family heparan suffate (glucosamine) 3-O-sutfot	· 5.0 5.0
40	418097	R45137	Hs.21868	ESTs	5.0 5.0
	453331	AI240665		ESTs	4.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.9
	426044	AA502490	Hs.170290	ESTs	4.9
45	444161	N52543	Hs.142940	EST _{\$}	4.9
45	428227 432242	AA321649 AW022715	Hs.2248	small inducible cytokine subfamily 8 (Cy	4.9
	447752	M73700	Hs.162160 Hs.105938	ESTs, Weakly similar to ALU4_HÜMÄN ALU S tactotransferrin	4.9
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.9 4.9
	402274			C19000498":gi]4567179 gb AAD23607.1 AC00	4.9
50	444656	AI277924	Hs.145199	ESTS	4.9
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	4.9
	443744	AI084326	Hs.271548	ESTs, Weakly similar to 178885 serine/th	4.9
	416871 409112	H98716 BE243971	Hs.50849	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.9
55	403481	00243371	115.30043	quinone axidoreductase homolog Target Exon	4.8 4.8
	443740	R56434	Hs.21062	ESTs	4.8
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	4.8
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Horno s	4.8
60	451418	BE387790	Hs.25369	hypothetical protein FLJ20287	4.8
50	428403 430968	AI393048 AW972830	Hs.326159	leucine rich repeat (in FLII) Interactin	4.8
	425212	AW962253	Hs.171618	gb:EST384925 MAGE resequences, MAGL Homo ESTs	4.8
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	4.8 4.8
	431176	AI026984	Hs.293662	ESTs	4.8
65	420092	AA814043	Hs.88045	ESTs	4.8
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	403011 405348			ENSP00000215330*:Probable serine/threoni	4.7
70	447072	D61594	Hs.17279	C7001664:gil12698061 db BAB21849.1 (AB tyrosylprotein sulfotransferase 1	4.7
	443318	AI051603	Hs.133141		4.7 4.7
	421027	AA761198	Hs.55254	ESTs	4.7
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cONA 5730	4.7
75	429170	NM_001394		dual specificity phosphatase 4	4.7
75	411852	AA528140	Hs.107515		4.7
	450166 438456	AA429504 AA913381	Hs.20594	ESTs	4.7
	446839	BE091926	Hs.16244	ESTs mitotic spindle colled-coil related prot	4.7
	438527	Al969251	Hs.115325	RAB7, member RAS oncogene family-like 1	4.7 4.7
80	458946	AA009716	Hs.42311	ESTs	4.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	4.7
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.7
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.6

The second secon

	422648	D86983	Hs.118893	Mainsons recognist ages	4.6
	431319	AA873350	Hs.302232	Melanoma associated gene ESTs	4.6 4.6
	445666	R59960	Hs.282386	ESTs	4.6
•	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.6
5	422887	AI751848	Hs.49215	ESTs	4.6
	422938 405141	NM_001809 Y14443	Hs.1594	centromere protein A (17kD) zinc finger protein 200	4.6
	440210	AW874562	Hs.125296	ESTs	4.6 4.6
• •	432527	AW975028	Hs.102754	ESTs	4.6
10	439726	AW449893	Hs.293707	ESTs, Weakly similar to 138598 zinc fing	4.6
	435143	R12375	Hs.194600	ESTs	4.6
	422170 452874	Al791949 AK001061	Hs.112432 Hs.30925	anti-Mullerian hormone hypothetical protein FLJ 10199	4.6
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.6 4.6
15	412568	A1878826	Hs.74034	cavaolin 1, caveolae protein, 22kD	4.5
	426215	AW963419	Hs.155223	stanniocalcin 2	4.5
	413076 456759	U10564 BE259150	Hs.75188	wee1 (S. pombe) homolog	4.5
	419735	AW750056	Hs.127792 Hs.169577	delta (Drosophila)-like 3 Homo sapiens cDNA FLJ 14743 fis, clone NT	4.5 4.5
20	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.5
	441217	AJ922183	Hs.213246	ESTa	4.5
	435542	AA687376		ESTs	4.5
	440435 400288	AL042201 X06256	Hs.21273 Hs.149609	transcription factor NYD-sp10 integrin, alpha 5 (fibronectin receptor,	4.5
25	416114	AI595549	Hs.183868	glucuronidase, beta	4.5 4.5
	437323	AA371145	Hs. 194397	leptin receptor	4.5
	425139	AW630488	Hs.25338	protease, serine, 23	4.5
	423678 403961	AW963357	Hs.7847	ESTs	4.5
30	443462	AI064690	Hs.171176	Target Exon ESTs	4.5 4.5
	418483	W26076	Hs.221847	ESTs	4.5
	428873	A1701609	Hs.98908	ESTs	4.5
	410268 408298	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.5
35	449145	A1745325 A1632122	Hs.271923 Hs.198408	Homo sapiens cDNA: FLJ22785 fis, clone K ESTs	4.5
	439574	A1469788	Hs.165190	ESTs	4.4 4.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.4
	453387 447444	AI990741 AK000318	Hs.252809	ESTs	4.4
40	433507	AI817336	Hs.18616 Hs.191791	hypothetical protein FLJ20311 ESTs	4.4 4.4
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 8-cel	4.4
	421064	AI245432	Hs.101382	turnor necrosis factor, alpha-induced pro	4.4
	402604 446291	BE397753	Hs.14623	Target Exon	4.4
45	424503	NM_002205	Hs.149609	interferon, gamma-inducible protein 30 integrin, alpha 5 (fibronectin receptor,	4.4 4.4
	423500	AI633559	Hs.310359	ESTs	4.4
	403361 408432	AW195262		NM_002210*:Homo sapiens Integrin, alpha	4.4
	424489	T48851	Hs.274470	gb:xn67b05.x1 NCI_CGAP_CML1 Homo septens D-siglec precursor,	4.4 4.3
50	442264	AJ278777	Hs.263455	ESTs. Weakly similar to ALU1_HUMAN ALU S	4,3
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.3
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	4.3
	414020 439566	NM_002984 AF086387	Hs.75703	small inducible cytokine A4 (homologous gb:Homo sapiens full length insert cDNA	4.3
55	425242	D13635	Hs.155287	KIAA0010 gene product	4.3 4.3
	423529	T87318	Hs.120411	ESTs	4.3
	439538 453682	AA837323 179703	Hs.56407	ESTs	4.3
	425259	AL049280	Hs.155397	gb:yd71e08.r1 Soares fetal liver spleen Homo sapiens mRNA; cDNA DKFZpS64K143 (fr	4.3
60	417918	AA209205	Hs.163754	hypothetical protein FLJ 12606	4.3 4.3
	426649	AJ914936	Hs.97152	ESTs	4.3
	438875 445868	AA827640 BE169357	Hs.189059	ESTs	4.3
	426509	M31166	Hs.207428 Hs.2050	ESTs pentaxin-related gene, rapidly induced b	4.3
65	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4,3 4,3
	432058	AW665996	Hs.130729	ESTs. Weakly similar to ALU1_HUMAN ALU S	4.3
	430694 441523	AA810624 AW514263	Hs.30936	ESTs, Weakly similar to H28H_HUMAN HISTO	4.3
	443950	NM_001425	Hs.301771 Hs.9999	ESTs, Wealty similar to ALUF_HUMAN !!!! epithelial membrane protein 3	4.2
70	419896	Z99362	14.3333	gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	4.2 4.2
	452994	AW962597	Hs.31305	KIAA1547 protein	4.2
	420841 441255	Al625251 R06350	Hs.94037	hypothetical protein FLJ23053	4.2
	416426	AA180256	Hs.171635 Hs.210473	ESTs Homo sapiens cDNA FLJ14872 fis, clone PL	4.2
75	411789	AF245505	Hs.72157	Adiican	4.2 4.2
	409638	AW450420	Hs.21335	ESTs	4.2
	439192 440684	AW970536	Hs.105413		4.2
	437470	A1253123 AL390147	Hs.127356 Hs.134742		4.2
80	432343	NM_002960	Hs.2961	S100 celcium-binding protein A3	4.2 4.2
	401454	0500.000		NM_014226":Homo sapiens renal tumor anti	4.2
	431770 442326	BE221880 H92962	Hs.268555 Hs.124813	5-3' expribonuclease 2	4.2
		•	110.124013	hypothesical protein MGC14817	4.2

	419402	Z68155	Hs.90291	taminin, beta 2 (taminin S)	4.2
	435703 444609	AW630133	Hs.83313	GK003 protein	4.2
	404407	AW571659	Hs.278081	ESTs Target Expn	4.2 4.2
5	450581	AF081513	Hs.25195	TGF-beta 4	4.2
-	407838	8E146411	Hs.40342	putative nuclear protein	4.1
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.1
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.1
	438898	AI819863	Hs.106243	ESTs	4.1
10	421674	T10707	Hs.296355	hypothetical protein FLJ23138	4.1
	445921	AW015211	Hs.146181	ESTs	4.1
	453055	AW291438	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	4.1
	413450	Z99716	Hs.75372	N-acetytgalactosaminidase, alpha-	4.1
15	427463	AA442224	Hs.97900	ESTs	4.1
13	450639 417576	AI703186	Hs.277174	EST8	4.1
	437269	AA339449 AA334384	Hs.82285 Hs.149420	phosphoribosylglycinamide formytransfer ESTs	4.1 4.1
	415688	AA166963	15.143420	gb:zo86d01.s1 Stratagene ovarian cancer	4.1
	414300	Al304870	Hs.188680	ESTs	4.1
20	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.1
	415024	AI983981	Hs.189114	ESTs	4.1
	408102	U46351	Hs.621	tectin, galactoside-binding, soluble, 3	4.1
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.1
25	451433	AA021140	Hs.269265	ESTs, Weakly similar to A46010 X-linked	4.1
25	446523	NM_003063	Hs.334629	sarcofipin	4.1
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	4.1
	402239	44754102		Target Exon	4.1
	423713 437814	AW754182 Al088192	Un 195474	gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.1
30	414948	C15240	Hs.135474 Hs.182155	ESTs, Wealthy similar to DDX9_HUMAN ATP-D ESTs	4.1
50	421307	BE539976	Hs.103305	Homo sapians mRNA; cDNA DKFZp434B0425 (f	4.0 4.0
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	449655	AI021987	Hs.59970	ESTs	4.0
35	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.0
	432842	AW574093	Hs.334822	hypothetical protein MGC4485	4.0
	422282	AF019225	Hs.114309	spolipoprotein t	4.0
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	4.0
40	449256	AA059050	Hs.59847	ESTs	4.0
40	453385	AW296101	Hs.252806	ESTs	4.0
	443715	AJ583187	Hs.9700	cyclin E1	4.0
	451778	AJ826131	Hs.62954	ESTs, Wealdy similar to zinc finger prot	4.0
	441287 418661	AW293132 NM_001949	Hs.131373	ESTS	4.0
45	420894	AA744597	Hs.1189 Hs.88854	E2F transcription factor 3 ESTs	4.0
1.5	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	4.0 4.0
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	4.0
	453948	AI970797	Hs.64859	ESTs	4.0
	444170	AW813879	Hs.102408	ESTs	4.0
50	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	418216	AA662240	Hs.283099	AF15q14 protein	4.0
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	4.0
55	430890	X54232	Hs.2699	glypican 1	3.9
23	429490	AI971131	Hs.23889	ESTs, Wealty similar to ALU7_HUMAN ALU S	3.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.9
	436265 407304	AA731331	Hs.190668	ESTs	3.9
	433244	AA565832 AB040943	Hs.271649 Hs.271285	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens KIAA1510 protein	3.9 3.9
60	446960	AW294936	Hs.156762	ESTs	3.9
••	406627	T64904	Hs.163780	ESTs	3.9
	420552	AK000492	Hs.98806	hypothetical protein	3.9
	402082			C18000743 :gij6678363 ref NP_033416.1 t	3.9
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.9
65	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.9
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.9
	422564	Al148006	Hs.222120	ESTs	3.9
	418781	T41160	Hs.8404	ESTs	3.9
70	431820	AW410408	Hs.271167		3.9
70	413095	AA494359 BE160091	Hs.30715	potassium voltage-gated channel, lsk-rel	3.9
	430637 443539	BE160081 AI076182	Hs.256290		3.9
	422173	BE385828	Hs.134074 Hs.250619		3.9
	433388	AJ432672	Hs.288539		3.9 3.8
75	403849		113.200333	Target Exon	3.8
	406646	M33600	Hs.308026		3.8
	445075	AI651827	Hs.344767	ESTs	3.8
	420004	AW975532	Hs.164039		3.8
00	449670	F07693	Hs.85603	Homo sapiers mRNA; cDNA DKFZp434K2172 (1	3.8
80	424479	AF064238	Hs.149098		3.8
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	3.8
	418641	8E243136	Hs.86947	a disintegrin and metalloproteinase doma	3.8
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.8

	403000				
	427286 453920	AW732802 AI133148	Hs.2132 Hs.36602	epidermal growth factor receptor pathway I factor (complement)	3.8 3.8
	453857	AL080235	Hs.35861	OKFZPS86E1621 protein	3.8
_	406872	AI760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
5	403696			C4001100":gi[5852342 gb]AAD54015.1 (AF0	3.8
	417791	AW965339	Hs.111471	ESTs	3.8
	418036 404209	Z37976	Hs.83337	latent transforming growth factor beta b	3.8 3.8
	431454	AW975980	Hs.292918	Target Exxon ESTs	3.8
10	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.8
	406739	A1566709	Hs.182426	ribosomal protein S2	3.8
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.8
	457876 435718	AI821940 R06569	Hs.269534	ESTs, Moderately similar to ALU8_HUMAN A	3.8
15	429716	R25685	Hs.211933	ESTs collagen, type XIII, alpha 1	3.8 3.8
	442710	AI015631	Hs.23210	ESTs	3.8
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.8
	419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	3.8
20	436674 408896	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	3.8
20	425300	AI610447 AW601773	Hs.48778 Hs.270259	niban protein ESTs	3.8 3.8
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.8
	424090	X99699	Hs.139262	XIAP associated factor-1	3.7
25	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	3.7
25	427584 420579	BE410293 AA278449	Hs.179718 Hs.137429	v-myb avlan myeloblastosis viral oncogen	3.7
	405038	Y14443	113.137423	ESTs zinc finger protein 200	3.7 3.7
	412590	AL134388	Hs.135033	ESTs, Wealdy similar to I38022 hypotheti	3.7
20	406714	Al219304	Hs.266959	hemoglobin, gamma G	3.7
30	412014	AI620650	Hs.43761	ESTs, Wealdy similar to A46010 X-linked	3.7
	419713 449115	AW968058 AW959952	Hs.92381 Hs.37528	nudix (nucleoside diphosphate linked moi	3.7 3.7
	408955	BE315170	Hs.8087	ESTs, Weakly similar to AF090944 1 PRO06 Target CAT	3.7 3.7
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.7
35	413774	AA131782	Hs.182314	ESTS	3.7
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	· 3.7
	414528 436137	AA148950 AI056769	Hs.188836 Hs.133512	ESTs ESTs	3.7
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.7 3.7
40	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	3.7
	443361	A1792628	Hs.133273	ESTs	3.7
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.7
	409557 420300	BE182896 AA258245	Hs.211193 Hs.127573	ESTs Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7 3.7
45	427695	R88483	Hs.172862	ESTs	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
	434563 444371	AW083994 BE540274	Hs.9469 Hs.239	plackstrin homology domain-containing, f	3.6
50	437816	AI823445	Hs.280599	forkhead box M1 ESTs	3.6 3.6
	405605			C2001342:gi[127814]sp P26434]NAH4_RAT SO	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	430540	AW245422	Hs.106357	Homo sapiens cDNA: FLJ22105 fis, clone H	3.6
55	429747 453785	M87507 Al368236	Hs.2490 Hs.283732	caspase 1, apoptosis-related cysteine pr ESTs, Moderately similar to ALU1_HUMAN A	3.6 3.6
-	403267	74000200	110.200732	Target Exon	3.6
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.6
	447497	AW167254	Hs.205722	ESTs	3.6
60	428600 428715	AW863261 AW293716	Hs.242413 Hs.53126	hypothetical protein DKFZp434K1421 ESTs	3.6
UU.	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	3.6 3.6
	453438	AI469935	Hs.22792	ESTs	3.6
	427299	AA830210	Hs.214263		3.6
65	434577 452785	R37316	Hs.179769		3.6
05	434467	AL359942 BE552368	Hs.296434 Hs.231853	erythroid differentiation and denucleati Homo saciens cDNA FLJ 13445 fis. clone PL	3.6 3.6
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.6
	418287	AI872319	Hs.78935	methionine aminopeptidase; etF-2-associa	3.6
70	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.6
70	441224 458072	AU076964 A1890347	Hs.7753 Hs.271923	catumenin	3.6
	435677	AA694142	Hs.293726		3.6 3.6
	433325	AW206986	Hs.143905		3.6
75	420683	AA830168	Hs.271305	ESTs	3.6
75	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.6
	454078 404584	AA501518	Hs.22209	secreted modular calcium-binding protein Target Exon	3.6
	428311	NM_005651	Hs.183671		3.5 3.5
٥٨	425922	AL157466	Hs.162751	Homo sapians mRNA; cDNA DKFZp761E2423 (f	3.5
80	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.5
	412971 451593	AA889628 AF151879	Hs.35125 Hs.26706	ESTs CGI-121 protein	3.5
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	3.5 3.5
	- 2.				

	427809	M26380	Us 400000		
	443303		Hs.180878	Epoprotein lipase	3.5
	422765	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	3.5
	445936	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.5
5		BE543594	Hs.61478	hypothetical protein FLJ22329	3.5
,	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.5
	432250	AA452088	Hs.274170	Opa-Interacting protein 2	3.5
	458438	AJ141520	Hs.151464	ESTs, Wealthy similar to ALUC_HUMAN !!!!	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to \$65657 alpha	
10	410507	AA355288	Hs.76064	transitional epithelia response protein	3.5
10	412436	AA665089		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	3.5
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.5
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.5
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.5
	440074	AA863045	Hs.10669	ESTs, Wealdy similar to T00050 hypotheti	3.5
15	422448	AW372922	Hs.116774	integrin, alpha 1	3.5
	420676	AJ434780	Hs.4248	ASA 5 oucodeus	3.5
	417663	R07483	Hs.180461	ESTs	3.5
	451089	AA903705	Hs.4190		3.5
	451446	AI826288	Hs.171637	Homo sapiens cDNA: FLJ23269 fs, clone C	3.5
20	414727	BE466904	Hs.190162	hypothetical protein MGC2628	3.5
	421778	AA428000		gb:hz28f03.x1 NCI_CGAP_GC8 Homo septens	3.5
	427413	BE547647	Hs.283072	actin related protein 2/3 complex, subun	3.5
	414039		Hs.177781	hypothetical protein MGC5618	3.5
	456304	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	3.5
25	449162	AI820973	4. 44	gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.5
		AI632740	Hs.10476	ESTs	3.5
	437774	AW978199	Hs.291648	ESTs, Weakly similar to 138022 hypotheti	3.5
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	3.4
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.4
30	450325	AI935962	Hs.26289	ESTs	3.4
30	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.4
	419726	U50330	Hs.1274	bone morphogenetic protein 1	
	417409	8E272506	Hs.82109	syndecan 1	3.4
	412811	H06382		ESTs	3.4
26	430758	T91568	Hs.270616	ESTs, Moderately similar to A34087 hypot	3.4
35	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.4
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.4
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.4
	447674	BE270640	Hs.19192	Cyclin-dependent kinase 2	3.4
	443378	AW392550	Hs.9280	Composed formation of the state	3.4
40	446134	AW161234	Hs.13993	proteasome (prosome, macropain) subunit, TBP-like 1	3.4
	418669	U85992	Hs.87197		3.4
	425006	R38685	Hs.222746	Human clone (MAGE:35527 unknown protein	3.4
	435256	AF193766	Hs.13872	ESTS	3.4
	453379	AA035261		cytokine-like protein C17	3.4
45	448224	R48700	Hs.61753	ESTs	3.4
	455899		Hs.20733	Homo sapiens cDNA: FLJ22356 fis, clone H	3.4
	422017	BE155112	11- 440	gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.4
	417395	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.4
	405046	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	3.4
50		41000440		C3000978:gij9280045 dbj BAB01579.1 (AB0	3.4
50	423178	A1033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	455142	AW861840		gb:CM0-CT0337-250200-243-g01 CT0337 Homo	3.4
	418819	AA228776	Hs.191721	ESTs	3.4
	428289	M26301	Hs.2253	complement component 2	3.4
55	412799	A1267606		gb:aq91h03.x1 Startley Frontal SB pool 1	3.4
٠,٠	403108			ENSP00000241415":Hypothetical 67.7 kDa o	3.4
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	3.4 3.4
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	
60	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4
vv	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.4
	439867	AA847510	Hs.161292	ESTs	3.4 3.4
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	
	420982	AW576160	Hs.100729	KIAA0692 protein	3.4
CE	440826	AW383618	Hs.346256	ESTs. Moderately similar to ALU2_HUMAN A	3.4
65	427687	AW003867	Hs.1570	histamine receptor H1	3.4
	400533			ENSP00000209376":PRED65 protein (Fragmen	3.4
	436314	AI983409	Hs.189226	ESTs	3.3
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	3.3
70	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.3
70	402229	BE262804		mitochondrial ribosomal protein S2	3.3
	410687	U24389	Hs.65436	hysyl oxidase-like 1	3.3
	424614	X54486	Hs.151242		, 3.3
	443338	R99575	Hs.302908	serine (or cysteine) proteinase inhibito ESTs	3.3
	433062	AK001757	Hs.281348		3.3
75	405303		·	hypothetical protein FLJ 10895	3.3
	410889	X91662	Hs.66744	Target Exon	3.3
	406673	M34996	Hs.198253	twist (Drosophila) homolog (acrocephatos	3.3
	431721	AB032996		major histocompatibility complex, class	3.3
	426746	J03826	Hs.268044	KIAA1170 protein	3.3
80	425262	D87119	Hs.2057	uridine monophosphate synthetase (orotat	3.3
	424947	R77952	Hs.155418	GS3935 projetn	3.3
	437634	AW293046	Ha 355450	ESTs, Wealthy similar to atternatively sp	3.3
	437014		Hs.255158	ESIS	3.3
	701014	AA808757	Hs.222531	ESTs, Wealthy similar to S59501 interfero	3.3
				=	

	435456	418							- Odonnelidate enh
	408601 420886	453 423				429415 422081		Hs.196011 E	rocollagen C-endopeptidase enh STs
5	437162 445704	_ 418	49			436258	AW867491	Hs.107125 p	lasmatemma vesicle associated b:MR4-ST0121-141099-010-G0
•	440700	. D 441.			5	410886 442609		Hs.8518 8	selenoprotein N
	414747 431553	449 446				416188 441544		Hs.127137	r-myc avian myelocytomatosis vi ESTs
10	405605	437	62			437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 hypothetical protein
10	431467 457561	I U 450 433			10	419652 44 3 623	AL157485 AA345519	Hs.9641	complement component 1, q sub-
	412507 413448	444 423			" -	415198 441701	AW009480 AW339828		natural killer cell transcript 4 ESTs
15	444168	454	92			426384	AI47207B	Hs.303662	hypothetical protein FLJ13189 (F ESTs, Wealty similar to T29012
13	400090 433642	I D 412 429			15	420886 428896	AA805453 AW291932	Hs.98936	ESTs
	422938 426318	413 433				458253 456895	AW296952 AA354771	Hs.195802 Hs.43047	ESTs Homo sapiens cDNA FLJ13585
20	428896 449277	449	91			434818	AA650097	Hs.5996	ESTs hypothetical protein FLJ20716
20	426509	424	94		20	424278 434131	AK000723 AI858275	Hs.144517 Hs.143659	ESTs
	412216 428845	454 410				447111 443021	AJ017574 AA368546	Hs.17409 Hs.8904	cysteine-rich protein 1 (intestina lg superfamily protein
25	431512	a.c. 456	08			416677	T83470	Hs.334840 Hs.164680	ESTs, Moderately similar to 178 ESTs
25	41B113 450661	420	71		25	429973 422 5 45	AJ423317 X02761	Hs.287820	fibronectin 1
	448448 422631	442 425				444008 420116	BE395085 NM_013241	Hs.10086 Hs.95231	type I transmembrane protein I FH1/FH2 domain-containing pr
30	419687 450963	30 407	20			401841	-	Hs.76084	NM_015113:Homo sapiens KI/ hypothetical protein MGC2721
50	435060	439	¹⁶⁴		30	414418 431019		Hs.2714	forkhead box G1B
	440274 437438	410 422				453707 432188		Hs.126522 Hs.2928	Homo sapiens, clone MGC:16 solute carrier family 7 (cationic
35	435401 416737	3.5 451	8			407378	AA299264	Hs.57776 Hs.293971	ESTs, Moderately similar to 13 ESTs
23	445314	407	21		35	430701 429569	AA454993	Hs. 138343	FSTs. Wealdy similar to 17888
	425870 425294	452 459			•	458918 43976		Hs.252692 Hs.22744	ESTs, Weakly similar to 13802 hypothetical protein MGC131
40	416404 413995	40 419	98			45222	C21322	Hs.288057	hypothetical protein FLJ2224: ENSP0000034663:Zinc fing
	422798	440	18		40	40396 42735	9 AW020782	Hs.79881	Homo sapiens cDNA: FLJ230
	426384 430147	449 450				41439 44415		Hs.76057 Hs.10414	galactose-4-epimerase, UDP hypothetical protein FLJ1074
45	42526 40691	45 449	id :			41440	3 AW969551	Hs.76064	ribosomal protein L27a gb:RC1-HT0256-081199-011
	42526	454	3 '		45		5 AW629223	Hs.64794	zinc finger protein 183 (RINC
	40155 43934	419 423				44488 4403		Hs.192809 Hs.190499	5 ESTs
50	41486 45397	50 424				4162 4391	07 NM_01474	5 Hs.79077 Hs.12470	Homo sapiens, clone MGC:: 7 ESTs
	40428 43289	453	54)		50) 4575	79 AB030816	Hs.36761	HRAS-like suppressor
	45149	447 419	38			4067 4201			secreted and transmembrar
55	44257 42836	55 451				4280 4441			
	44375 41786	432	30		5	5 4091	54 U72882	Hs.50842	2 Interteron-induced protein 3
	44389	446 457	72	1		4494 4587		Hs.1988(Hs.1113	34 ferritin, light polypeptide
60	43886 45390	60 44		•		450 425			ab:EST374201 MAGE rest
	44771 42658	438 434	ro		6	0 445	211 BE04560	1 Hs.1182	
	42112	422	77 ₁ .	4		441 450	625 AW97010	17	gb:EST382188 MAGE res
65	41076 43146	65 433 427				437 444	640 AA76489 672 Z95636	3 Hs.2721 Hs.1166	ig taminin, alpha 5
	45222 41232	414 420	13		•	55 407	047 X65965		gb:H.saplens SOD-2 gene
	42860	456	20			439	755 AW7484	82 Hs.7787	73 B7 hamolog 3
70	42650 40555	70 436				41.	5520 AA29799 1598 A109422		
	42148 44858	439 451			•	70 44	0948 AW1883	11 Hs.128	
	45210	415	25			41	7336 R70429	Hs.819	88 disabled (Drosophila) hor
75	4295 4507	75 433	57,	•		41	7944 AU0771 1671 BE0490		ESTS
	4293 4374	426 435	io	*****		75 43	0444 AW2984	121 Hs.121	
	4321 4046	439	1			40	7721 Y12735	Hs.380)18 dual-specificity tyrosine-(
80	4526	80 400	1			44	19093 AA5341 19523 NM_00	0579 Hs.544	143 chemokine (C-C motif) n
	4214 4190	417 425				80 4	15664 A10320 53085 AW954	37 Hs.269	9819 ESTs KIAAO251 protein
	4535	415				4:	30314 AA3690	601 Hs.23	9138 pre-B-cell colony-enhanc
						4	47627 A17028	96 Hs.42	A21 E319

	*****	D60468	Uh 04101	FOY-		
	415114 448958	AB020651	Hs.94181 Hs.22653	ESTs KIAA0844 protein	6.0 5.9	6.0 5.9
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.9	6.0
•	447138	A1439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
5	414545	AA149287	Hs.76605	ESTs	5.8	3.6
	418202 410389	N48521 AW954049	Hs.26549 Hs.8177	KIAA1708 protein ESTs, Weakly similar to PIHUB6 salivary	5.8 5.7	5.8 9.6
	444124	R43097	Hs.6818	ESTs	5.7	9.3
10	408065	AW954272		gb:EST386342 MAGE resequences, MAGC Homo	5.6	5.6
10	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.6	9.6
	425523 459697	AB007948 AA406062	Hs.158244 Hs.98002	KIAA0479 protein ESTs	5.6 5.6	35.0
	408428	NM_014787	Hs.44896	OnaJ (Hsp40) homolog, sublamily 8, membe	5.6	5.4 5.6
	420111	AA255652		gb:zs2th11.r1 NOI_CGAP_GC81 Homo sapiens	5.5	3.2
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	5.3	5.3
	438202 448605	AW169287 AL109678	Hs.22588 Hs.21597	ESTs Homo sapiens mRNA full length insert cDN	5.3 5.3	5.3 5.3
	425580	L11144	Hs.1907	galanin	5.3	3.5
20	418868	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.3	3.8
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3	4.9
	448786 427283	BE048842 AL119796	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.2	5.2
	415666	H72693	Hs.174185	ectonucleotide pyrophosphatase/phosphodi gb:yu03c11.r1 Soares fetal fiver spieen	5.2 5.2	3.0 5.2
25	410240	AL157424	Hs.61289	synaptojanin 2	5.2	4.6
	428784	Y12851	Hs.193470	purtnergic receptor P2X, ligand-gated to	5.2	7.7
	446692	Z44514	11- 404660	Homo sapiens mRNA for KIAA1763 protein,	5.2	33.0
	428508 446353	BE252383 AJ290919	Hs.184668 Hs.153661	SBBI31 protein ESTs	5.2	4.1
30	423135	N67655	Hs.26411	EST8	5.1 5.1	5.1 8.2
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	5.1	5.1
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	5.1	5.1
35	411379 408068	AI816344 AW148652	Hs.12554 Hs.167398	ESTs, Weakly similar to NPL4_HUMAN NUCLE ESTs	5.0 5.0	11.2 5.0
-	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.0	27.4
	439607	BE540565	Hs.159460	ESTS	5.0	5.6
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	4.9	29.3
40	414631 437117	AW970130	Hs.65406	ESTs	4.9	4.9
40	418527	AL049256 AA450386	Hs.122593 Hs.7149	ESTs Homo sapiens cDNA: FLJ21950 fis, clone H	4.9 4.9	3.8 4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
	455384	H72176	Hs.4273	hypothetical protein FLJ13159	4.9	4.9
45	443150	AI034467	Hs.34650	ESTs	4.9	7.6
43	422411 414931	AW749443 AK000342	Hs.22511 Hs.77646	ESTS	4.9	12.0
	430456	AA314998	Hs.241503	Homo sapiens mRNA; cDNA DKFZp761M0223 (I hypothetical protein	4.9 4.8	3.4 4.7
	428186	AW504300	Hs.295605		4.8	3.9
50	433516	AA595802	Hs.33410	ESTs, Wealty similar to T17279 hypotheti	4.6	4.8
50	427287 416101	NM_014903	Hs.174188		4.8	4.8
	447252	R24854 R90916	Hs.268806 Hs.12449	ESTs Homo sapiens transmembrane protein HTMP1	4.B 4.8	3.3 3.2
	458268	AA428403	Hs.106131	ESTs	4.7	3.9
66	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.7	8.2
55	445102	AW204610	Hs.22270	ESTs	4.7	19.2
	419643 414949	F06066 C15314	Hs.91791 Hs.323349	chromosome 11 open reading frame 25 ESTs	4,7 4,7	4,7 3.8
	453534	NM_014796		KIAA0748 gene product	4.7	4.7
~	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	4.7	4.0
60	451032	W03692	Hs.323079		4.7	4.9
	434792 447104	AA549253 R19085	Hs.132458 Hs.210706		4.7	3.8
	430537	X62692	Hs.2593	phosphodieslerase 68, cGMP-specific, rod	4.7 4.6	3.0 4.6
	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
65	453302	NM_000838		glutamate receptor, metabotropic 1	4.6	4.6
	429876	AB028977	Hs.225974		4.6	16.8
	451516 433670	AI800515 AA604405	Hs.12024	ESTs gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	4.6 4.6	6.3 3.9
	437380	AL359577	Hs.112198		4.5	3.8
70	410366	AI267589	Hs.302689		4.5	10.4
	419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5
	429290 424932	AF203032 R14070	Hs.198760		4.5	3.3
	432738	AA788898	Hs.315369 Hs.179902	Homo sapiens cDNA: FLJ23075 fis, clone L transporter-like protein	4.5 4.4	10.2 4.0
75	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC: 15606, mRNA, com	4.3	3.3
	435040	A1932350	Hs.152825		4.3	4.7
	451301 452381	AI769514 H23329	Hs.209890 Hs.290880		4.3	4.3
80	410305	AF030409	Hs.62185		4.3 4.3	4.3 7.8
-	433109	N58907	Hs. 162430		4.3	3.9
	431342	AW971018	Hs.21659		4.3	8.0
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	4.3	3.4

	422414 439274	AW875237	Hs.13701	ESTs	4.2	5.3
	439274	AF086092 AA328082	Hs.48372 Hs.209569	ESTs	4.2 4.2	18.3 4.2
_	429955	AI374651	Hs.22542	ESTs	4.2	3.2
5	427317	AB028955	Hs.175780	KIAA1032 protein	4.2	5.3
	426847 408206	S78723 AF041853	Hs.298623 Hs.43670	5-hydroxytryptamine (serotonin) receptor kinesin family member 3A	4.1 4.1	7.9 4.1
	433803	AJ823593	Hs_27688	ESTs	4.1	4.1
10	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	4.1	4.0
10	448117 450600	H49129	Hs.172982	ESTs	4.1	4.1
	429550	BE079478 AW293055	Hs.24880 Hs.119357	ESTs ESTs	4.1 4.1	3.9 6.4
	448681	AL109781	Hs.21754	Homo saplens mRNA full length insert cDN	4.0	7.2
15	458694	F12832	Hs.3610	ESTs	4.0	4.0
13	452197 423728	AW023595 AW891294	Hs.232048 Hs.132138	ESTs solute carrier family 4, sodium bicarbon	4.0 4.0	4.0 7.9
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	4.0	13.1
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
20	419863 442412	AW952691 R77677	Hs.93485 Hs.346644	Homo sapiens mRNA; cDNA DKFZp761D191 (fr ESTs	3.9	21.4
20	424001	W67883	Hs.137476	paternally expressed 10	3.9 3.9	3.9 5.4
	440293	Al004193	Hs.22123	ESTs	3.9	3.9
	422890 426054	Z43784	LL 100100	ankyrin 3, node of Ranvier (ankyrin G)	3.9	3.6
25	412949	U12431 AJ471639	Hs.166109 Hs.71913	ELAV (embryonic lethal, abnormal vision, ESTs	3.9 3.8	3.9 3.7
	427457	AW779105	Hs.164682	ESTs	3.8	11.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyrne)	3.8	4.4
	442676 434998	A1733585 AW975157	Hs.130897 Hs.26037	ESTs ESTs	3.8 3.7	3.8 3.7
30	424945	AJ221919		hypothetical protein FLJ10582	3.7	30.5
	415257	F03016	Hs.27513	ESTs	3.7	8.6
	407886 400844	AW969688	Hs. 100826	ESTs NM_003105*:Homo sapiens sortiin-related	3.7 3.7	20.2
	456765	Al497900	Hs.33067	ESTs	3.7	3.1 3.7
35	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.6	7.6
	452667 436773	T87219 AW078629	Hs.13219	ESTs	3.6	3.6
	424120	T80579	Hs.290270	PC4 and SFRS1 interacting protein 1 ESTs	3.6 3.6	3.6 14.7
40	446574	Al310135	Hs.335933	ESTs	3.6	3.5
40	432453 408119	AI885537 W26213	Hs.27172	ESTs, Moderately similar to PC4259 ferri	3.6	3.9
	449093	AB035356	Hs.101672 Hs.22998	ESTs, Weakly similar to T00331 hypotheti neurexin 1	3.6 3.6	3.6 3.6
	439239	AI031540	Hs.235331	ESTs	3.6	49.5
45	451625	R56793	Hs.106576	alanine-glyoxytate aminotransferase 2-li	3.6	4.1
43	435059 423346	Z45270 AI267677	Hs.235873 Hs.127416	hypothetical protein FLJ22672 synaptolanin 1	3.6 3.6	4.8 20.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	442106	AW205881	Hs.326728	ESTs	3.5	3.2
50	449117 405819	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.5 3.5	3.5 13.5
	452311	AW304029	Hs.252744	ESTa	3.5	3.5
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	3.5	21.8
	410224 400098	M55513	Hs.150208	potassium voltage-gated channel, shaker- Eos Control	3.4 3.4	3.4 3.4
55	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.4	5.9
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.4	14.0
	443682 417417	Al383061 F05745	Hs.47248 Hs.89512	ESTs, Highly similar to similar to Cdc14 ATPase, Ca transporting, plasma membrane	3.4	3.3
	419529	AB020695	Hs.91662	KIAA0888 protein	3.3 3.3	17.1 13.4
60	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.3	4.1
	417063 435071	N50515 D60683	Hs.45061 Hs.35495	ESTs ESTs	3.3	3.3
	446377	AW014022	Hs.170953	ESTS	3.3 3.3	3.3 3.3
65	412453	R20205	Hs.75236	ESTA	3.3	3.3
05	450561 423829	R49674 R44107	Hs.25909	ESTs	3.3	3,3
	415527	F11624	Hs.240905	gb:HSC2ZD101 normalized infant brain cDN	3.3 3.3	4.4 3.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
70	425121	AI797511	Hs.154679		3.2	3.9
, 0	452856 442879	AF034799 AF032922	Hs.30881 Hs.8813	protein tyrosine phosphatase, receptor t syntaxin binding protein 3	3.2 3.2	10.7 3.2
	417284	N62889	Hs.107242		3.2	3.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.2	6.7
75	429477 453169	AI275514 AB037815	Hs.6658 Hs.32156	ESTs KIAA1394 protein	3.2	3.2
. •	408039	AA131424	Hs.336636		3.2 3.2	5.7 3.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DXFZp566A1046 (1	3.2	22.1
	409746 416874	NM_004794 H98752	Hs.56294 Hs.42568	RAB33A, member RAS oncogene family ESTs	3.2	10.6
80	453919	AW959912	Hs.7076	KIAA 1705 protein	3.2 3.2	6.0 3.2
	444861	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2	3.2
	433315 419103	R96754 Z40229	Hs.239706 Hs.96423		3.2	3.1
	413103	C-10573	.13.30423	hypothetical protein FLJ23033	3.2	8.4

	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	3.2	56.0
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	3.2	4.1
	432809 445225	AA565509	Hs.131703	ESTs	3.1	9.9
5	424087	AI216555 N69333	Hs.202398 Hs.143434	ESTs	3.1	5.5
	437924	A1935344	Hs.164118	contactin 1	3.1	3.1
	419683	AA248897	Hs.48784	ESTs, Weakly similar to SL51_HUMAN SODIU ESTs	3.1	3.2
	420173	AA256151	Hs.22999	ESTs	3.1 3.1	5.9
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1	4.1 6.6
10	416220	N49776	Hs.170994	hypothetical protein MGC10946	31	4.5
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	3.1	4.2
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.1	3.1
	445194	AJ215667	Hs.175044	ESTS	3.1	3.1
1.0	438054	AA776626	Hs.169309	ESTs	3.1	10.2
15	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.1	12.2
	445725	AK000956	Hs.13209	hypothetical protein FLJ 10094	3.0	3.0
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.0	11.7
	447673	AJ823987	Hs.182285	ESTs	3.0	3.0
20	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	3.0	42.3
20	418410 429024	AA811441 Al652297	Hs.107393	chromosome 3 open reading frame 4	3.0	3.9
	426919	AL041228	Hs.119302	complement-c1q tumor necrosis factor-rei	3.0	3.7
	424724	T06532	Hs.287709	ELAV (embryonic lethal, abnormal vision,	3.0	9.0
	410011	AB020641	Hs.57856	Homo sapiens cDNA: FLJ22674 fis, clone H	3.0	3.0
25	408947	AL080093	Hs.49117	PFTAIRE protein kinase 1 Homo sapiens mRNA; cDNA DKFZp564N1662 (f	3.0 3.0	10.0 13.5
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	2.9	81.1
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	29	6.6
	410711	A8002316	Hs.65746	KIAA0318 protein	29	6.1
	415486	H12214	Hs.13284	ESTs. Wealdy similar to 2109260A B cell	29	15.7
30	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.9	3.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ 10392	2.9	11.5
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	2.9	3.6
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.9	5.1
26	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.9	3.2
35	429401	AW296102	Hs.99272	ESTs, Wealdy similar to \$32567 A4 protei	2.9	6.1
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.9	5.9
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.8	28.5
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	2.8	23.1
40	416836	D54745	Hs.80247	cholecystokinin	2.8	6.8
40	449277	AA001064	Hs.43570	ESTs	2.8	8.5
	451952	AL120173	Hs_301663	ESTs	2.7	19.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.7
	413408 410343	R51793	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.7	3.0
45	420489	AA084273 AA815089	Hs.76561	ESTs, Weakly similar to S47072 finger pr	2.7	3.2
73	447359	NM_012093	Hs.193513	ESTs	2.7	4.1
	423731	T08814	Hs.18268	adenylate kinase 5	2.7	17.2
	409953	AA332277	Hs.57691	gb:EST06706 Infant Brain, Bento Soares H cadherin 18, type 2	2.7 2.7	4.0
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	27 27	5.5 11.5
50	449714	AB033015	Hs.23941	KIAA1189 protein	. 27	7.5
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.7	3.7
	432447	X92681	Hs.2998	contactin 2 (axonal)	27	4.1
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.7	5.1
~ ~	438068	AI927209	Hs.306210	Homo saplens cDNA: FLJ23133 fis, clone L	2.6	5.1
55	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.6	7.9
	447761	AF061573	Hs.19492	protocadherin 8	2.6	6.3
	448743	AB032962	Hs.21896	KIAA1136 protein	2.6	23.2
	408547	AA574291	Hs.57837	ESTs	2.6	4.0
60	426380	AI291267	Hs.149990	EST8	2.6	6.9
UU	420898	A8002379	Hs.100113	KIAA0381 protein	2.6	3.7
	440357	AA379353	Hs.20950	phospholysine phospholistidine inorganic	2.6	3.7
	424572 418338	M19650	11- 04454	2.3-cyclic nucleotide 3 phosphodieste	2.6	5.9
	427658	NM_002522 H61387	Hs.84154 Hs.30868	neuronal pentraxin I	2.5	6.1
65	410359	R38624	Hs.106313	nogo receptor	2.5	3.0
	449717	AB040935	Hs.23954	ESTs cerebral cell adhesion molecule	2.5	6.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.5	4.5
	450133	AW969769	Hs.105201	ESTs	2.5 2.5	10.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.5 2.5	40.5
70	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	2.5 2.5	17.4 9.5
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.5	3.9
	414683	\$78298	Hs.76888	hypothetical protein MGC12702	2.5	7.1
	422927	AW247388	Hs.301423		25	3.0
76	449568	AL157479	Hs.23740	KIAA1598 protein	25	3.6
75	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.5	3.6
	428495	NM_013279	Hs.184640	hypothetical protein MGC10781	2.5	3.2
	431096	AA324358	Hs.249227		2.4	3.6
	452371	R40990	Hs.21658	ESTs	2.4	3.3
80	424997	AL138167	Hs.96920	ESTs	2.4	6.2
30	450310	N62341	Hs.94116	ESTs	24	3.6
	452898	AA814497	Hs.78792	ESTs	2.4	3.9
	436734	AI937612	Hs.273758		2.4	4.7
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	2.4	3.1

	439428	AA835825	Hs.190490	ESTS	2.4	3.0
	445255 438420	NM_014841 AA443966	Hs.12477 Hs.31595	synaptosomal-associated protein, 91 kDa ESTs	2.4 2.4	8.1
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	24	3.7 3.0
5	451407	AA131376	Hs.343809	fibroblast growth factor 12B	24	7.2
	419757	AA773820	Hs.63970	ESTs	24	3.3
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.4	3.6
	439199	R40373	Hs.26299	ESTs .	2.3	9.5
10	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.3	5.6
10	454048 412675	H05626 AA460716	Hs.6921 Hs.9788	ESTS	23	9.9
	434811	AW971205	Hs.114280	hypothetical protein MGC10924 similar to ESTs	23 23	3.3 6.7
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	23	3.1
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	23	3.1
15	447028	AJ973128	Hs.167257	brain link protein-1	23	5.6
	451050	AW937420	Hs.69662	ESTs	2.3	4.4
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	2.3	4.8
	408838	AI669535	Hs.40369	ESTS	2.3	3.0
20	408777 453924	U71204 R49295	Hs.47626 Hs.24886	Ric (Drosophila)-like, expressed in neur	23	3.8
20	422709	AA315331	Hs.153485	ESTs ESTs	23 23	13.4 4.4
	438911	AF085841	Hs.301920	ESTs	2.3	3.3
	439108	AW163034	Hs.6467	synaptogyrin 3	22	6.9
~~	420297	A1528272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2	4.1
25	404819			NM_002588*:Homo sapiens peanut (Drosophi	2.2	5.8
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.2	11.8
	433597	AA708205	Hs.100343	ESTs	22	11.0
	440152 418375	AB002376 NM_003081	Hs.7006 Hs.84389	KIAA0378 protein	22	14.2
30	409892	AW956113	Hs.7149	synaptosomal-associated protein, 25kD gb:EST368183 MAGE resequences, MAGD Homo	2.2 2.2	82.9 4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.2	6.0
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	2.2	5.0
	438703	AI803373	Hs.31599	ESTs	2.2	6.2
35	428845	AL157579	Hs.153610	KIAA0751 gene product	2.2	6.7
33	417865	AW086059	Hs.6529	ESTs, Weakly similar to 178885 serine/th	2.2	3.5
	425897 419271	AA935315 N34901	Hs.48965 Hs.238532	Homo sapiens cDNA: FLJ21693 fis, clone C ESTs	2.2	3.2
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-ch)	2.2 2.2	7.5 7.3
	439415	F05538	Hs.4273	ESTs	2.2	7.3 31.3
40	415170	R44386	Hs.164578	ESTs	22	10.9
	423641	AL137256	Hs.130489	ATPase, aminophosphotipid transporter-li	2.1	6.2
	443728	AJ083876	Hs.148383	ESTs	2.1	4.1
	452108	AW135982	Hs.203013	hypothetical protein FLJ 12748	21	5.7
45	429037 418900	X81895 BE207357	Hs.194765 Hs.3454	H.sapiens GENX-5624 mRNA, 3' UTR	21	7.1
43	421268	AJ126821	Hs.30514	KIAA1821 protein ESTs	21 21	4.3 4.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	15.6
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	2.1	6.5
60	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.1	3.3
50	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	3.5
	447877	AJ435184	Hs.164252	ESTs.	2.1	5.1
	422421 432882	AA325138 NM_013257	Hs.235873 Hs.279696	hypothetical protein FLJ22672	2.1	8.3
	410631	AA086469	Hs.47171	serum/glucocorticoid regulated kinase-li ESTs	2.1 2.1	4.2 5.8
55	407808	AA663559	Hs.279789	histone deacetylase 3	2.1	5.7
	424379	Z42034	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.1	3.2
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	2.1	3.0
	433932	AW954599	Hs.169330	neuronal protein	2.1	6.9
60	425130 402027	AA448208	Hs.99163	ESTs	2.1	3.1
UU	435191	R15912	Hs.4817	Target Exon Homo sapiens clone 24461 mRNA sequence	2.0	3.5
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	2.0 2.0	7.5 10.7
	404541		110.00100	NM_030795:Homo sepiens stathmin-like 4 (2.0	6.0
	420050	AL118615	Hs.94653	neurochondrin	2.0	6.5
65	417868	AI078534	Hs.122592	ESTs	20	5.6
	416602	NM_006159		nei (chicken)-like 2	2.0	3.2
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	2.0	4.2
	439340 429900	AB032436 AA460421	Hs.6535	brain-specific Na-dependent inorganic ph	2.0	6.3
70	437762	T78028	Hs.30875 Hs.154679	ESTs synaptotagmin 1	20	4.2
	425172	AA447729	Hs.12714	ESTs	2.0 2.0	4.6 3.1
	419587	\$62907	Hs.91343	gamma-aminobutyric acid (GABA) A recepto	2.0	3.1
	451734	NM_006176		neurogranin (protein kinase C substrate,	2.0	4.9
75	423603	AB007880	Hs.129883		2.0	4.3
13	438277	AL022326	Hs.6139	synaptogyrin 1	2.0	3.4
	423767 434933	H18283 R91095	Hs.132753		2.0	3.2
	426575	M74826	Hs.4276 Hs.170808	KIAA1701 protein glutamate decarboxylase 2 (pancreatic is	2.0	6.1
	~~~~	7050	113.170000	Anguaran according a fibermant of	2.0	4.6

80 TABLE 188:
Play:
CAT number:
Accession:
Unique Eos probeset identifier number
Gene duster number
Genbank accession numbers

	Pkey	CAT Number	Accession											
	408065	103646_1		03154 AA059300 AA046911										
_	415527	1539393_1		2 H08936 R56332 H09256 R52303 R13075										
5	415666	1543492_1		3 H72694 F20990 R08580										
	418512	176394_1		1332 RS8460 AA350990 T33788 T30936 AA350905 T08	3592 T09274 AA22429	97 D54678 T08951	R15346 AW953188 AA350074							
			AW890649											
	418856	179788_1	T65754 AA229											
10	420111	190755_1		280911 AW967920 AA262684	*****	C020 A 400C204 A	********							
10	422890	222707_1		2 AW572911 AA449369 H17037 R19603 Al632565 AW										
				53735 AI263703 AA319159 AW964436 AI903440 AW59	M 1 / 1 MIDD/ 44/ MY12	MU/1 AW330110 C	, 130 IB UB 1 142 H I / (A3B A17 102343							
	402224	224455 4	T87230 AI3	O AL 190525 AA220210 AUDICIES MIZIED										
	423731	231456_1		8 AL120536 AA330218 AW961552 N47159	E1200E 0C2EE2C4 0	E361303 T66340 A	A 200EDE A A 200ACE DE ANDERA							
15	424572	24097_1		50 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 2037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303										
13					TO ATTOO TOO ATTOO	1330 11000 11 1111 01	01000012174270000140000							
	424945	245223_1		62 AA019090 AA001 9 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227										
				32626 D81263 D53937 D52496 AA974487 AW043854 N										
			Al193667 Al3											
20	426919	273507_1	AL041228 D8	2004 D61361 AI203314 AI990307 AW900295 AI018308	AW087473 AW18353	0 AA393346 H500!	55 AA935601							
	433670	372721_1	AA604405 BE	062234 AW748386										
	433921	377350_1		14549 R36464 R36465										
	433940	37787_1	H05129 N634	33 A1651350 AA984734 A1368716 NA0915 A1989705 F0	19042 T03905 R88588	AF112220	•							
26	435773	426857_1		857375 N64357 AA731069										
25	446692	689623_1	Z44514 A/352	097 A1803984 AW235923 AW196558 A1954637 A13369	83									
	TABLE 18	.c.												
	Pkey:		nua animber corre	sponding to an Eos probeset										
	Ret:			he 7 digit numbers in this column are Genbank Identifier	(GI) numbers. "Dunh	am, et al.º refers lo	the publication entitled 'The DNA							
30				chromosome 22" Dunham, et al. (1999) Nature 402:489-										
	Strand:	Indi	cates DNA strand	from which exons were predicted.										
	Nt_positio	n: Indi	cates nucleotide	positions of predicted exons.										
	Oleman	Ref	C	Attiti										
35	Pkey 400844	9188505	Strand Plus	Nt_position 24746-24872,25035-25204										
73	402027	7622350	Plus	51645-51888,52917-53006										
	404541	8318559	Plus	103456-103664										
	404819	4678240	Ptus	16223-16319,16427-16513,16736-16859,16941-17075	,17170-17287,17389-	17529,18261-18357	7,18443-18578							
40	405560	183148	Plus	5495-5655,6077-6241,6495-6692										
40	405819	4007557	Plus	2830-2967										
	406311	9211559	Minus	137114-139033										
	TARI E 1	9A· ARCHIT 35	A CHS.ENRICHI	D GENES SIGNIFICANTLY DOWN-REGULATED IN G	LIORI ASTOMA COM	PARED TO NORM	ALADUIT ONS							
				genes significantly down-regulated in glioblastoma comp										
45	the Affvir	retrix/Eos Hu03	GeneChip array	such that the ratio of "average" normal CNS to "average	° ofioblastoma was or	eater than or equal	to 2. The "average" normal CNS level was							
	sel to the	85° percentile	amongst various	normal CNS tissues. The "average" gliobiastoma level	was set to the 85h per	centile amongst va	rious tumor samples. To enrich for CNS							
	specific g	enes, the ratio	of "average" CN	S to "average" non-CNS normal adult fissues was calcula	ated to be greater than	or equal to 3. The	"average" CNS level was sel to the 85°							
				The "average" normal non-CNS adult tissue level was s										
50				of non-specific hybridization, the 10th percentile value an	nongst non-malignant	issues was subtrac	ted from both the numerator and the							
50	Oenomin Pkey:		ratios were evalu											
	ExAcon:			et identifier number n number, Genbank accession number										
	Unigene		INFO ACCESSOR INTELLED, SCHOOL ACCESSOR INTELLED											
	Unigene		igene gene title											
55	R1:		tio of CNS to Gli	oblastoma			•							
	R2:	Ra	atio of CNS to NC	IN-CNS NORMAL ADULT TISSUES										
	~			41 to 1										
	Pkey 425489	ExAccn M58594	UnigenelD Hs.1905	Unigene Title protectin	R1 24.8	R2 10.5								
60	410330	AW023630		ESTs	23.4	23.4								
00	430538	AB032435		differentiation-associated Na-dependent	22.6	22.6								
	417275		Hs.295449	parvalbumin	22.4	6.0								
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8	21.8								
15	408040		Hs.22905	ESTs, Wealdy similar to RHG6_HUMAN RHO-G	19.4	19.4								
65	435145		Hs.116631	ESTs .	18.5	3.8								
	407039			gb:Human protectin gene 5' region.	18.1	18.1								
	409263 432298			ESTs Homo sapiens mRNA; cDNA DKFZp761G1111 (f	16.8 15.1	16.8 15.1								
	424645			KIAA0535 gene product	15.1	15.1								
70	416018			proprotein convertase subtilisin/kexin t	14.0	14.0								
	405560			hypothetical protein FLJ20628	13.9	8.0								
	452022		Hs.293875	ESTs	13.8	13.8								
	413324		Hs.75294	corticotropin releasing hormone	13.2	13.2								
75	411498			ecotropic viral Integration site 2A	12.9	19.4								
13	423449		Hs.33067	ESTS	12.4	14.5								
	433940 410657		Hs.65248	cyclic AMP-regulated phosphoprotein, 21 dynein, cytoplasmic, intermediate polype	12.0 11.5									
	449078			KIAA1576 protein	11.0									
	410635		Hs.334372	chorionic somatomammotropin hormone 1 (p	11.0									
80	453165		Hs.32042	aspartoacylase (aminoacylase 2, Canavan	10.7	10.7								
	417167	AW20643		ESTs	10.4									
	420033		Hs.292590		10.4									
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	10.0	10.0								
				201										

	418207	C14685	Hs.34772	ESTs	9.8	9.8
	417175 444330	R44558	Hs.94002 Hs.49265	ESTs ESTs	9.6	8.9
	427322	AI597655 AK002017	Hs.176227	hypothetical protein FLJ11155	9.1 8.9	9.1 8.9
5	429096	A8011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AA584272	Hs.335224	transmembrane protein with EGF-like and	8.6	8.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	8.6	22.2
	410309	BE043077	Hs.278153	ESTs	8.5	8.5
10	416851	AW963951	Hs.85618	ESTs	8.5	8.5
10	427061 400438	AB032971 AF185611	Hs.173392 Hs.115352	KIAA1145 protein	8.4	8.4
	440209	H05049	Hs.247837	Target neurexin 3	8.3 8.2	5.1 18.7
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.1	5.8
	435648	H24347	Hs.27524	ESTs	8.1	8.1
15	429470	AI878901	Hs.203862	guarrine nucleotide binding protein (G pr	8.0	8.0
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	7.9	8.6
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	7.9	15.7
20	435427	AI344378	Hs.143399	ESTs	7.8	7.8
20	434367 429875	AB020700 AB028977	Hs.3830 Hs.225974	KIAA0893 protein KIAA1054 protein	7.8 7.8	5.6
	441005	241305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7	16.8 7.7
	442023	A1187878	Hs.144549	ESTs	7.7	5.6
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
25	450642	R39773	Hs.7130	copine IV	7.6	5.6
	437073	AI885608	Hs.94122	ESTs	7.5	7.5
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
	424153	AA451737	Hs.141496	MAGE-like 2	7.3	5.1
30	450474 450715	AW872844 AI266484	Hs.117494 Hs.31570	ESTs ESTs, Wealthy similar to KIAA1324 protein	7.2 7.2	7.2 7.2
50	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	7.0	7.0
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0
2.0	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	6.9	6.1
35	457012	R41480	Hs.302754	ESTs	6.9	6.9
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
	409031 453590	AA376836 AF150278	Hs.288856 Hs.33578	ESTs KIAA0820 protein	6.8 6.6	6.8 22.3
40	450181	H05254	Hs.201198	ESTs	6.6	7.2
	425580	L11144	Hs.1907	galanin	6.5	3.5
	445279	R41900	Hs.22245	ESTs	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
AE	434104	AF116691	Hs. 115459	hypothetical protein PRO2198	6.4	4.D
45	443244	A1457235	Hs.166479	ESTs	6.3	3.0
	447750 415114	AI422234	Hs.143434	contactin 1	6.2	9.8
	450600	D60468 BE079478	Hs.94181 Hs.24880	ESTs ESTs	6.0	6.0
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	5.9 5.9	3.9 7.7
50	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
	447138	AI439112	Hs.93828	ESTs, Wealtly similar to 2109260A B cell	5.8	5.8
	414545	AA149287	Hs.76605	ESTs	5.8	3.6
	410389	AW954049	Hs.8177	ESTs, Wealtly similar to PIHUB6 salivary	5.6	9.6
55	450590	AI701507	Hs.273740		5.6	3.8
"	408428 442026	NM_014787 AI243749	Hs.44896 Hs.8074	OnaJ (Hsp40) homotog, subfamily B, membe brain-specific angiogenesis inhibitor 3	5.6 5.5	5.6
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	6.5 5.4
	414699	AJ815523	Hs.76930	synuclein, elpha (non A4 component of am	5.3	4.5
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
60	448605	AL109678	Hs.21597	Homo sapiens mRNA full tength insert cDN	5.3	5.3
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.3	3.8
	448786	BE048842	Hs. 179075		5.2	5.2
	406311 443682	Al383061	Hs.47248	NM_021979*:Home sapiens heat shock 70kD	5.2 5.2	11.5
65	415666	H72693	15.47240	ESTs, Highly similar to similar to Cdc14 gb:yu03c11.r1 Soares fetal liver spleen	5.2 5.2	3.3 5.2
•••	416101	R24854	Hs.268806	ESTs	5.2	3.3
	428508	BE252383	Hs.184668	SBBI31 protein	5.2	4.1
	419318	AW969742	Hs.291005		5.2	3.1
70	439238	N47305	Hs.302161		5.1	5.3
70	446353	Al290919	Hs.153661		5.1	5.1
	412049	N53437 AL353933	. Hs.18268	adenylate kinase 5	5.1	10.7
	437331 413988	M81883	Hs.21710 Hs.324784	hypothetical protein DKFZp761G0313 glutamate decarboxylase 1 (brain, 67kD)	5.1	5.1
	408068	AW148652	Hs.167398		5.1 5.0	5.1 5.0
75	414631	AW970130	Hs.65408	ESTs	5.0 4.9	4.9
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
	427224	AL135554	Hs.101937		4.9	3.9
80	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
00	427287 447252	NM_014903 R90916			4.8	4.8
	424932	R14070	Hs.12449 Hs.315369		4.8	3.2 10.2
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7 4.7	4.7
					7,7	7.7

	414949 453534	C15314	Hs.323349 Hs.33187	ESTs	4.7	3.8
	430537	NM_014796 X62692	Hs.2593	KIAA0748 gene product phosphodiesterase 68, cGMP-specific, rod	4,7 4,6	4.7 4.6
_	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
5	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.6	3.0
	418202 419191	N48521 U17195	Hs.26549 Hs.89666	KIAA1708 protein	4.6	5.8
	459080	AW192083	Hs.290855	A kinase (PRKA) anchor protein 6 ESTs	4.5 4.5	4.5 13.5
10	451783	R42554	Hs.210862	T-box, brain, 1	4.4	11.2
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	451050	AW937420	Hs.69662	ESTs	4.4	4.4
	423728 447746	AW891294 AW015920	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	7.9
15	451301	AF769514	Hs.161359 Hs.209890	ESTs EST	4.3 4.3	9.9 4.3
	452381	H23329	Hs.290880	ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	412155	R38167	Hs.12449	Homo saplens transmembrane protein HTMP1	4.3	27.9
20	426365 423589	AA376667 AA328082	Hs.10283	RNA binding motif protein 88	4.3	4.1
20	432453	AI885537	Hs.209569 Hs.27172	ESTs ESTs, Moderately similar to PC4259 femi	4.2 4.2	4.2 3.9
	420489	AA815089	Hs.193513	ESTs	4.1	4.1
	427457	AW779105	Hs.164682	ESTs	4.1	11.1
25	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
43	433803 407868	A1823593 NM_000950	Hs.27688 Hs.40637	ESTs	4.1	4.1
	448117	H49129	Hs.172982	profine-rich Gla (G-carboxyglutamic acid ESTs	4.1 4.1	3.3 4.1
	442106	AW205881	Hs.326728	ESTs	4.1	3.2
20	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.0	3.2
30	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	4.0	6.2
	458694 452197	F12832 AW023595	Hs.3610 Hs.232048	ESTs ESTs	4.0 4.0	4.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0 4.0
2.5	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	3.9	7.0
35	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293 433670	AI004193 AA604405	Hs.22123	ESTs	3.9	3.9
	459697	AA406062	Hs.98002	gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens ESTs	3.9 3.9	3.9
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.9 3.9	5.4 3.3
40	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
	424001	W67883	Hs.137476	paternally expressed 10	3.8	5.4
	442676 410240	A1733585	Hs.130897	ESTs ·	3.8	3.8
	409339	AL157424 AB020686	Hs.61289 Hs.54037	synaptojanin 2 ectonucleotide pyrophosphatase/phosphodi	3.8 3.7	4.6 3.6
45	434998	AW975157	Hs.26037	EST8	3.7	3.7
	439450	R51613	Hs.125304	EST\$	3.7	8.3
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.7	4.9
	400844 458765	A1497900	Hs.33067	NM_003105*:Homo saplens sortilin-related ESTs	3.7	3.1
50	452667	T87219	Hs. 13219	ESTs	3.7 3.6	3.7 3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.6	19.9
	432149 408119	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.6	12.2
55	449093	W26213 AB035356	Hs.101672 Hs.22998	ESTs, Weakly similar to T00331 hypotheti neuroxin 1	3.6 3.6	3.6 3.6
• •	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.6	15.3
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.6	10.0
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
60	451032 449117	W03692 AW449310	Hs.323079 Hs.210262	Homo sapiens mRNA; cDNA DKFZp564P116 (Ir ESTs, Wealdy similar to HSS2_HUMAN HEPAR	3.5 3.5	4.9 3.5
	416490	AF090116	Hs.79348	regulator of G-protein signatting 7	3.5	12.5
	412266	N59006	Hs.26133	EŠTs	3.5	30.9
	452311	AW304029	Hs.252744		3.5	3.5
65	425649 410224	U30930 M55513	Hs.158540 Hs.150208	UDP glycosyltransferase 8 (UDP-galactose potassium voltage-gated channel, shaker-	3.5	38.6
•	451516	AI800515	Hs.12024	ESTs	3.4 3.4	3.4 6.3
	400098			Eos Control	3.4	3.4
	42491B	R13982	Hs.169309		3.4	5.3
70	452238 417063	F01811	Hs.345757		3.3	3.8
70	443992	N50515 AW022228	Hs.45061 Hs.322922	ESTs ESTs	3.3 3.3	3.3
	412453	R20205	Hs.75236	ESTs	3.3	13,1 3.3
	450561	R49674	Hs.25909	ESTs	3.3	3.3
75	415527	F11624	11	gb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
13	427386 423346	AW836261 AJ267677	Hs.6727 Hs.127416	ESTS	3.3	3.3
	431342	AW971018	Hs.12/416	synaptojanin 1 ESTs	3.2 3.2	20.1 8.0
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.2	9.6
80	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.2	3.2
٥V	417284	N62889	Hs.107242		3.2	3.2
	429477 410343	AI275514 AA084273	Hs.6658 Hs.76561	ESTs ESTs, Wealdy similar to \$47072 finger pr	3.2 3.2	3.2
	427317	AB028955	Hs.175780		3.2 3.2	3.2 5.3

	408039	AA131424	Hs.336636	ESTs .	3.2	3.2
	428976	AL037824	Hs.194695	ras homolog gene family, member 1	3.2	17.4
	420297	A1628272	Hs.88323	ESTs. Weakly similar to ALU1_HUMAN ALU S	3.2	4.1
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
,	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	3.2	3.3
	423829 424087	R44107 N69333	Hs.240905	ESTs contactin 1	3.1 3.1	4.4
	419852	AW503756	Hs.143434 Hs.286184			3.1
	444783	AK001468	Hs.62180	hypothetical protein dJ551D2.5 anillin (Drosophila Scraps homolog), act	3.1 3.1	4.1 43.2
10	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.1	3.1
	446692	Z44514	113.110201	Homo sepiens mRNA for KIAA1763 protein,	3.1	33.0
	437117	AL049256	Hs.122593	ESTA	3.1	3.8
	405819		12.166550	NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	452752	AW044058	Hs.33578	KIAA0820 protein	3.1	13.4
15	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.1	4.5
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKF2p547M073 (fr	3.0	3.8
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.0	5.9
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
	447673	AI823987	Hs.182285	ESTs	3.0	3.0
20	427283	AL119796	Hs.174185	ectonucieotide pyrophosphatase/phosphodi	3.0	3.0
	424724	T06532	Hs.287709	Homo sapiens cONA: FLJ22674 fs, clone H	3.0	3.0
	408547	AA574291	Hs.57837	ESTs	3.0	4.0
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.0	3.1
25	439274	AF086092	Hs.48372	ESTs	3.0	18.3
25	410765	At694972	Hs.66180	nucleosome assembly protein 1-like 2	3.0	8.0
	458268	AA428403	Hs.106131	ESTs	3.0	3.9
	424641	AB001106	Hs.151413	glia maturation factor, beta	3.0	5.6
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.0	14.9
30	442593	R39804	Hs.31961	ESTs	2.9	6.7
30	426380	AI291267	Hs.149990	ESTs	2.9	6.9
	428536	Al143139	Hs.2288	visinin-like 1	2.9	22.1
	417417	F05745 AI816344	Hs.89512	ATPase, Ca transporting, plasma membrane	29	17.1
	411379 422414	AW875237	Hs.12554 Hs.13701	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.9	11.2
35	428186	AW504300	Hs.295605	ESTs	2.9 2.9	5.3 3.9
55	419518	U79289	Hs.90798	mannosidase, alpha, class 2A, member 2 Human clone 23695 mRNA sequence	2.9	3.6
	426919	AL041228	ris.30730	ELAV (embryonic lethal, abnormal vision,	2.9	9.0
	446544	AJ631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	2.8	12.4
	422411	AW749443	Hs.22511	ESTs	2.8	12.0
40	416874	H98752	Hs.42568	ESTs	2.8	6.0
	448902	Z45998	Hs.22543	Homo sepiens mRNA; cDNA DKFZp76111912 (f	2.8	21.8
	430456	AA314998	Hs.241503	hypothetical protein	2.8	4.7
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.8	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.8	13.1
45	437948	AA772920	Hs.303527	ESTs	2.8	24.8
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.8	8.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.8	3.4
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.8	4.4
60	446574	A1310135	Hs.335933		2.8	3.5
50	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	2.8	3.6
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP).	2.7	45.2
	408554	AA836381	Hs.315111		2.7	3.7
55	434460	AA478486	Hs.3852	KIAA0368 protein	2.7	4.8
"	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	10.5
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.7	3.4
	437924 424945	A1935344 A1221919	Hs.164118		2.6	3.2
	425984	AW836277	Hs.165636	hypothetical protein FLJ 10582 hypothetical protein DKFZp761C07121	2.6 2.6	30.5 29.3
60	447761	AF061573	Hs. 19492	protocatherin 8	2.6	6.3
•••	425138	H08849	Hs.167464		2.6	4.2
	436568	H12049	Hs.91564	ESTs	26	6.8
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	26	5.6
	430287	AW182459	Hs.125759		2.6	7.6
65	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	2.6	3.8
	420173	AA256151	Hs.22999	ESTs	2.6	4.1
	429550	AW293055	Hs.119357		2.6	6.4
	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.6	5.1
70	424264	D80400	Hs.239388		2.6	7.3
70	432809	AA565509	Hs.131703	ESTs	2.6	9.9
	407886	AW969688	Hs.100826		2.5	20.2
	445225	AI216555	Hs.202398		2.5	5.5
	415257	F03016	Hs.27513	ESTs	2.5	B.6
75	423135	N67655	Hs.26411	ESTs	2.5	8.2
75	438283	AI458931	Hs.37282	ESTs	2.5	7.5
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.4	3.6
	443150	A1034467	Hs.34650	ESTS	2.4	7.6
	429956	AJ374651	Hs.22542	ESTs	2.4	3.2
80	428392	H10233 AJ754847	Hs.2265	secretory granule, neuroendocrine protei	2.4	42.3
50	437268 426529	AF090100	Hs.22757 Hs.17024		2.4	14.0
	430347	NM_002039			2.4	5.1 3.2
	422949			gb:EST21657 Adrenal gland turnor Horno sap	2.4 2.4	3.2 7.4
	422043			Anima i and i anima and Artino militar Liditio 25th	24	7.4

	451952	AL120173		ESTs	2.4	19.2
	434277	X77748		glutamate receptor, metabotropic 3	2.4	28.5
	422927 425121	AW247388 AJ797511	Hs.301423 Hs.154679	calcium binding protein 1 (calbrain) synaptotagmin t	2.4 2.4	3.0 3.9
5	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	2.4	4.8
	446377	AW014022	Hs.170953	ESTs	2.4	3.3
	452371	R40990	Hs.21658	ESTs	24	3.3
	419103 427658	Z40229 H61387	Hs.96423 Hs.30868	hypothetical protein FLJ23033 nogo receptor	2.4 2.4	8.4 3.0
10	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.3	3.6
	439607	BE540565	Hs.159460	ESTs	2.3	5.6
	412949	AI471639	Hs.71913	ESTs	23	3.7
	419757 410037	AA773820 AB020725	Hs.63970 Hs.58009	ESTs KIAA0918 protein	2.3 2.3	3.3 12.2
15	451385	A8029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.3	3.1
	409953	AA332277	Hs.57691	cadherin 18, type 2	23	5.5
	419629	AB020695	Hs.91662	KIAA0888 protein	2.3	13.4
	434792 429006	AA649253 AA443143	Hs.132458 Hs.50929	ESTs hypothetical protein FLI13842	2.3 2.3	3.8 6.6
20	445194	AI215667	Hs.175044	ESTs	23	3.1
	422491	AA338548	Hs.117546	neuronatin	2.3	3.6
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	27.4
	434933 424922	R91095 BE386547	Hs.4276 Hs.217112	KIAA1701 protein hypothetical protein MGC10825	2.2 2.2	6.1 3.7
25	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	22	81.1
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	22	56.0
	418410	AAB11441	Hs.107393	chromosome 3 open reading frame 4	22	3.9
	409746 439239	NM_004794 AI031540	Hs.56294 Hs.235331	RAB33A, member RAS oncogene family ESTs	2.2 2.2	10.6 49.5
30	450310	N62341	Hs.94116	ESTs	2.2	3.6
	453924	R49295	Hs.24886	ESTs	2.2	13.4
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.2	6.6
	404819 449568	AL157479	Hs.23740	NM_002688*:Homo sapiens peanut (Drosophi KIAA1598 protein	2.2 2.2	5.8 3.6
35	419271	N34901	Hs.238532	ESTs	2.2	7.5
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.2	3.6
	438208	AL041224	Hs.65379	ESTs	2.2	5.8
	424458 421790	M29273 AW896201	Hs.1780 Hs.22654	myelin associated glycoprotein sodium channel, voltage-gated, type I, a	2.2 2.2	10.1 4.1
40	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	21	4.2
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.1	21.4
	449277	AA001064	Hs.43670	ESTs	2.1	8.5
	420156 452738	AW449258 AL133800	Hs.6187 Hs.7086	ESTs hypothetical protein MGC12435	2,1 2,1	12.5 3.5
45	410366	AI267589	Hs.302689	hypothetical protein	21	10.4
	452106	AJ141031	Hs.21342	ESTs	2.1	3.4
	413409 423641	Al638418 Al.137256	Hs.1440 Hs.130489	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	21 21	9.4 6.2
	410909	AW898161	Hs.53112	ATPase, aminophospholipid transporter-li ESTs, Moderately similar to ALU8_HUMAN A	2.1	12.5
50	410631	AA086469	Hs.47171	ESTs	2.1	5.8
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.1	3.3
	448299 444124	AA497044 R43097	Hs.20887 Hs.6818	hypothetical protein FLJ10392 ESTs	2.1 2.1	11.5 9.3
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	8.5
55	432736	AA788898	Hs.179902	transporter-like protein	21	4.0
	429024	AI652297	Hs.119302		21	3.7
	420071 408822	AB028985 AW500715	Hs.94806 Hs.57079	ATP-binding cassette, sub-family A (ABC1 Homo sapiens cONA FLJ13267 fis, clone OV	2.1 2.1	5.1 3.0
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	21	23.1
60	426814	AF036943	Hs.172619	myelin transcription factor 1-like	2.1	14.2
	425130	AA448208 AB033015	Hs.99163	ESTs	2.1 2.0	3.1
	449714 439108	AW163034	Hs.23941 Hs.6467	KIAA1189 protein synaptogyrin 3	20	7.5 6.9
	415669	NM_005025		serine (or cysteine) proteinase inhibito	20	10.2
65	435040	AI932350	Hs.152825	ESTs	2.0 ·	4.7
	440152	AB002376	Hs.7006	KIAA0378 protein	2.0	14.2
	445102 436734	AW204610 AJ937612	Hs.22270 Hs.273758	ESTs hypothetical protein FLJ23112	2.0 2.0	19.2 4.7
=0	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	2.0	6.4
70	418512	AW498974		diacylglycerol kinase, zeta (104k0)	20	7.9
	453169	AB037815	Hs.32156	KIAA1394 protein	2.0	5.7 e.c
	420050 429900	AL118615 AA460421	Hs.94653 Hs.30875	neurochondrin ESTs	2.0 2.0	6.5 4.2
	432447	X92681	Hs.2998	contactin 2 (axonal)	2.0	4.1
75	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	2.0	3.1
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	20	10.7
	448681 453754	AL109781 AW972580	Hs.21754 Hs.17275	Homo sapiens mRNA full tength insert cDN  B ESTs	2.0 2.0	7.2 3.4
	422544	AB018259	Hs.11814		20	11.8
80	416836	D54745	Hs.80247	cholecystokinin	2.0	6.8
	454048 425741	H05626 AF052152	Hs.6921	ESTS Home seriene close 24628 mPNA secuence	2.0	9.9 6.5
	723/41	W 032132	Hs.159412	2 Homo sapiens clone 24628 mRNA sequence	2.0	0.3

	74045 400												
	TABLE 198 Pkey:		Eas probeset i	fentifier number									
	CAT numbe		luster number										
_	Accession:	Genbar	nik accession nu	mbers									
5	Pkey	CAT Number	Accession										
	408065			03154 AA059300 AA046 <del>9</del> 11									
	415527			H08936 R56332 H09256 R52303 R13075									
10	415666			3 H72694 F20990 R08580									
10	418512			1498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074									
	418866		AYY890649 T65754 AA229857 AA229658										
	422890			2 AW572911 AA449369 H17037 R19603 Al63256	5 AW004030 BE5029	30 225032	AA805324 AA4	19241 AI651825 AI2648	63 AW196918				
1.5				53735 A1263703 AA319159 AW964436 A1903440 A	AW594171 AI867447	AW204071	AW956110 C15	5616 D81142 H17038 AV	W162343				
15	422949		T87230 AI3	456 AA319377 AW961532 T48452 AA894424									
	42 <i>2</i> 949 424945			195 AA319377 AW961332 146432 AW654424 1867 AA348780 AW964077 AW166028 BE540193 P	194800 AA452368 NS	99604 AI341	345 AW298800	AA724961 AA931158 A	N741227				
			AI806660 AI98	2626 D81263 D53937 D52496 AA974487 AW043	354 N50483 Z39997	AJ492961 AJ	361526 F04002	AA452141 T23551 AI4	72655				
20			AI193667 AI34										
20	426919 433670	273507_1 372721_1		1004 D61361 AJ203314 AJ990307 AW900295 AJ01 162234 AW748386	8308 AW087473 AW	183530 AA3	193346 H50U55	AA935601					
	433921	377350_1		14549 R36464 R36465									
	433940	37787_1	H05129 N634	33 AI651350 AA984734 AI368716 N40915 AI98970	05 F09042 T03905 R	B8588 AF11	2220						
25	436773	426857_1		357375 N64357 AA731069	*****								
23	446692	689623_1	244514 AI352	097 AI803984 AW235923 AW196558 AI954637 AI	336963								
	TABLE 19	C:											
	Pkey:			sponding to an Eos probeset					- 0114				
30	Ref:			ne 7 digif numbers in this column are Genbank Ide: turomosome 22° Dunham, et al. (1999) <u>Nature</u> 402		Dunnam, et	a. reters to un	e publication entitled in	IS UNA				
	Strand:			from which exons were predicted.									
	Nt_positio	n: Indica	rtes nucleotide	ositions of predicted exons.									
	Pkey	Ref	Strand	Nt_position									
35	400844	9188605	Plus	24746-24872,25035-25204									
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-1	7075,17170-17287,1	7389-17529	,18261-18357,1	8443-18578					
	405560 405819	183148 4007557	Plus Plus	5495-5655,6077-6241,6495-6692 2830-2967									
	406311	9211559	Minus	137114-139033									
40													
45	Table 20/ 59680 pm CNS leve CNS spe 85th perce	A lists about 328 obesets on the Af I was set to the 8 cific genes, the re entile amongst va	CNS-enriched ( flymetrix/Eos H 15 th percentile a atio of "average prious CNS tisse	D GENES SIGNIFICANTLY DOWN-REGULATED enes significantly down-regulated in lower grade ( and GeneChip array such that the ratio of "average mongst various normal CNS tissues. The "average CNS to "average" norn-CNS normal adult tissues uss. The "average" normal non-CNS adult tissues to see the "average" normal non-CNS adult tissue is	plioblastoma (LGG) on a normal CNS to "avent to the command to the command to the command to the second to the sec	ompared to a rage" LGG to the 85h po preater than h percentile	normal adult CN was greater tha ercentile among or equal to 3. T amongst variou	IS tissues. These were : n or equal to 2. The "av- st various tumor sample the "average" CNS level s non-CNS normal tissue	selected from erage" normal as. To enrich for was set to the es. In order to				
		ene-specific daci ninator before th		of non-specific hybridization, the 10 th percentile valuated.	te suiduider Asudre u	on-mangnar	11 USSUES WAS SI	IOU BORD I FORT DOOR UP T	mineralty and				
50	Pkey:	Uniq	ue Eos probese	t identifier number									
	ExAccn: Unigenel			number, Genbank accession number									
	Unigene		ene number ene gene title										
<i>c c</i>	R1:	Ratio	o of CNS comp	ared to LOWER GRADE GLIOBLASTOMA									
55	R2:	Ratio	o of CNS comp	ared to NON-CNS NORMAL ADULT TISSUE									
	Pkey	ExAcon	UnigeneiD	Unigene Title		R1	R2						
	425580	L11144	Hs.1907	gatanin		33.1	3.5						
60	425489 430538	M58594 AB032435	Hs.1905 Hs.242821	protactin differentiation-associated Na-dependent		24.7 22.6	10.5 22.6						
•	417275	X63578	Hs.295449	parvalbumin		22.4	6.0						
	428505	AL035461	Hs.2281	chromogranin 8 (secretogranin 1)		21.8	21.8						
	408040 435145	AI266496 AI277259	Hs.22905 Hs.116631	ESTs, Wealthy similar to RHG6_HUMAN RHO-G ESTs		19.4 18.5	19.4 3.8						
65	407039	X00368	15.110031	gb:Human protactin gene 5' region.		18.1	18.1						
	428976	AL037824	Hs.194695	ras homolog gene family, member I		17.4	17.4						
	409263 424645	AA069573 NM_014682	Hs.50319 Hs.151449	ESTs KIAA0535 gene product		16.B 15.1	16.8 15.1						
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t		14.0	14.0						
70	405560	AW887701		hypothetical protein FLJ20628		13.9	8.0						
	452022	AW072330	Hs.293875	ESTs cyclic AMP-regulated phosphoprotein, 21		13.8	13.8 12.0						
	433940 413324	H05129 V00571	Hs.75294	cyclic Amir-regulated phosphoprotein, 21 cordicatropin releasing hormone		12.0 12.0	13.2						
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype		11.5	11.5						
75	410330	AW023630	Hs.159425	ESTs		11.1	23.4						
	453165 420297	\$74727 A1628272	Hs.32042 Hs.88323	aspartoacylase (aminoacylase 2, Canavan ESTs, Weakly similar to ALU1_HUMAN ALU S		10.7 10.5	10.7 4.1						
	417167	AW206437	Hs.4290	ESTS		10.4	10.4						
00	420033	D59502	Hs.292590	ESTs		10.4	10.4						
80	413293 426380	AL047483 AJ291267	Hs.302498	GTP-binding protein homologous to Saccha	•	10.0 9.8	10.0 6.9						
	426380 410635	D58863	Hs.149990 Hs.334372	ESTs chorionic somatomammotropin hormone 1 (p		9.5	6.6						
	422756		Hs.119689	glycoprotein hormones, alpha polypeptide		9.1	5.8						
				0.	0.0								

	444000			F07		
	444330 427322	A1597655	Hs.49265	ESTs hypothetical analyje E1 1111EE	9,1	9.1
	421522	AK002017 AF121860	Hs. 176227 Hs. 106260	hypothetical protein FLJ11155 sorting nexin 10	8.9 8.6	8.9 6.7
	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
5	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	410309	BE043077	Hs.278153	ESTs	8.5	8.5
	424932	R14070	Hs.315369	Homo sapiens cONA: FLJ23075 fis, clone L	8.5	10.2
	417175 427061	R44558 AB032971	Hs.94002 Hs.173392	ESTs KIAA1145 protein	8.4 8.4	8.9 8.4
10	400438	AF185611	Hs.115352	Target	8.3	5.1
	418207	C14685	Hs.34772	ESTS	8.2	9.8
	440209	H05049	Hs.247837	neuraxin 3	8.1	18.7
	429876	AB028977	Hs.225974	KIAA1054 protein	8.1	16.8
15	429470 430004	A1878901 U27768	Hs.203862 Hs.227571	guarrine nucleotide binding protein (G pr regulator of G-protein signatiling 4	8.0 7.9	8.0 15.7
13	436427	AI344378	Hs.143399	ESTs	7.8 7.8	7.8
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	7.8	8.6
	434367	AB020700	Hs.3830	KIAA0893 protein	7.7	5.6
20	441005	Z41305	Hs.303172	Homo sapiens mRNA; cONA DKFZp547G133 (fr	7.7	7.7
20	416851 429033	AW963951 NM_007374	Hs.85618 Hs.194756	ESTS	7.7 7.6	8.5
	437073	AI885608	Hs.94122	sine oculis homeobox (Drosophila) homolo ESTs	7.5 7.5	5.5 7.5
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
25	450715	AI266484	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	7.2	7.2
25	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	410011 423003	AB020641 AL120077	Hs.57856 Hs.122967	PFTAIRE protein kinase 1	7.1 7.0	10.0
	433921	AA618174	ns.122501	ketch (Drosophila)-like 2 (Mayven) gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0 7.0
	457012	R41480	Hs.302754	ESTS	6.9	6.9
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	6.9	6.1
	433558 409031	AA833757 AA376836	Hs.201769	ESTs, Wealdy similar to T24435 hypotheti ESTs	6.9	6.9
	419347	C15944	Hs.288856 Hs.90005	superforcervical ganglia, neural specifi	6.8 6.5	6.8 22.2
35	445279	R41900	Hs.22245	ESTs	6.4	8.4
	437414	AW894071	Hs.48448	hypothetical protein DKFZpS47C176	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
	434104 443244	AF116691	Hs.116459 Hs.166479	hypothetical protein PRO2198	6.4	4.0
40	447761	AI457235 AF061573	Hs.19492	ESTs protocadherin 8	6.3 6.3	3.0 6.3
	450600	BE079478	Hs.24880	ESTs	6.2	3.9
	427457	AW779105	Hs.164682	ESTs	6.2	11.1
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	6.1	8.0
45	432453 432298	AI885537 AL118812	Hs.27172	ESTs, Moderately similar to PC4259 ferri	6.0	3.9
45	415114	D60468	Hs.274293 Hs.94181	Homo sapiens mRNA; cDNA DKFZp761G1111 (f ESTs	6.0 6.0	15.1 6.0
	416101	R24854	Hs.268806	EST8	5.9	3.3
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
50	447138	A1439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
20	414545 424153	AA149287 AA451737	Hs.76605	ESTs	5.8	3.6
	424641	AB001106	Hs.141496 Hs.151413	MAGE-like 2 glia maturation factor, beta	5.7 5.6	5.1 5.6
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.6	9.6
<i>c e</i>	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	5.6	12.2
55	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	5.6
	443912 442023	R37257 A1187878	Hs.184780 Hs.144549		5.5	6.1
	450642	R39773	Hs.7130	copine IV	5.5 5.4	5.6 5.6
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.4	9.8
60	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605 418866	AL10967B T65754	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3 5.3	5.3
	448786	BE048842	Hs.179075	gb:yc11c07.s1 Stratagene lung (937210) H Homo sepiens cDNA FLJ11881 fis, clone HE	5.3 5.2	3.8 5.2
65	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	5.2	3.3
	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
	428508	BE252383	Hs.184668		5.2	4.1
	446353 442106	Al290919 AW205881	Hs.153661 Hs.326728		5.1	5.1
70	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1 5.1	3.2 5.1
	419318	AW969742	Hs.291005		5.0	31
	408068	AW148652	Hs.167398		5.0	5.0
	434149	Z43829	Hs.244624		5.0	5.0
75	439238 414631	N47305 AW970130	Hs.302161 Hs.65408	ESTs ESTs	4.9	5.3
, ,	447104	R19085	Hs.210706		4.9 4.9	4.9 3.0
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073		Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
80	433516		Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4,8	4.8
50	427287 447252		3 Hs.174188 Hs.12449	KIAA0938 protein     Homo sapiens transmembrane protein HTMP1	4.8 4.8	4.8 3.2
	419643		Hs.91791	chromosome 11 open reading frame 25	4.6 4.7	3.2 4.7
	414949		Hs.323349		4.7	3.8

					4.5	4.5
	429900 422949	AA460421 AA319435		ESTs pb:EST21657 Adrenal gland tumor Homo sap	4.7 4.7	4.2 7.4
	430537	X62692		phosphodiesterase 68, cGMP-specific, rod	4.6	4.6
_	419191	U17195		A kinase (PRKA) anchor protein 6	4.5	4.5
5	421952	AA300900		ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	406311	AW937420		NM_021979*:Homo sepiens heat shock 70kD ESTs	4.4 4.4	11.5 4,4
	451050 423728	AW891294		solute carrier family 4, sodium bicarbon	4.4	7.9
	411498	NM_014210		ecotropic viral integration site 2A	4.3	19.4
10	451301	A1769514		EST	4.3	4.3
	452381	H23329		ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.3 4.3	4.3 3.9
	433109 423589	N58907 AA328082	Hs.162430 Hs.209569	EST ESTs	4.2	4.2
	427224	AL135554	Hs. 101937	sine oculis homeobox (Drosophila) homolo	4.2	3.9
15	420489	AA815089	Hs.193513	ESTs .	4.1	4.1
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
	418202 448117	N48521 H49129	Hs.26549 Hs.172982	KIAA1708 protein ESTs	4.1 4.1	5.8 4.1
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.0	27.9
20	458694	F12832	Hs.3610	ESTs	4.0	4.0
	452197	AW023595	Hs.232048	ESTs .	4.0	4.0
	408547 433447	AA574291 U29195	Hs.57837 Hs.3281	ESTs neuronal pentravin II	4.0 4.0	4.0 3.7
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
25	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	AI004193	Hs.22123	ESTs	3.9	3.9
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.9 3.9	4.1 3.1
	400844 426054	U12431	Hs.166109	NM_003105°:Homo sapiens sortilin-related ELAV (embryonic lethal, abnormal vision,	3.9	3.9
30	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.8	3.3
• •	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	3.8	3.8
	442676	AI733585	Hs.130897	ESTs	3.8	3.8
	414699 436476	AI815523	Hs.76930	symuclein, alpha (non A4 component of am	3.8 3.8	4. <b>5</b> 3.3
35	434998	AA326108 AW975157	Hs.33829 Hs.26037	bHLH protein DEC2 ESTs	3.6 3.7	3.3 3.7
55	412049	N53437	Hs.18268	adenylate kinase 5	3.7	10.7
	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.7	4.5
	459697	AA406062	Hs.98002	ESTs	3.7	5.4
40	435648 442042	H24347 Al990506	Hs.27524 Hs.8077	ESTs Homo sepiens mRNA; cDNA DKFZp547E184 (tr	3.7 3.7	8.1 6.2
40	456765	AJ497900	Hs.33067	ESTs	3.7	3.7
	434933	R91095	Hs.4276	KIAA1701 protein	3.6	6.1
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.6	3.6
45	452667	T87219	Hs.13219	ESTs	3.6	3.6
47	436773 408119	AW078629 W26213	Hs.101672	PC4 and SFRS1 interacting protein 1 ESTs, Weakly similar to T00331 hypotheti	3.6 3.6	3.6 3.6
	453534	NM_014796		KIAA0748 gene product	3.6	4.7
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
50	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
30	447746 449117	AW015920 AW449310	Hs.161359 Hs.210262	ESTs ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5 3.5	9.9 3.5
	447750	AI422234	Hs.143434	contactin 1	3.5	9.8
	453590	AF150278	Hs.33578	KIAA0820 protein	3.5	22.3
55	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.5	3.6
33	410240	AL157424	Hs.61289	synaptojanin 2	3.5 3.4	4.6 3.4
	410224 400098	M55513	Hs.150208	potassium voltage-gated channel, shaker- Eos Control	3.4	3.4
	450181	H05254	Hs.201198	ESTs	3.4	7.2
۲0	459080	AW192083	Hs.290855		3.4	13.5
60	417063 424918	N50515 R13982	Hs.45061	ESTs	3.3 3.3	3.3 5.3
	453431	AF094754	Hs.169309 Hs.32973	myelin-associated oligodendrocyte basic glycine receptor, beta	3.3	4.6
	412453	R20205	Hs.75236	ESTs	3.3	3.3
65	450561	R49874	Hs.25909	ESTs	3.3	3.3
65	415527	F11824	11- 477074	gb:HSC2ZD101 normalized infant brain cDN	3.3 3.3	3.3 15.3
	426968 427386	U07616 AW836261	Hs.173034 Hs.6727	amphiphysin (Stifl-Mann syndrome with br ESTs	3.3 3.3	3.3
	424001		Hs.137476		3.2	5.4
=0	439450		Hs.125304		3.2	8.3
70	442879		Hs.8813	syntaxin binding protein 3	3.2	3.2
	417284 410343		Hs.107242 Hs.76561	Homo sapiens cDNA FLJ12965 fis, clone NT ESTs, Wealdy similar to S47072 finger pr	3.2 3.2	3.2 3.2
	410909			ESTs, Moderately similar to ALUS_HUMAN A	3.2 3.2	12.5
	453919			KIAA1705 protein	3.2	3.2
75	424087	N69333	Hs.14343	contactin 1	3.1	3.1
	428963				3.1	3.3
	419852 422234				3.1 3.1	4.1 3.1
	423829		Hs.24090		3.1	4.4
80	443297	AI049864	Hs.13302	9 ESTs	3.1	3.1
	453302		8 Hs.32945	glutamate receptor, metabotropic 1	3.1	4.6
	405819 445729		Hs.13209	NM_002578:Homo sapiens p21 (CDKN1A)-ecti hypothetical protein FLJ10094	3.1 3.0	13.5 3.0
	-HJ125		113.13203	HARMAN COMMITTER STATES AND ADDRESS OF THE S	3.0	J.4

	447672	A1000000	Hs.182285	Ent.	••	
	447673 433670	AI823987 AA604405	rs.102203	ESTs gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.0 3.0	3.0 3.9
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.0	3.2
-	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	3.0	3.0
5	433315	R95754	Hs.239706	GRB2-associated binding protein 1	3.0	3.1
	451032 423346	W03692 AI267677	Hs.323079 Hs.127416	Homo sapiens mRNA; cDNA DKFZp564P116 (fr synaptojanin 1	3.0	4.9
	439274	AF086092	Hs.48372	ESTs	3.0 3.0	20.1 18.3
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	2.9	38.6
10	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	2.9	14.9
	407868	NM_000950	Hs.40637	profine-rich Gla (G-carboxyglutamic acid	2.9	3.3
	410765 428001	A1694972 H97428	Hs.66180 Hs.219907	nucleosome assembly protein 1-like 2 ESTs, Moderately similar to Transforming	2.9 2.8	8.0
	448533	AL119710	Hs.21365	fucleosome assembly protein 1-fike 3	2.8	5.9 9.6
15	425130	AA448208	Hs.99163	ESTs	2.8	3.1
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8	3.7
	452238	F01811	Hs.345757	ESTs	2.8	3.8
	446544 433803	AJ631932 AJ823593	Hs.7047 Hs.27688	ESTs, Weakly similar to Unknown [H.saple ESTs	2.8 2.8	12.4 4.1
20	407728	AW071502	Hs.175931	ESTs	2.7	10.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.7	3.4
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	452738 451516	AL133800 AI800515	Hs.7086 Hs.12024	hypothetical protein MGC12435 ESTs	2.7	3.5
25	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.7 2.7	6.3 3.6
	450474	AW872844	Hs.117494	ESTs	2.7	7.2
	422414	AW875237	Hs.13701	ESTS	2.7	5.3
	428186 431342	AW504300	Hs.295605	mannosidase, atpha, class 2A, member 2	2.7	. 3.9
30	423449	AW971018 Al497900	Hs.21659 Hs.33067	ESTs ESTs	2.7 2.6	8.0 14.5
	427283	AL119796	Hs.174185	ectonucleofide pyrophosphatase/phosphodi	2.6	3.0
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.6	9.0
	437117	AL049256	Hs.122593	ESTs	2.6	3.8
35	422491 438068	AA338548 Al927209	Hs.117546 Hs.306210	neuronatin Horno sepiens cDNA: FLJ23133 fis, clone L	2.6 2.6	3.6
	432809	AA565509	Hs.131703	ESTs	2.5	5.1 9.9
	433551	AI985544	Hs.12450	protocadherin 9	2.5	18.1
	444783	AK001468	Hs.62180	anillin (Orosophila Scraps homolog), act	2.5	43.2
40	417417 413554	F05745 AA319146	Hs.89512 Hs.75426	ATPase, Ca transporting, plasma membrane	2.5	17.1
70	448902	Z45998	Hs.22543	secretogranin II (chromogranin C) Homo sapiens mRNA: cDNA DKFZo761I1912 (f	2.5 2.5	5.7 21.8
	442910	Al365130	Hs.11307	ESTs, Wealthy similar to T19326 hypotheti	2.5	14.5
	423135	N67655	Hs.26411	ESTs	2.5	8.2
45	452311 418940	AW304029 H17739	Hs.252744 Hs.288513	ESTs Human DNA sequence from clone RP5-899C14	2.5 2.5	3.5 7.0
	432882	NM_013257	Hs.279696	serum/glucoconticoid regulated kinase-li	2.5	4.2
	422411	AW749443	Hs.22511	ESTS	2.5	12.0
	451386 404819	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.4	3.1
50	429656	X05608	Hs.211584	NM_002688*:Homo sapiens peanut (Drosophi neurofilament, light polypeptide (68kD)	2.4 2.4	5.8 13.1
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.4	10.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.4	11.2
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	24	45.2
55	429859 430287	. NM_007050 AW182459	Hs.225952 Hs.125759	protein tyrosine phosphatase, receptor t ESTs, Wealdy similar to LEUS_HUMAN LEUKE	2.4 2.4	5.1 7.6
•••	422890	243784	110.120100	ankyrin 3, node of Ranvier (ankyrin G)	24	3.6
	427658	H61387	Hs.30868	nogo receptor	2.4	3.0
	446100 412266	AW967109 N59006	Hs.13804	hypothetical protein dJ462O23.2	2.3	3.6
60	435059	Z45270	Hs.26133 Hs.235873	ESTs hypothetical protein FLJ22672	2.3 2.3	30.9 4.8
• •	420173	AA256151	Hs.22999	ESTs	2.3	4.1
	452371	R40990	Hs.21658	ESTs	2.3	3.3
	430456	AA314998	Hs.241503		2.3	4.7
65	409953 429006	AA332277 AA443143	Hs.57691 Hs.50929	cadherin 18, type 2 hypothetical protein FLJ13842	2.3	5.5
-	445194	AI215667	Hs.175044		2.3 2.3	6.6 3.1
	428392	H10233	Hs.2265	secretory granute, neuroendocrine protei	2.3	42.3
	434460	AA478486	Hs.3852	KIAA0368 protein	2.3	4.8
70	416490 437924	AF090116 AI935344	Hs.79348 Hs.164118	regulator of G-protein signalting 7 ESTs, Wealthy similar to SLS1_HUMAN SODIU	2.3	12.5
. •	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.3 2.2	3.2 16.9
	424945	AI221919		hypothetical protein FLJ10582	2.2	30.5
	416530	U62801	Hs.79361	katlikreln 6 (neurosin, zyme)	2.2	4.4
75	422927 438831	AW247388 BE263273	Hs.301423		22	3.0
, 5	449078	AK001256	Hs.6439 Hs.22975	synapsin II KIAA1576 protein	2.2 2.2	3.4 16.1
	410631	AA086469	Hs.47171	ESTs	2.2	5.8
	419271	N34901	Hs.238532		2.2	7.5
80	452752 44667A	AW044058 Al310135	Hs.33578	KIAA0820 protein	2.2	13.4
30	446574 452106	AI310135 AI141031	Hs.335933 Hs.21342	B ESTs	2.2 2.2	3.5 3.4
	415910	U20350	Hs.78913	chemokina (C-X3-C) receptor 1	2.2	28.9
	44445B	8E041526	Hs.31746	hypothetical protein DKFZp547F072	2.2	7.7

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						***	
	446692	Z44514	44- 400446	Homo sapiens mRNA for KIAA1763 protein,	22 22	33.0 8.5	
	412788 419103	AA120960 Z40229	Hs.198416 Hs.96423	ESTs hypothetical protein FLJ23033	2.2	B.4	
	424474	AA308883	Hs.148680	calcyon; D1 doparnine receptor-interactin	2.2	3.6	
5	451783	R42554	Hs.210852	T-box, brain, 1	2.1	11.2	
	434792	AA649253	Hs.132458	ESTs	21 21	3.8 3.7	
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	21	4.9	
	455364 413988	H72176 M81883	Hs.4273 Hs.324784	hypothetical protein FLJ13159 dutamate decarboxylase 1 (brain, 67kD)	21	51	
10	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	2.1	3.6	•
	443150	AI034467	Hs.34650	ESTs	21	7.6	
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	2.1 2.1	19.9 6.5	
	420050 408449	AL118615 NM_004408	Hs.94653 Hs.166161	neurochondrin dynamin 1	21	5.1	
15	423841	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2	
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	21	3.2	
	449568	AL157479	Hs.23740	KIAA1598 protein	21 21	3.6 3.3	
	412675 429550	AA460716 AW293055	Hs.9788 Hs.119357	hypothetical protein MGC10924 similar to ESTs	21	6.4	
20	446782	A1653048	Hs.144006	ESTs	2.1	9.0	
20	453924	R49295	Hs.24886	ESTs	2.1	13.4	
	437948	AA772920	Hs.303527	ESTs	21	24.8	
	451952	AL120173	Hs.301663	ESTs	2.0 2.0	19.2 3.4	
25	453754 448765	AW972580 R15337	Hs.172753 Hs.21958	ESTs Homo sapiens mRNA; cDNA DKFZp547D086 (tr	20	3.9	
23	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	20	3.4	
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.0	11.5	
	411668	AF106564	Hs.71346	neurofilament 3 (150kD medium)	20 20	6.6 10.1 ·	
30	424458 434277	M29273 X77748	Hs.1780 Hs.3786	myelin associated glycoprotein glutamate receptor, metabotropic 3	2.0	28.5	
50	440152	AB002376	Hs.7006	KIAA037B protein	2.0	14.2	
	429956	Al374651	Hs.22542	ESTs	2.0	3.2	
	450590	AJ701507	Hs.273740	ESTs	2.0 2.0	3.8 3.7	
` 35	429024 430643	AI652297 AW970065	Hs.119302 Hs.287425	complement-c1q tumor necrosis factor-rel MEGF10 protein	2.0	4.1	
55	415734	NM_014747		KIAA0237 gene product	20	27.4	
	419757	AA773820	Hs.63970	ESTs	2.0	3.3	
	421264	AL039123	Hs.103042		2.0 2.0	23.8 5.6	
40	439607 435624	BE540565 AF218942	Hs.159460 Hs.24889	ESTs tormin 2	2.0	12.2	
70	425121	AI797511	Hs.154679	synaptotagmin I	2.0	3.9	
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	20	3.1	
	442593	R39804	Hs.31961	ESTs	20	6.7 10.4	
45	410366	AI267589	Hs.302689 Hs.170808		· 20 20	4.6	
40	426575 452856	M74826 AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	20	10.7	
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	2.0	3.8	
	424893	AW295112			2.0	3.8 4.7	
50	436734 422544	AI937612 AB018259	Hs.273758 Hs.118140		2.0 2.0	11.8	
50	440105	AA694010	Hs.6932	Homo sapiens cione 23809 mRNA sequence	2.0	8.2	
	425741	AF052152	Hs.159412		2.0	6.5	
	450310	N62341	Hs.94116	ESTs	2.0	3.6	
55	TABLE	30D-					
23	Pkey:		nique Eos prob	eset identifier number			
	CAT nu	mber: G	ene cluster nun	nber			
	Accessi	ion: G	enbank access	ion numbers			
60	Pkey	CAT Numb	er Accession	•			
•	415527			43212 H08936 R56332 H09256 R52303 R13075			
	415656			108673 H72694 F20990 R08580			
	418868		165754 A	A229857 AA229658 113382 AW572911 AA449369 H17037 R19603 AI6325	KS AWAAAAA RESA253A 729	5032 AAR05324 AA449241 AI651825	AI264883 AW196918
65	422890	222707_1	243764 F AA94826	7 AI953735 AI263703 AA319159 AW984438 AI903440	AW594171 AI867447 AW20	4071 AW956110 C15616 D81142 H	7038 AW162343
			T87230 A				
	422949		AA31943	5 N56456 AA319377 AW961532 T48452 AA894424	A104000 A A 453350 MOOCOA	A124124E A18700000 AA7740E1 AA6	131150 A1741337
	424945	245223_1	A1221919	Z19967 AA348780 AW964077 AW166028 BE540193 AI982626 D81263 D53937 D52496 AA974487 AW04	1854 NEMARI 739997 AMPS	61 A1361526 F04002 AA452141 T23	551 AI472655
70			A100000		Q004 (1304Q0 £0330), 7043£0		••
	426919	273507_1	AL04122	8 D82004 D61361 AI203314 AI990307 AW900295 AI0	18308 AW087473 AW18353	0 AA393346 H50055 AA935601	
	433670	372721_1		5 BE062234 AW748386			
	433921		AA51817	'4 A1114549 R36464 R36465 N63433 A1651350 AA984734 A1368716 N40915 A1989	705 E00042 T03905 B89588	AF112220	
75	433940 436773			29 AI857375 N64357 AA731069	103 103042 100300 100000	~	
	44669			AL352097 AL803984 AW235923 AW196558 AL954637	AI 336983		
		_					
	TABLE		Inlaus come	assessmenting to an Englishment			
80	Pkey: Ref:	,	Seansnos com Seansnos annos.	corresponding to an Eos probeset ce. The 7 digit numbers in this column are Genbank Id	entifier (GI) numbers. "Dunha	am, et al." refers to the publication en	litled "The DNA
			sequence of hu	man chromosome 22° Dunham, et al. (1999) Nature 40	12:489-495.		
	Strand	l: Î	ndicates DNA	strand from which exons were predicted.			
	Nt_po:	SIUUTI: (	moveres nucle	otide positions of predicted exons.			
				20	W)		

#### WQ 03/025138

445529 447750

444409 409031

453220

429611 414290

450715 428508

425649 459247

434064

448958 410657

447138

440736

407245

441976 450642

432799 428465

407868

AW294909 AW500305

H14421 Al422234

AJ792140 AA376836

AB033089 AW072330 NM_014787 AI921750 AI911527

A1187878 H79667

AI889077 AI568801 AI266484 BE252383

U30930

N48243

AL049045

AW630088 NM_001683 M22440 AA446644

AB020651

AF063228

Al439112 D56919

X90568 AA428403 R39773

NM_016161 AW970976 NM_000950

55

60

65

70

75

80

ESTs

**ESTs** 

contactin 1 ESTs

syntaxin 7
ATP-binding cassette, sub-family A (ABC)

ESTs
Homo sapiens mRNA for KIAA1263 protein,
ESTs
OnaJ (Hsp40) homolog, subfamily B, membe
Homo sapiens cDNA FLJ13752 fls, clone PL
ESTs

Homo sapiens cDNA FLJ12052 fis, clone HE Homo sapiens BAC clone CTB-60N22 from 7q

ESTs, Wealdy similar to KIAA1324 protein SB8317 protein UDP glycasytrans/lerase 8 (UDP-galactose ESTs, Highty similar to T42626 secreted hypothetical protein PRC0082 Homo sapiens mRNA; cDNA DKFZp56481264 (I ATPase, Ce transporting, plasma membrane transforming growth factor, alpha GA733-2 antigen; epithetial glycoprotein KJAA0844 protein dynein, cytoplasmic, intermediate polype ESTs, Wealdy similar to 2109260A B cell myomegalin titin

copine IV alpha-1,4-N-acetytglucosaminyttransferas ESTs

proline-rich Gla (G-carboxyglutamic acid

ESTs, Wealthy similar to KIAA1324 protein

Hs.132206 Hs.18906 Hs.180513 Hs.143434 Hs.49265 Hs.288856 Hs.32452

Hs.293875 Hs.44896 Hs.144871 Hs.11805

Hs.144549 Hs.237642

Hs.211388 Hs.71721

Hs.31570

Hs.184668 Hs.158540

Hs.110373 Hs.180758

Hs.76550 Hs.89512 Hs.170009

Hs.692

Hs.22653

Hs.65248 Hs.93828

Hs.265848 Hs.172004

Hs.106131 Hs.7130

Hs.278960 Hs.293653

Hs.40637

	Pkey	Ref	Strand	Nt. position	
	400844	9188605	Plus	24746-24872,25035-25204	
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075.	17170 17707 17700 17500 10001 10009 10110 10570
5			Plus	5495-5655,6077-6241,6495-6692	1/1/0-1/20/,1/303-1/323,16251-1635/,16443-185/8
•	405819	4007557	Plus	2830-2967	
	406311	9211559	Minus	137114-139033	
	400011	3211333	mawa	13/114-135033	
10	<del>==</del>				
10	IABLE 21	A: ABOUT 410	GENES SIGNI	FICANTLY DOWN-REGULATED IN GLIOBLASTONA M	ULTIFORMA COMPARED TO NORMAL ADULT CNS
	1808 ZIA	IISIS BOOUL 41U (	genes signinca	nny down-regulated in glioblastoma multiforma (GBM) co	impared to normal adult CNS tissues. These were selected from 59680 probesets
	OR USE ALI	meduzeos Huu.	a GeneCuth su	ray such mat the rapo of "average" normal CNS to "avera	ge* GBM was greater than or equal to 2. The "everage" normal CNS level was set
	Bone 12	percenue amon	gsi vanous noi	mai UNS tissues. The "average" GBM level was set to to	to 95% percentile amongst various tumor samples. In order to remove gene-specific
15	the ratio w	ras evaluated.	specific myonou	usion, the 10" percentile value amongst vanous non-mail	gnant lissues was subtracted from both the numerator and the denominator before
10	Pkey:		m Eco ambara	ri identifier number	
	ExAcen:			n number, Genbank accession number	
	Unigenet		sne number	Horioer, Gendan accession manager	
	Unigene T		ne gene tila		
20	R1:	Ratio	of CNS to GI	OBLASTOMA MULTIFORMA	
		,		SOLIO CHE MOLIN CHAR	
	Pkey	ExAcon	UnigenetO	Unigene Title	R1
	417275	X63578	Hs.295449	parvalbumin	18.6
~-	428505	AL035461	Hs.2281	chromogranin 8 (secretogranin 1)	13.8
25	415672	N53097	Hs.193579	ESTs	13.5
	459080	AW192083	Hs.290855	ESTs	12.9
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	11.7
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	10.9
30	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
30	424645	NM_014682		KIAA0535 gene product	8.2
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	413324 417167	V00571	Hs.75294	corticotropin releasing hormone	7.5
	422728	AW206437 AW937826	Hs.4290	ESTs	7.3
35	410330	AW023630	Hs. 103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	6.8
55	450590	A1701507	Hs.159425 Hs.273740	ESTS ESTS	6.5
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	. 6.5
	454076	AW204712	Hs.61957	ESTs	6.5
	419956	AL137939	Hs.40096	ESTs	6.3 6.3
40	416851	AW963951	Hs.85618	ESTs	6.2
	428874	W32133	Hs.194366	transthyretin (prealburnin, amytoidosis t	6.0
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	449078	AK001256	Hs.22975	KIAA1576 protein	5.6
	448072	AI459306	Hs.24908	ESTs	5.6
45	412622	AW664708	Hs.171959	ESTs	5.6
	428414	AL049980	Hs.184216	DKFZP564C152 protein	5.5
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	411498	NM_014210		ecotropic viral integration site 2A	5.4
50	453344	BE349075	Hs.44571	ESTs	5.4
50	441790	AW294909	Hs.132208		5.3
	443037	AW500305	Hs.8906	syntaxin 7	6.3

4.0

	******	AA833757	Hs.201769	ESTR	Wealthy similar to T24435 hypotheti	4.0
	433558 429470	AI878901	Hs.203862	muani	ne nucleotide binding protein (C pr	4.0 3.9
	415665	H72693		ab:vu	13c11.r1 Soares tetal tiver spieces	3.9
_	407988	N47760	Hs.285107	hypol	hetical protein FLJ13397 1145 protein	3.9
5	427061 430261	AB032971 AA305127	Hs.173392 Hs.237225		hetical protein HT023	3.9
	440624	AF017987	Hs.7306	SECTE	ted frizzled-related protein 1	3.8 3.8
	431668	AW969610	Hs.151179	ESTS	o sepiens mRNA for KIAA1763 protein,	3.8
••	446692	Z44514	Hs.238797	Hom	Moderately similar to 138022 hypot	3.8
10	408739	W01556 NM_006379	Hs.171921	Sent	domain, immunoglobulin domain (lg).	3.8
	426716 450103	R08665	Hs.17244	hypo	thetical protein FLJ 13605	3.7 3.7
	426775	AA384564	Hs.3628	EST		3.7
1.5	403459		Hs.201198		et Exon	3.7
15	450181	H05254 AW169287	Hs.22588	EST		3.7
	438202 445279	R41900	Hs.22245	EST	ĺs	3.7 3.7
	422546	AB007969	Hs.301478		A0500 protein	3.6
20	435712	AA694607	Hs.176956			3.6
20	417620	R02530 AA300900	Hs.19119 Hs.98849	ES	is. Moderately similar to AF161511 1 H	3.6
	421952 453655	AW960427	Hs.34287	4 tran	isforming growth factor, beta recepto	3.6 3.6
	426365	AA376667	Hs.10283	RN	A binding motif protein 8B	3.6
25	416982	J05401	Hs.80691 Hs.83623	cre	atine kinase, mitochondrial 2 (sarcom clear receptor subfamily 1, group 1, m	3.6
25	438085 424704	AA336519 AI263293	Hs.15209	6 cv1	ochrome P450, subfamily IU (arachido	3.6
	414631	AW970130				3.6 3.6
	453698	AA037615	Hs.42746		Ts .	3.5
20	438704	AI435060	Hs.32829		iTs iTs	3.5
30	437073 434460	A1885608 AA478486	Hs.9412 Hs.3852	· KI	AAN36R protein	3.5
	414541	BE293116		2 8	dehyde dehydrogenase 1 family, member	3.5 3.5
	423665				STS	3.5
25	446390				rpothetical protein FLJ 11151 STs	3.5
35	441264 433629		) Hs.2329 Hs.1335		CT.	3.5
	411811			g	b:PM4-SN0016-100500-004-h09 SN0016 Homo	3.5 3.4
	410140	) AL134435	Hs.2478		eurexin 3	3.4
40	415114		Hs.9411		STs b:RC1-BT0313-110500-017-c04 BT0313 Homo	3.4
40	455649 433679			Š	b:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.4
	41717		Hs.940	02 E	STs	3.4 3.4
	42717	6 AW3815		34 [	STs Iomo sapiens prostein mRNA, complete cds	3.4
45	44851		65 Hs.278 Hs.302		ESTs	3.3
45	45701 40535		M3.302		CX000321:dil6671578trefINP_031518.1  ari	3.3
	44587		3 Hs.288	871	Homo sapiens cDNA FLJ 11997 fts, clone rte	3.3 3.3
	43380	)3 A182359			ESTs	3.3
50	44901			EOE	ESTs ESTs	3.3
50	41454 4090			3441	Home saciens, Similar to RIKEN cONA 1700	3.3 3.3
	4261		1982 Hs.19	9067	v-erb-b2 avian erythroblastic leukerma v	3.3
	4224				ESTs	3.3
55	4288				gb:stearoyl-CoA desaturase (human, adipo	3.2
در	4069 4295				ESTs	3.2 3.2
	4341	04 AF1166	91 Hs.11	6459	hypothetical protein PRO2198	3.2
	4272				ESTs hypothetical protein DKFZp547F072	3.2
60	) 4444 ) 433				ESTs. Weakly similar to S65824 reverse t	3.2
Ů.	412			85729	ESTs. Weakly similar to unnamed process	3.2 3.2
	440	BOB AKOO1			hypothetical protein FLJ 10477 ESTs; hypothetical protein for IMAGE:447	3.1
	442		4964 Hs.1	28899 25974	KIAA1064 omtein	3.1
6:	5 429	876 AB028 757 BE081		1570	ESTs, Wealdy similar to KIAA1324 protein	3.1
U.		327 BE408		85254	ESTs. Weakly similar to 124435 hypomen	3.1 3.1
		<b>399 BE40</b> 1		53998	creatine kinase, mitochondrial 1 (ubiqui	3.1
		1582 BE54		48016	ESTs KIAA0820 protein	3.0
7		2752 AW04 3165 AA02		33578 35162	KCNO1 overlapping transcript 1	3.0
,		9165 AAUZ 9403 AA66		5634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.0 3.0
	42	2414 AW8	75237 Hs.:	13701	ESTA	3.0
	40	7173 T643		21542	gb:yc10d08.s1 Stratagene lung (937210) H KIAA1035 protein	3.0
7				21542 145319	ESTs	3.0
,				246970	mitogen-activated protein kinase kinase	3.0
		2258 AA37	76768 Hs.	324841	hypothetical protein FLJ22622	3.0 3.0
	42	9968 AA3	22503 Hs	227011		29
•				.181799 .11223	P ESTs	2.9
•				.24282	differentiation-associated Na-dependent	2.9
				17924	ESTs. Moderately similar to ALU1_HUMAN A	2.9 2.9
		05403			Target Exon	
					7	102

						2.9
	452197	AW023595 AL359559	Hs.232048 Hs.331666	ESTs Home:	sapiens mRNA; cDNA DKFZp762O2215 (f	2.9
	437357 436427	AL355555 Al344378	Hs.143399	ESTs		29 29
_	417787	R14948	Hs.23883	ESTs		29
5	439272	AA832474	Hs.25851 Hs.46735	ESTS	ss locus associated putative guani	2.9
	454247 415839	AJ243950 R40611	Hs.94694	ESTs		29
	408814	N62499	Hs.176227	h-modi	netical protein FLJ11155	2.9 2.9
	408468	AI909712	Hs.93837	phosp	hatidylinositol transfer protein, m 24-HT0373-130200-011-a03 HT0373 Homo	2.9
10	431304	BE157283	Hs.61289	go:rcc	tojanin 2	29
	410240 444783	AL157424 AK001468	Hs.62180	enillin	(Drosophita Scraps homolog), act	2.8 2.8
	408438	AB011180	Hs.100960	KIAA	0608 protein	2.8
	458793	N80159	Hs.121849	micro	hibule-associated proteins 1A/18 fi (S. cerevisiae)-fike	2.8
15	429788	U87791 D80400	Hs.221040 Hs.239388	Hum	an DNA sequence from clone RP1-304B14	2.8
	424264 433109	N58907	Hs.162430	EST		2.8 2.8
	427974	BE093023	Hs.188767	EST		2.8
00	432266	AK000385	Hs.274222	CCT	thetical protein FLJ20378	2.8
20	414764 411918	AW013887 AW876354	Hs.31522	ab:P	M4-PT0019-141299-009-F08 PT0019 Homo	2.8
	404563	Andros		Targ	et Exon	2.8 2.8
	446468	A1765890	Hs_16341	MAY	VD binding protein ( (caselnolytic protease X, E. cofi)	2.8
26	444755	AA431791	Hs.113823 Hs.13423	Hon	n saniens clone 24468 (NKNA Sequence	2.7
25	445898 427283	AF070623 AL119796	Hs. 17418	ecto	nucleotide pyrophosphatase/phosphodi	27 27
	400138	74710700		Eos	Control	2.7
	458676	AI692464	Hs.20226			2.7
20	459697	AA406062	Hs.98002 Hs.14876			2.7
30	444420 430371	A1148157 D87466	Hs.24011	2 1/14	A0276 protein	27 27
	449117	AW449310	Hs.21026	2 ES	Ts. Wealdy similar to HSS2_HUMAN HEPAR	27
	424994			v ua	EST366595 MAGE resequences, MAGC Homo A histone family, member F, pseudogene	2.7
35	400339 417494		Hs.24820 Hs.22213			2.7
23	427166			E F	Te.	2.7 2.7
	404746			c	000138*:gij7512767 pir  T12477 hypothe CM2-LT0066-030100-109-d06 LT0066 Homo	2.7
	411361			14 SI	argardt disease 3 (autosomal dominant)	2.7
40	428358 406625		Hs.1195	97 st	earcyl-CoA desaturase (delta-9-desatur	2.7 2.7
40	416101		Hs.2688	06 €	STs _	2.7
	404500		_	T ₁	rget Exon xnq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
	43392				STs	2.7
45	41427 41804		Hs.484		STs	2.7 2.7
45	42108	9 AB03777		799 K	IAA1350 prolein b:RCD-MT0013-280300-021-c10 MT0013 Horno	2.7
	41224				CTAIRE protein kinase 3	2.6
	43243 42415				AGE-like 2	2.6
50	42718		Hs.563	5 1	STs	2.6 2.6
	4544	54 AW6122			STs adikrein 3, (prostate specific antigen	2.6
	4267			1 220	GE recentor activating protein 1	2.6
	4567 4057		110.10		FNSP00000005198":Mixed lineage kinase Mi.	26 26
55	4254	94 N55540		26	ESTs, Weatly similar to similar to ankyr	26
	4308				HSPC125 protein ESTs	2.6
	4357 4101				ESTs	2.6 2.6
	4321		072 Hs.11	5960	KIAA0939 protein	26
60					kruppel-related zinc finger protein hcKr ESTs, Weakly similar to T43458 hypotheti	2.6
	4149 429				ESTs	2.6
		269			Eos Control	2.5 2.5
_	443	992 AW022		2922	ESTs Homo sapiens, Similar to clone FLB3816,	2.5
6:		926 AW134		5125 16631	FSTe	2.5
		145 A12772 309 AW043			ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5 2.5
		709 BE410	1592 Hs.2		hypothetical protein PP5395	2.5 2.5
_	_ 416	5530 U5280		9361	kallikrein 6 (neurosin, zyme) squalene epoxidase	2.5
7		1678 Al907 8119 W262		1465 01672	ESTs, Weakly similar to T00331 hypotheti	2.5
		8119 W262 6624 T6429			fatty acid binding protein 1, liver	2.5 2.5
	45	8268 AA42	8403 Hs.	06131	ESTs	2.5
-	45	1336 AJ264		3610 106056	ESTs ESTs, Highly similar to match to EST AA3	2.5
/		6924 A1631 5040 AW8	510 Hs. 52286	196956	gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
		0033 D595		292590	ESTs .	2.5 2.5
	44	18786 BEO4	8842 Hs.	179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5
				232165 43670	polycythemia rubra vera 1; cell surface kinesin family member 3A	2.5
•		08206 AF04 40205 T869		105448	ESTs. Wealdy similar to B34087 hypotheti	2.5
		42138 AA4	45973 Hs	.13303	Homo sapiens cDNA: FLJ21784 ffs, clone H	2.5 2.4
		20912 AW8	153156 Hs	.90787	ESTs	
					203	į.

	400100	AJ393742	Hs.199067 v	-erb-b2 avian erythroblastic teukemia v	2.4
	439180 421025	AW958975	Hs.29397	tomo sapiens cDNA FLJ 13226 fis, clone OV	24 24
	439973	AJ733308	N= 12/EE3 (	CTe	24
•	446847	T51454	Hs.82845	tomo sapiens cDNA: FLJ21930 fis, clone H ESTs, Moderately similar to ALU5_HUMAN A	2.4
5	414672 451522	AI218038 BE\$65817	Hs.48504 Hs.26498	hypothescal protein FLJ21657	24
	433068	NM_006456	Hs.288215	sialytransferase	24 24
	446620	AA128808		transporter-like protein	24
10	423803	NM_005709	Hs.132945 Hs.41717	POZ-73 protein phosphodiesterase 1A, calmodulin-depende	24
10	407978 42 <del>59</del> 07	AW385129 AA365752		ESTs	2.4
	433819	AW511097	Hs.112765	ESTs	24 24
	446066	A1343931	Hs.149383	ESTs	2.4
15	430573	AA744550 R37658	Hs.136345 Hs.21375	ESTs ESTs	2.4
13	444992 434975	AA657884	Hs.314413	ESTs	24
	458227	Z40670	Hs.181340	ESTs	24 24
	443244	A1457235	Hs.156479	ESTs ESTs, Weakly similar to A46010 X-linked	24
20	432408 401600	N39127 BE247275		US snRNP-specific protein, 116 kD	2.3
20	419066	298492	Hs.6975	PRO1073 protein	2.3
	424823	NM_006226	Hs.153322	phospholipase C, epsãon	2.3 2.3
	402124	1100440	Lt. 000100	NM_031891:Homo sapiens cadherin 20, type ESTs	2.3
25	416678 444897	N80448 AW137088	Hs.269106 Hs.144857	ESTs	23
23	425111	BE018485	Hs.30977	ESTs. Weakly similar to 834087 hypotheti	2.3 2.3
	400536			NM_000681*:Home sapiens adrenergic, alph ESTs, Wealdy similar to 178885 serine/th	23
	427544	AI767152 AI142379	Hs.181400	gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.3
30	459511 415111	R39039	Hs.279041	EST	23
50	433331	A1738815	Hs.117323	ESTs	23 23
	440293	AJ004193	Hs.22123	ESTs heat shock protein (hsp110 family)	2.3
	411770 416964	NM_014278 D87467	3 Hs.71992 Hs.80620	guarrine nucleotide exchange factor for R	2.3
35	419386	AA236867		ESTs, Weakly similar to 138022 hypotheti	2.3 2.3
	402493	AJ743260		mannosidase, alpha, class 1A, member 1	2.3
	401783	AA278248	Hs.920	NM_003771°:Homo sapiens keratin, hair, a ESTs	2.3
	420548 419763	AK039691	Hs.127486	ESTs	2.3
40	421750		Hs.107872	hypothetical protein FLJ20761	2.3 2.3
	406023		202007	Target Exon hypothetical protein FLJ23403	23
	454024 401586		Hs.293907	Target Exon	2.3
	404091			Target Exon	23 23
45	456773	AI038192	Hs.129764		2.3
	414108				2.3
	454288 441879		Hs.10714	novel protein similar to archaeal, yeast	2.3 2.3
	42472	4 T06532	Hs.28770		2.3
50	415693		Hs.47374 Hs.16725	7 heals link protein-1	2.2
	41628 40465		NS. 10723	ENSP00000239999":HYPOTHETICAL 34.7 kDa P	2.2
	42995	6 AJ374651		ESTs	2.2 2.2
55	42967		Hs.21159 Hs.21156		2.2
55	42965 45892				2.2
	43646	3 H06502	Hs.6656	ESTs	2.2 2.2
	40899				2.2
60	41330 41815			nuclear receptor subfamily 1, group I, m	2.2
00	41840			8 nuclear transcription factor Y, beta	2.2 2.2
	4229				2.2
	4463 4292			4	2.2
65	4497		15 Hs.2394	1 KIAA1189 protein	2.2 2.2
	4084				2.2
	4100			9 DKFZP586L2024 protein gb:MR4-ST0125-021199-017-e07 ST0125 Homo	2.2
	4109 4471		770 Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.2
70	) 4217			356 CED-6 protein	2.2 2.2
	4037	728	107 11. 740	Tørget Éxon 72 ESTs	2.2
	4533 4113				2.2
	413			interleukin 13	22
7:	5 409	028 AB014	513 Hs.499	98 Z-band alternatively spliced PDZ-motif	2.2 2.2
	413		964 Hs.756	16 setatin-1 Target Exon	2.2
	403 408	463 068 AW148	3652 Hs.167	398 ESTs	2.2
_	407	819 R4218	5 Hs.102	7720 ESTs	2.2 2.2
8		203 BE262 2045 AJ297			2.2
		1045 AJ 297 1835 AW 979			2.2
		3547 AW20			2.2

	414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens c	2.2
	427493	H09037		Target CAT	2.2
	458441	AW842283	Hs.288232	cyclin I	21
5	410705 444647	BE004107	Hs.11506	gb:CM0-BN0102-150300-288-I12 BN0102 Homo	2.1
,	405502	H14718	ns.11506	Human clone 23589 mRNA sequence C7000609":gij626012[pirl]A53933 myosin 1	2.1 2.1
	400818			Target Exon	21
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	21
10	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	21
10	445200 453396	AA084460 AW162768	Hs.12409 Hs.22620	somatostatin ESTs	2.1 2.1
	443819	AB033076	Hs.9873	Ekely homolog of rat kinase D-interacti	2.1
	401929			C17001690:gq6005701 ref NP_009099.1  AT	2.1
15	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	2.1
13	433862 458694	D86960 F12832	Hs.3610 Hs.3610	KIAA0205 gene product	21
	417063	NS0515	Hs.45061	ESTs ESTs	21 21
	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	21
20	414446	AA147534	Hs.142019	ESTs, Weakly similar to 1207289A reverse	2.1
20	434681	AA642402	Hs.59142	ESTs	2.1
	413835 426137	AJ272727 AL040683	Hs.249163 Hs.167031	fatty acid hydroxytase OKFZP566D133 protein	2.1 2.1
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	21
26	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	2.1
25	407786	AA687538	Hs.38972	tetraspan 1	21
	421296 444200	NM_002666 AA327113	Hs.103253 Hs.149057	perilipin ESTs	21 21
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.1
20	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	2.1
30	414759	AW295157	Hs.47587	ESTs	2.1
	449511 451606	A1436187 AA018791	Hs.296261 Hs.7945	guardine nucleotide binding protein (G pr	2.1
	437924	A1935344	Hs.164118	AIE-75 binding protein Protein ESTs, Wealdy similar to SL51_HUMAN SODIU	2.1 2.1
2.5	449119	AI631195	Hs.232193	ESTs	2.1
35	431568	AW972316	Hs.283703	ESTs	2.1
	447932 433516	AA837474 AA595802	Hs.20021	vesicle-associated membrane protein 1 (s	2.1
	441987	AW452234	Hs.33410 Hs.128293	ESTs, Wealdy similar to T17279 hypotheti ESTs	21 21
	414055	AW818687	Hs.5366	hypothetical protein FLJ21522	2.1
40	445066	BE178734	Hs.197422	ESTs	2.1
	455546	AW994075		gb:RC3-BN0036-090200-011-g06 9N0036 Homo	2.1
	413607 456401	T64741 W28146		gb:yc48f11.r1 Stratagene liver (937224) gb:43f11 Human retina cDNA randomly prim	2.1 2.0
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.0
45	425055	AW961959	Hs.96940	EST\$	2.0
	426917	AA913814	Hs.172854	DKFZP58680923 protein	2.0
	419647 412266	AA348947 N59006	Hs.91816 Hs.26133	hypothetical protein ESTs	2.0
	449658	A1964033	Hs.195730	ESTs, Wealdy similar to CTXN RAT CORTEXI	2.0 2.0
50	424505	AA446131	Hs.124918	KIAA1795 protein	2.0
	438219	AI916151	Hs.257194	ESTs	2.0
	425068 412949	AL048716 AJ471639	Hs.154387	KIAA0103 gene product	2.0
	418866	T65754	Hs.71913	ESTs gb:yc11c07.s1 Stratagene lung (937210) H	2.0 2.0
55	445071	A1280246	Hs.149504	ESTs	2.0
	456529	AF014643	Hs.100072		20
	406475 429656	X05608	Un 314504	C15000508*:gij2558825 gb AAC53387.1  (AF	20
	431542	H63010	Hs.211584 Hs.5740	neurofilament, light polypeptide (68kD) ESTs	2.0 2.0
60	452625	AA724771	Hs.61425	ESTs	2.0
	410378	R23324	Hs.41693	Dna.i (Hsp40) homolog, subfamily B, membe	2.0
	409767	AW501470	11- 20224	gb:UI-HF-8P0p-ajd-b-03-0-UI.r1 NIH_MGC_5	2.0
	446873 453938	AI554439 AF082569	Hs.30724 Hs.36794	ESTs O-type cyclin-interacting protein 1	2.0 2.0
65	423605	AF047826	Hs.129887		2.0
	420061	AW024937	Hs.29410	EST ₅	2.0
	439559	AW364675	Hs.173921		2.0
	449901 428304	AI674072 AI743177	Hs.98422	gbtwd15h01x1 Soares_NFL_T_GBC_S1 Homo s ESTs	20
70	432278	AL137506	Hs.274256		2.0 2.0
	458480	AI792298	1,0,2,1,2,0	p30 D8C protein	20
	404559			Target Exon	2.0
	445831	NM_006055		LanC (bacterial tantibiotic synthetase c	20
75	427523 413055	BE242779 AV655701	Hs.179526 Hs.75183	upregulated by 1,25-dihydroxyvitamin D-3 cytochrome P450, sublamily IIE (ethanol-	2.0 2.0
- •	444904	AW452054	Hs.161139		2.0
	443713	AJ082810	Hs.204934	ESTs	20
	448743	AB032962	Hs.21896	KIAA1136 protein	2.0
80	428186 448770	AW504300 AA3266B3	Hs.295605 Hs.21992	mannosidase, alpha, class 2A, member 2 likely ortholog of mouse variant polyade	2.0 2.0
	453994	BE180964	Hs.165590		2.0
	420290	AW977318	Hs.194480	ESTs	2.0
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	2.0

					0.0
	447965	AW292577	Hs.94445	ESTs	20 20
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr hypothetical protein FLJ14547	20
	459256	AW967468	Hs.99821	gb:QV2-PT0012-020500-186-a08 PT0012 Homo	20
5	411906 441984	AW875765 AB037763	Hs.8059	synaptotagmin IV	2.0
,	437900	AI763301	Hs.107331	ESTS	2.0
	436092	Al345995	Hs.127383	ESTs	20
	415529	AW009370	Hs.115772	ESTs	2.0
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	20
10	444749	Al190672	Hs_65926	ESTs	2.0
	446277	AI284218	Hs.159204	ESTs	20
	452550	AA026735	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	20
	445725	AK000956	Hs.13209	hypothetical protein FLJ 10094	2.0 2.0
1.5	409265	178737	Hs.321062	ESTs	2.0
15	426736	AA431615	Hs.130722	ESTS	2.0
	447098	A1939409	Hs.157803	ESTs Target Exon	2.0
	403582			taget Com	
	TABLE 21	R:			
20	Pkey:		ue Eos probes	et identifier number	
	CAT num!		e cluster numb		
	Accession	: Genl	bank accessio	n numbers	
25	Pkey	CAT Number	Accession	A14P00001 A18/400000	
25	409767	1154015_1	AW501470	AW502931 AW499500 BE004105 AW901093 AW797879 AW901094 AW7	7881 AW797880 RE004108
	410705	1217235_1	8EUU41U7	AW810337 AW810295 AW810333 AW810335 AW	10296 AW816053
	410912 411361	1226543_1 1240611_1	AVV01UZZ4	AW839234 AW839230 AW878302 AW839109 AW	43897
	411811	1259427_1	AWR64370	AW864319 AW864504	
30	411906	1265204_1	AWR75769	H50294 AW875444	
20	411918	1265807_1	AW876354	AW876179 AW876318 AW876290 AW876234 AW	76125 AW876199 AW876198
	412244	1284692_1	AW948175	; AW947637 AW902869 AW947537 AW947531 AW	947532 AW947530
	413607	1379911_1		158393 BE152805	
~ ~	414276	14321151			
35	415666	1543492_1		08673 H72694 F20990 R08580	
	416935	163179_1	DETERDED	AA190665 AA252564 BE166832 AA319621 AA401166 AIR11901 H7885	X56199 R93797 AW896675 AA401072 AW374411 H52942 AW896685 AA348138
	418154	17249_1	A12007C4	**************************************	MR705 AA029093 AW444847 HE1757UU AV651636 AV651647 AAJ32VJ3 AV943227
			*******		RE21R742 AA3339R AAN95633 AAD91968 M/8602 105342 W1/U94 AA140501
40			AVAP274CE	E ALAEDONS AWIRTEONN ALTREMAN ALDROPER ALAESTR	3 AA693541 Al681019 AV658257 AV658133 BEU45335 BEU89546 AA3UU63U AA3G1376
40			BE218739	AW207622 AA765340 AW612733 BE348741 AI80	054 AI871563 AA808652 AI500693 AW342032 AA147066
	418856	179788_1	T65754 A	A229857 AA229658	
	419386	184356_1	AA23686	7 AA237066 AA354236 AW957759 H08961	
	424994	245786_1	AW95452	5 Al372685 AA349501 Al372687 H10564	
45	427493	279541_2		W974937 AA657521 H86138 H86513 H09016 AA4	4410 AA404454
	431304	331286_1	BE15728	3 BE157287 AA502438	
	432408	346286_2		20776 AI082691 AA865520 F36964 F33894	
	433670	372721_1	4 4 6 4 6 4 7	5 BE062234 AW748386 4 AI114549 R36464 R36465	
50	433921 436624	377350_1 4237_5	704007 6	. ADDAMA I NILA MM 1443 MINDEN AWRAZING AIFORS	5 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
50	430024	423/_3	A1768596	AA101894 W90338 AI742193 AW752206 AA0994	3 T53220 AW082135 AW272775 T29562 T55862 Al343047 Al345671 T68235 T68121
			AW8422		
	446692	689623_1		1352097 AIB03984 AW235923 AW196558 AI9S463	7 A1336983
	449901		AI67407	2 BE268487	
55	454339	1122972_1	AW3819	80 BE152244 BE152235 BE152238 BE152232	
	455040			86 AW851934 AW852096 AW852274	
	455546		1 AW9940	75 AW994386	ACTA DECCACTE
	455649			31 BE155165 BE064764 BE155231 BE064648 BE0	407 1 BE004030
60	456401 458480		2 W28146	W20107 8 H14121 Al375113 AA960851 AA744592 AV6487:	A A 1298360 AW 293609
00	430401	) 33043_1	AII JEEU	0111412113010113113133	
	TABLE	21C:			
	Pkey:		Inique number	corresponding to an Eos probeset	
	Ref:	9	equence sour	ce. The 7 digit numbers in this column are Genban	Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
65		8	equence of hu	man chromosome 22° Dunham, et al. (1999) <u>Natur</u>	402:489-495.
	Strand			strend from which exons were predicted.	
	Nt_pa	sition: t	ndicates nucle	olide positions of predicted exons.	
	_	- ·	C1	All assistan	
70	Pkey	Ref	Strand Minus	Nt_position 170994-172025	
70			Plus	172644-172765,173085-173200	
	40081 40158		Minus	93974-94099	
	40160		Minus	27363-27518 28727-28891 29526-29731	
	40178		Plus	139369-139827,140509-140591,140834-140	90,141496-141657,141757-141882,142063-142283
75	40192	9 3810670	Minus	3167-3286,4216-4310	
	40212	4 4033680	Plus	164205-164459	
	40249			205146-205240,205428-205542	
	40346			102596-102879	
80	4034			4831-7707 19309 19459	
٥U				18308-18458 34481-34671	
	4037: 4040:			82121-8322 <del>9</del>	
	4045	• • • • • • • • • • • • • • • • • • • •		73499-73651,89575-89739	
		3		-	206



	404563	9838310	PNUS	100130-100343
	404606	9212936	Minus	22310-23269
	404659	9797068	Minus	65026-67930
	404746	7219894	Minus	32643-32834
5	405354	2642452	Plus	52213-53089
,	405403	6850244	Minus	37491-37670,40951-41031
	405502	9211311	Minus	50360-50584
	405715	4156209	Plus	26293-26706
	405/13	.8272661	Ptus	205623-205936
10			Plus	125417-125563,128052-128180
10	406475	9797684	FIUS	149411-120000,120002-120100

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS
Table 22A list a about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS listues. These were selected from 59680 probesets on the
AffymentivEns t-No3 GeneChip array such that the ratio of "average" normal CNS is "average" abolitations are greater than or equal to 2. The "average" normal CNS level was set
to the 75th per centitie amongst various normal CNS tissues. The "average" soloblastoma level was set to 95th percentitie amongst various tumor samples. In order to remove geneto the 75th per centitie amongst various normal CNS tissues. The "average" soloblastoma level was set to 95th percentitie amongst various tumor samples. In order to remove geneto the 75th per centitie amongst various normal CNS tissues. The "average" normal cNS tissues was subtracted from both the numerator and the denominator
before the ratio was evaluated.

Play:

Unique Eos probaset identifier number

Unique Eos probaset identifier number.

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	KI.	74000			
	Dha.	ExAcon	UnigeneiD	Unigene Title	R1
25	Pkey 418318			transmembrane 4 superfamily member 3	10.1
23		H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	9.4
	445529	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	415274	AW 206437	Hs.4290	ESTs	7.3
	417167 453165	\$74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	6.5
30		AW204712	Hs.61957	ESTs	6.3
30	454076		Hs.295449	parvalbumin	6.2
	417275	X63578	115.233443	desmoplatin (DPI, DPII)	6.0
	412636	NM_004415	Hs.183506	hypothetical protein FLJ14213	5.9
	409743	N48721	Hs.151449	KIAA0535 gene product	5.6
25	424645	NM_014682	Hs.176227	hypothetical protein FLJ11155	5.5
35	427322	AK002017	Hs.14992	hypothetical protein FLJ11151	5.2
	446390	AA233393	Hs.49265	ESTs	5.2
	444409	AI792140		ESTS	5.1
	409031	AA376836	Hs.288856 Hs.44898	Onal (Hsp40) homolog, subfamily B, membe	4.8
40	408428	NM_014787		DKFZP564C152 protein	4.8
40	428414	AL049980	Hs.184216	transityretin (prealburnin, armyloidosis t	4.6
	428874	W32133	Hs.194366	HSPC156 protein	4.6
	420605	BE391491	Hs.99291	Homo saplens cDNA FLJ12052 fis, clone HE	4.6
	445618	H79667	Hs.237642	POTE MEMORIA CONTROL TO MANAGEMENT CONTROL	4.4
45	450715	A1266484	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	4,4
45	428508	BE252383	Hs.184668	SBB131 protein	4.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.2
	410330	AW023630	Hs.159425	ESTs	4.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
50	448958	AB020651	Hs.22653	KIAA0844 protein	4.0
	428465	AW970976	Hs.293653	ESTs	4.0
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.9
	432298	AL118812	Hs.274293		3.9
	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
55	430261	AA305127	Hs.237225		3.8
	435145	A1277259	Hs.116831		3.6
	416101	R24854	Hs.268806	ESTs	3.8
	426716	NM_006379	Hs.171921		3.8
	438202	AW169287	Hs.22588	ESTs	3.7
60	433558	AA833757	Hs.201769		3.7
	419958	AL137939	Hs.40096	ESTs	3.7
	430573	AA744550	Hs.136345		3.7
	422546	AB007969	Hs.301476		3.6
	453344		Hs.44571	ESTs	3.6
65	417620		Hs.19119		3.6
	421952		Hs.98849		3.6
	414631				3.5
	437073		Hs.94122		3.5
	441264	AA927170	Hs.23290		3.5
70	433629		Hs.13359		3.4
	415114		Hs 94181		3.4
	411770		8 Hs.71992	heat shock protein (hsp110 family)	3.4
	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	3.4
	416851				3.4
75	44303			syntaxin 7	3.4
	44951		Hs.29626		3.4
	42717				3.3
	43870		Hs.3282		3.3 3.3
	41717	5 R44558	Hs.9400		3.3 3.3
80	43086		Hs.5232		3.3
	45701		Hs.3027	54 ESTs	
	40535			CX000321:gij6671579 ref]NP_031518.1  ari	3.3 3.3
	43279		61 Hs.2789	60 alpha-1,4-N-acetylglucosaminyltransleras	3.3
		_		207	

					22
			Hs.225974 1	KIAA 1054 protein pulative b,b-caretene-9.10'-dioxygenase	3.3 3.3
	434348 441071	BE393191 D79550	Hs.181795 Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clione H	3.3
	445279	R41900	Hs 22245	FSTs	3.2
5	414541	BE293116		aldehyde dehydrogenase 1 family, member	3.2 3.2
	448072 402429	AJ459308	Hs.24908	ESTs Target Exon	3.2
	433328	AW298159	Hs.23644	ESTs, Wealdy similar to \$65824 reverse t	3.2
10	400138		405064	Eos Control ESTs, Wealdy similar to T24435 hypotheti	3.1 3.1
10	414327 459399	BE408145 BE407712	Hs.185254 Hs.153998	creating kinase, mitochondrial 1 (ublqui	3.1
	433582	BE548749	Hs.148016	ESTs .	3.1
	434104	AF116691	Hs.116459	hypothesical protein PRO2198	3.0 3.0
15	404606	T64349		Target Exon gb:yc10d08.s1 Stratagene tung (937210) H	3.0
13	407173 415672	N53097	Hs.193579	ESTs	3.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	3.0 3.0
	429043	A1824977	Hs.145319 Hs.95162	ESTs KCNQ1 overlapping transcript 1	29
20	439165 449561	AA029517 A1022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	29
20	436427	Al344378	Hs.143399	ESTs .	29 29
	405403	*******	Hs.232048	Target Exon ESTs	29
	452197 437357	AW023595 AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp762O2215 (f	2.9
25	439272	AA832474	Hs.25851	ESTs	29 2.9
	415839	R40611	Hs.94694	ESTs gb:QV2-PT0012-020500-186-s08 PT0012 Homo	2.9
	411906 409403	AW875765 AA668224	Hs.6834	Homo sapiens cDNA: FLJ22547 fls, clone H	2.9
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	2.B 2.8
30	435836	AW292532	Hs.343667 Hs.162430	homolog of yeast long chain polyunsatura EST	2.8
	433109 404563	N58907	N3.102430	Target Exon	2.8
	427974	BE093023	Hs.188767	ESTs	2.8 2.7
25	413324	V00571	Hs.75294 Hs.50319	corticotropin reteasing hormone ESTs	2.7
35	409263 454247	AA069573 AJ243950	Hs.46735	dealness locus associated putative guarti	2.7
	449180	A1633836	Hs.195649	ESTs	2.7 2.7
	416004	D11880 AW954525	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L gb:EST366595 MAGE resequences, MAGC Homo	2.7
40	424994 430371	D87466	Hs.240112	KIAA0275 protein	2.7
	449117	AW449310	Hs.210262		2.7 2.7
	451007	H38108 AL133721	Hs.32759 Hs.224680	ESTs ESTs	2.7
	414502 458793	N80159	Hs.121849		2.7
45	459053	AI807052	Hs.210361		2.7 2.7
	427229	A1799751 U30930	Hs.5635 Hs.15854	ESTs ) UDP glycosyttransferase 8 (UDP-galactose	2.7
	425649 444922		Hs.14487	Homo sapiens cDNA FLJ13752 fis, clone PL	2.7
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo saplens	2.7 2.7
50	414272		Hs.46988 Hs.4847	ESTs ESTs	2.7
	418047 421089			9 KIAA1350 protein	27
	416498	U33632	Hs.79351		2.6 2.6
55	414290 433703		Hs.71721 Hs.3532	ESTs nemo-like kinase	2.6
,,	408739		Hs.23879	7 ESTs, Moderately similar to 138022 hypot	2.6 2.6
	414602			) Homo sapiens mRNA; cDNA DKFZp56481264 (f	2.6
	422137 44202				2.6
60	42170	9 AA15939	4 Hs.1070	56 CED-6 protein	26 26
	42674	7 AA53521		95 Italiikrein 3, (prostate specific antigen gb:RC0-MT0013-280300-021-c10 MT0013 Homo	2.6
	41224 41938			ESTs. Wealdy similar to 138022 hypotheti	2.6
	42366			O ESTs	2.6 2.6
65					2.6
	40846 41065				2.6
	44887		9 Hs.1592	65 kruppel-related zinc finger protein hcKr	2.6 2.6
70	41451				2.5
/(	7 45908 4550-			gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
	4357		07 Hs.176	as6 ESTs	2.5 2.5
	4316	62 AA5134	06 Hs.152		25 25
75	4359 4366		67 Hs.297	/25 ES13 fatty acid binding protein 1, liver	2.5
-	4431			72 ESTs	25 25
	4391	83 AW9700			25 25
	4263 4200				2.5
80	O 4084	38 AB0111	80 Hs.100	960 KIAA0608 protein	2.5 2.5
	4402				2.5 2.5
	4487 4322				2.5
	702			200	

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	427115	AW972853	Hs.112237	ESTs .	2.4
	433670	AA604405	LL 202025	gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	24
	452022 408814	AW072330 N62499	Hs.293875 Hs.176227	ESTs hypothetical protein FLJ11155	24
5	403469	1102103	***************************************	Target Exon	2.4 2.4
	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	24
	451926 443622	AW134519	Hs.96125 Hs.11805	Homo sapiens, Similar to clone FLB3816,	2.4
	456791	AI911527 H05202	Hs.133968	ESTs FGF receptor activating protein 1	24 24
10	414672	AI218038	Hs.48504	ESTs. Moderately similar to ALU5_HUMAN A	24
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	24
	422414 425383	AW875237 D83407	Hs.13701 Hs.156007	ESTs	24
	428363 438086	AA336519	Hs.83623	Down syndrome critical region gene 1-lik nuclear receptor subfamily 1, group 1, m	24 24
15	410240	AL157424	Hs.61289	synaptolanin 2	24
	432408	N39127		ESTs, Wealdy similar to A45010 X-linked	2.4
	458227 431325	Z40670 AW026751	Hs.181340 Hs.5794	ESTs	24
	401600	BE247275	ris.57 <del>54</del>	ESTs, Wealdy similar to 2109260A B cell U5 snRNP-specific protein, 116 kD	24 23
20	422963	M79141	Hs.13234	ESTs	23
	444897	AW137088	Hs.144857	ESTs	23
	418207 445071	C14685 AJ280246	Hs.34772 Hs.149504	ESTs ESTs	23
~-	407868	NM_000950	Hs.40637	profine-rich Gla (G-carboxyglutamic acid	23 23
25	433331	A1738815	Hs.117323	ESTs	2.3
	440293 428850	AI004193	Hs.22123	ESTs	23
	420030	AA934975	Hs.185076	ESTs NM_003771":Homo sepiens keratin, hair, a	2.3 2.3
20	419763	AI039691	Hs.127486	ESTs	2.3
30	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	2.3
	420912 442097	AW853156 AW015799	Hs.90787 Hs.128474	ESTs	2.3
	425907	AA365752	Hs.155965	ESTs ESTs	2.3 2.3
25	404091			Target Exon	2.3
35	414105	8E300325	Hs.77135	RNA binding protein	2.3
	454268 441040	BE222648 AW449782	Hs.241432 Hs.178803	ESTs, Highly similar to c380A1.1b (H.sap ESTs	2.3
	424724	106532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	2.3 2.3
40	441879	AJ521936	Hs.107149	novel protein similar to archaeal, yeast	2.3
40	407988 452420	N47760	Hs.285107	hypothetical protein FLJ13397	2.2
	458676	BE564871 A1692464	Hs.29463 Hs.202263	centrin, EF-hand protein, 3 (CDC31 yeast ESTs	2.2
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.2 2.2
A E	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.2
45	407978 420548	AW385129 AA278246	Hs.41717	phosphodiesterase 1A, calmodulin-depende	2.2
	422907	AI879263	Hs.920 Hs.77273	ESTs Human glucose transporter pseudogene	2.2 2.2
	446351	AW444551	Hs.35380	x 001 protein	2.2
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.2
30	429598 408480	AA811257 AI350337	Hs.269710 Hs.164568	ESTs	2.2
	411381	AW839073	113.104300	fibroblast growth factor 7 (keratinocyte gb:CM2-LT0066-030100-109-d06 LT0066 Homo	2.2 2.2
	459697	AA406062	Hs.98002	ÉST <b>s</b>	2.2
55	409856 444760	AW502082 AI796296	U= 000000	gb:UI-HF-BR0p-aig-g-04-0-UI.r1 NiH_MGC_5	2.2
55	443258	AF169301	Hs.208062 Hs.9098	ESTs suffate transporter 1	2.2
	428206	AB020643	Hs.183006	KIAA0836 protein	2.2 2.2
	410119	F07841	Hs.13926	ESTs	2.2
60	413427 438021	U31120 AV653790	Hs.845	interteukin 13	2.2
~~	428652	AA584272	Hs.324275 Hs.336224	WW domain-containing protein 1 transmembrane protein with EGF-like and	2.2 2.2
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.2
	424153	AA451737	Hs.141496	MAGE-like 2	2.2
65	413303 427287	AW836130 NM_014903	Hs.75277 Hs.174188	hypothetical protein FLJ13910 KIAA0938 protein	2.2
	449658	A#964033	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEX	2.2 2.2
	441984	AB037763	Hs.8059	synaptotagmin [V	22
	449709 408068	BE410592	Hs.23918	hypothetical protein PPS395	2.2
70	407819	AW148652 R42185	Hs.167398 Hs.102720	ESTs ESTs	2.2
	414203	BE262170	Hs.78629	ATPase, Na? transporting, beta 1 polypep	2.2 2.2
	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	2.2
	448045 458480	AJ297436 AJ792298	Hs.20166	prostate stem cell antigen	2.2
75	458480 449835	AI/92298 AW979300	Hs.293813	p30 DBC protein ESTs	2.2
	458547	AW204314	Hs.170784	EST8	5.2
	411678	AI907114	Hs_71465	squalene epoxidase	2.1
	444783 424632	AK001468 AB014523	Hs.62180	anillin (Drosophila Scraps homolog), act	2.1
80	449901	A6014523 A674072	Hs.151406	KIAA0623 gene product gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.1 2.1
	410538	AW753115		gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.1
	426775	AA384564	Hs.3628	ESTs	2.1

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	433862	D88960	Hs.3610	VIAA0206 oons omder!	21
	458694	F12832	Hs.3610	KIAA0205 gene product ESTs	21
	417063	N50515	Hs.45061	ESTs	2.1
_	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	2.1
5	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	21
	431128 442310	AJ203545 AF033199	Hs.296169 Hs.8198	S-phase response (cyclin-related)	2.1
	432434	AL161977	Hs.2994	zinc finger protein 204 PCTAIRE protein kinasa 3	2.1 2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
10	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	21
	414759	AW295157	Hs.47587	EST ₅	2.1
	438219	AI916151	Hs.257194	ESTs	2.1
	451336 430538	AJ264643 AB032435	Hs.3610 Hs.242821	ESTs differentiation-associated Na-dependent	21
15	413493	8E144444	113.242021	gb:MR0-HT0168-141199-002-09 HT0168 Homo	2.1 2.1
	428501	AL041162	Hs.98587	ESTs	2.1
	431568	AW972316	Hs.283703	ESTs	21
	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	2.1
20	441976 421311	AA428403 N71848	Hs.106131	ESTs	2.1
LU	428358	AA993222	Hs.283609 Hs.101915	hypothetical protein PRO2032 Stargardt disease 3 (autosomal dominant)	21 21
	439973	AJ733308	Hs.124663	ESTs	21
	446185	Al279191	Hs.149454	ESTs, Weakly similar to DSR6_HUMAN DOWN	2.1
25	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.1
23	433516 441987	AA595802	Hs.33410	ESTs. Weakly similar to T17279 hypotheti	2.1
	457140	AW452234 AI279960	Hs.128293 Hs.178140	ESTs ESTs	2.1 2.1
	414055	AWB18687	Hs.5366	hypothetical protein FLJ21522	2.1
20	445066	BE178734	Hs.197422	ESTs	2.1
30	459265	AJ003616		gb:AJ003616 Selected chromosome 21 cDNA	2.0
	425337 409339	AA355442	Hs.169054	ESTs	2.0
	453023	AB020686 AW028733	Hs.54037 Hs.31439	ectonucleolide pyrophosphalase/phosphodi serine protease inhibitor, Kunitz type,	2.0 2.0
	425055	AW961959	Hs.96940	ESTs	2.0
35	425068	AL048716	Hs.154387	KIAA0103 gene product	2.0
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	2.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.0
	450103 448519	R08665 AW175665	Hs.17244 Hs.278695	hypothetical protein FLJ13605  Homo sapiens prostein mRNA, complete cds	2.0
40	440808	AK001339	Hs.7432	hypothetical protein FLI 10477	2.0 2.0
	429968	AA322503	Hs.227011	G-substrate	2.0
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.0
	433068	NM_006456	Hs.288215	sialytransferase	2.0
45	416982 423479	J05401 NM_014326	Hs.80691 Hs.129208	creatine kinase, mitochondrial 2 (sarcom	2.0
	407341	AA918886	Hs.204918	death-associated protein kinase 2 ESTs, Weakly similar to ALUS_HUMAN ALU S	2.0 2.0
	452625	AA724771	Hs.61425	ESTs	2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, merfibe	2.0
50	409767	AW501470		gb:UI-HF-BP0p-ajd-b-03-0-UI.r1 NIH_MGC_5	2.0
50	415925 405870	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L C2000627":gi[12034653]gb]AAG45951.1]AF22	2.0
	408206	AF041853	Hs.43670	kinesin family member 3A	20 20
	458560	AJ299739	Hs.99601	hypothetical protein FLJ12553	2.0
55	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	20
33	404559 403728			Target Exon	2.0
	413055	AV655701	Hs.75183	Target Exon cytochrome P450, subfamily IIE (ethanol-	2.0
	407786	AA687538	Hs.38972	tetraspan 1	2.0 2.0
<b>60</b>	413266	BE300352		gb:600944231F1 NIH_MGC_17 Homo sapiens c	2.0
60	453994	BE180964	Hs.165590	ribosomal protein S13	2.0
	451583 443244	A1653797	Hs.24133	ESTs	2.0
	453396	AI457235 AW162768	Hs.166479 Hs.22620	ESTs ESTs	2.0
	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	2.0 2.0
65	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.0
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	2.0
	451032 440509	W03692	Hs.323079		2.0
_	444647	BE410132 H14718	Hs.134202 Hs.11506	ESTs. Weakly similar to T17279 hypotheti Human clone 23589 mRNA sequence	20
70	447932	AAB37474	Hs.20021	vesicle-associated membrane protein 1 (s	2.0 2.0
	444749	AI190672	Hs.65926	ESTs	2.0
	446277	AI284218	Hs.159204		2.0
	452550 452943	AA026735	Hs.326048		2.0
75	453843 445725	D25215 AK000956	Hs.35804 Hs.13209	hect domain and RLD 3 hypothetical protein FLJ10094	2.0
	409265	T78737	Hs.321062		2.0 2.0
	TABLE 2	ZB:			

TABLE 228: Pkey: CAT number: Accession: Unique Eos probeset identifier number Gene cluster number Genbank accession numbers

Pkey CAT Number Accession

	409767	1154015_1	AW501470	AW502931 AW499500
	409856	1156268_1	AW502082	AW502979 AW502807 AW501876
	410538 411361	1207341_1 1240611_1		AW753113 R45779 AW839234 AW839230 AW878302 AW839109 AW843897
5	411906	1265204_1		H50294 AW875444
	412244 412636	1284692_1		AW947637 AW902869 AW947537 AW947531 AW947532 AW947530
	412030	13165_1	NM_00441:	5 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985
10			BE002107 /	AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047
10			AW607238	AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516
			8E001925	AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488
			AW995615	BE 184948 BE 159846 AW806653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 RS8704 AW36566 AW364859
15	•		AA025851 /	AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW649690
13			187267 AV	7853812 AA852213 W74149 BE009090 AA066401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576787 D26863 AW177787 AA026654 AW177788 BE092134 BE092137 BE092136 AW177784 A1022862 BE091653 AW376811 AW848592
			AA040018	BE 185331 8E 182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181
			BE167165	N84767 H27408 H30146 A1190590 C03378 A1554403 A1205263 AA128470 A1392926 AF139065 AW370813 AW370827 AW798417
20			AW798780	AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AJ760816 AJ439101 AW879451
~~			AA702424	A451923 A1340326 A1590975 T48793 A1568096 A1142882 AA039975 A1470146 AA946936 BE067737 BE067786 W19287 AA644381 Al417612 A1306554 A1686869 A1568892 AW190555 A1571075 A1220573 AA056527 A1471874 A1304772 AW517828 A1915596 A1627383
			AJ270345 A	W021347 AW166807 AW105614 AJ346078 AA552300 W95070 AJ494069 AI911702 AA149191 AA026864 AJ830049 AJ887258 AW780435
•			AI910434 A	UB19984 AUB58282 AU07B449 AU025932 AUB60584 AU635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892
25			AW015480	782066 AW243815 AW150038 AW268383 AW004633 A1927207 AA782109 AW473233 A1804485 AW169216 A1572669 AA602182 AW771865 A1270027 AA961816 AA283207 A1076962 A1498487 A1348053 A1783914 H44405 AW799118 AA128330 AA515500 AA918281
			W02156 AI	905927 AA022701 W38382 R20795 T77861 AW860878
	413266 413493	1356260_1 1373555_1		BE299274 BE075351 BE297444
	415666	1543492_1	BE 144444 H72693 R0	BE 144530 18673 H72694 F20990 R08580
30	416935	163179_1	AA190712	AA190665 AA252564
	419386 424994	184356_1 245786_1		AA237066 AA354236 AW957759 H08961
	432408	346286_2		A1372685 AA349501 A1372687 H10564 (0776 A1082691 AA865520 F36964 F33894
25	433670	372721_1	AA604405	BE062234 AW748386
35	433921 436624	377350_1 4237_5		A1114549 R36464 R36465
	400024	4231_3	A1768596	894931 NM_001443 M10050 AW843109 A1698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617 AA101894 W90338 A1742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 A1343047 A1345671 T68235 T68121
			AW842284	
40	449901 454339	818599_1 1122972_1	AI6740721	BE 268487 ) BE 152244 BE 152235 BE 152238 BE 152232
	455040	1250028_1		AW851934 AW852096 AW852274
	458480 459265	59843_1 966590_1		H14121 AJ375113 AA960851 AA744592 AV648739 AJ298360 AW293609
	453205	300330_1	A3003010	AJ003654 AJ003617
45	TABLE 2			
	Pkey: Ret:	Uni Sax	dne unusper c	orresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA"
	1.00.	880	ineuce of ymur	an chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
50	Strand:			and from which exons were predicted.
50	NL positio	on: ung	cates nucleon	de positions of predicted exons.
	Pkey	Ref	Strand	Nt_position
	401600 401783	4388746 7249190	Minus Plus	27363-27518,28727-28891,29526-29731
55	402429	9796372	Minus	139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283 57622-57793,59282-59402,59624-59827
	403469	9929739	Minus	4831-7707
	403728 404091	7534291 7684554	Minus	34481-34671
	404559	8748893	Minus Minus	82121-83229 73499-73651.89575-89739
60	404563	9838310	Plus	100136-100343
	404606 405354	9212936 2642452	Minus	22310-23269
	405403	6850244	Ptus Minus	52213-53089 37491-37670,40951-41031
CE	405670	4662655	Plus	96543-96870
65				
	TABLE 2	3A: ABOUT 44	I GENES SIC	SNIFICANTLY DOWN-REGULATED IN LOWER GRADE GUOBLASTOMA COMPARED TO NORMAL ADULT CNS
	Table 23	A lists about 44	it genes signit	icantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets
70	ON URB AT	iymetru/ttos H	uO3 GeneChip	array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2.5. The "average" normal CNS level was se
, ,	hadran.	ad levels of se	o consise bub	normal CNS tissues. The "average" LGG level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific

to the 75° percentile amongst various normal CNS tissues. The "average" normal CNS to "average" (LGG was greater than or equal to 2.5. The "average" normal CNS to "average" (LGG was greater than or equal to 2.5. The "average" normal CNS tevel was set to the 95° percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play:

Unique Eos probeset identifier number
Exacon:
Evemplar Accession number, Genbank accession number
Unique ID:
Unique number
Unique gene title
Rt:

Ratio of CNS to LOWER GRADE GLIOBLASTOMA

00	Pkey	ExAcon	UnigenelD	Unigene Title	R1
80	415388	AF018081	Hs.78409	collagen, type XVIII, alpha 1	10.3
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
	445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	9.9
	417433	8E270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	7.A

# WO 03/025138 PCT/US02/29560

	422746	NM_004484	Hs.119651	glypican 3	7.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	7.7
	430573	AA744550	Hs.136345	ESTs	7.6
5	415274 419290	AF001548 Al128114	Hs.78344 Hs.112885	myosin, heavy polypeptide 11, smooth mus	7.5
-	424670	W61215	Hs.116651	spinal cord-derived growth factor-8 epithelial V-like antigen 1	7.4 7.3
	417167	AW206437	Hs.4290	ESTs	7.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	7.3
10	424632 453165	AB014523 S74727	Hs.151406	KIAA0623 gene product	6.9
	411770	NM_014278	Hs.32042 Hs.71992	aspartoacylase (aminoacylase 2, Canavan heat shock protein (hsp110 family)	6.5 6.5
	439272	AA832474	Hs.25851	ESTs	6.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	6.4
15	454076	AW204712	Hs.61957	ESTs	6.3
13	446390 430865	AA233393 Al073424	Hs.14992 Hs.5232	hypothetical protein FLJ11151 HSPC125 protein	6.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	6.3 6.2
	417458	NM_005655	Hs.82173	TGFB inducible early growth response	6.1
20	412636	NM_004415		desmoplakin (DPI, DPII)	6.0
20	409743 430998	N48721 AF128847	Hs.183506	hypothetical protein FLJ14213	5.9
	434725	AK000796	Hs.204038 Hs.4104	indolethylamine N-methyltransferase hypothetical protein	5.8 5.6
	417175	R44558	Hs.94002	ESTs	5.6
25	417275	X63578	Hs.295449	parvalbumin	5.5
25	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	431009 420297	8E 149762 AI628272	Hs.48956 Hs.88323	gap junction protein, beta 8 (connexin 3 ESTs, Wealdy similar to ALU1_HUMAN ALU \$	5.4
	412472	AW975398	Hs.293836	ESTs	5.4 5.4
20	443258	AF169301	Hs.9098	sulfate transporter 1	5.3
30	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	5.3
	442064 438868	AI422867 AW246243	Hs.88594 Hs.334800	ESTs	5.2
	444409	A1792140	Hs.49265	hypothetical protein FLJ20974 ESTs	5.2 5.2
0.5	442310	AF033199	Hs.8198	zinc finger protein 204	5.1
35	409031	AA376836	Hs.288856	ESTs	5.1
	438460 411939	AB020702 AI365585	Hs.6224	KIAA0895 protein	5.1
	448429	D17408	Hs.146246 Hs.21223	ESTs calponin 1, basic, smooth muscle	5.0 5.0
40	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.0 5.0
40	408968	AI652236	Hs.49376	hypothetical protein FLJ20544	5.0
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, acti	4.9
	448960 416101	AF006513 R24854	Hs.22670 Hs.268806	chromodomain helicase ONA binding protei ESTs	4.9
	433558	AA833757	Hs.201769	ESTs, Wealthy similar to T24435 hypotheti	4.9 4.9
45	424845	NM_014682	Hs.151449	KIAA0535 gene product	4.8
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	4.8
	408428 414502	NM_014787 AL133721	Hs.44896 Hs.224680	OnaJ (Hsp40) homolog, subfamily B, membe ESTs	4.8
	442572	AJ001922	Hs.135121	hypothetical protein FLJ22415	4.8 4.8
50	412700	8E222433	Hs.239208	ESTs, Weakly similar to 138022 hypotheti	4.8
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.8
	420605 422482	BE391491 Al439905	Hs.99291 Hs.344476	HSPC156 protein	4.7
	416636	N32536	Hs.42645	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo saplen solute carrier family 16 (monocarboxylic	4.7
55	409263	AA069573	Hs.50319	ESTs	4,7 4.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.6
	457216 433423	AA452554 BE407127	Hs.283697	ESTs, Wealdy similar to A41796 neural re	4.6
	449901	AI874072	Hs.8997	heat shock 70kD protein 1A gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	4.6 4.6
60	445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 fis, clone HE	4.6
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	4.5
	424875 449 <b>5</b> 11	NM_005512	Hs.151641	glycoprotein A repetitions predominant	4.5
	401600	AI438187 BE247275	Hs.296261	guanine nucleotide binding protein (G pr U5 snRNP-specific protein, 116 kD	4.5
65	447135	T58148		gb:yb98g06.s1 Strategene lung (937210) H	4.5 4.5
	426689	8E245550	Hs.171825	basic hefix-loop-hefix domain containing	4.4
	429598	AA811257	Hs.269710	ESTs	4.4
	428206 450715	AB020643 Al266484	Hs.183006	KIAA0836 protein	4.4
70	428508	BE252383	Hs.31570 Hs.184668	ESTs, Wealdy similar to KIAA1324 protein SBBI31 protein	4.4
	435145	AJ277259	Hs.116631	ESTs	4.4 4.4
	405670	A ERC		C2000627*:gi 12034653igb AAG45951.1 AF22	4.4
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	4.3
75	427670 428465	8E612888 AW970976	Hs.180224 Hs.293653	myosin regulatory light chain ESTs	4.3
-	449180	AI633836	Hs.195649		4.3 4.3
	402354	AV653231		CCAAT/enhancer binding protein (C/EBP),	4.3 4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
80	419386	AA236867	LL 400007	ESTs, Wealdy similar to I38022 hypotheti	4.2
	441408 419631	AI733249 AW188117	Hs.126897 Hs.303154		4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2 4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2

	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	422278	AF072873	Hs.114218	frizzled (Drosophila) hornolog 6	4.2
	459053	A1807052	Hs.210361	ESTs	4.1
5	450600 415839	BE079478 R40611	Hs.24880	ESTs	4.1
,	450374	AA397540	Hs.94694 Hs.60293	ESTs Homo sapiens clone 122482 unknown mRNA	4,1
	422270	AF114494	Hs.114062	protein lyrosine phosphatase-like (profi	4,1 4.1
	405674			NM_022775:Homo sapiens hypothetical prot	4.1
10	453906	AW444952	Hs.257054	ESTs	4.1
10	419318	AW969742	Hs.291005	ESTs	4.0
	456382 435902	NM_001126 AA701867	Hs.90011 Hs.297726	adenylosuccinate synthase ESTs	4.0
	449483	AK001971	Hs.23607	hypothetical protein FLJ11109	4.0 4.0
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.0
15	403890			C5002036*:gi[10241574 emb CAC09416.1] (A	4.0
	429470 409856	AI878901 AW <b>5</b> 02082	Hs.203862	guanine nucleotide binding protein (G pr	4.0
	443682	A1383061	Hs.47248	gb:Ui-HF-BR0p-ajq-g-04-0-Ui.rt NtH_MGC_5 ESTs, Highly similar to similar to Cdc14	4.0 4.0
••	420230	AL034344	Hs.284186	forkhead box C1	4.0
20	410509	AW840743		gb:QV1-CN0002-080300-102-f07 CN0002 Homo	4.0
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.9
	400138 451522	BE565817	Hs.26498	Eos Control hypothetical protein FLJ21657	3.9
	436521	AW203986	Hs.213003	ESTs	3.9 3.9
25	401507			C15000810":gi]11131272 sp P79331 ATS2_BO	3.9
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	3.9
	434815 411906	AF155582 AW875765	Hs.46744	core 1 UDP-galactose:N-acetylgalactosamin	3.9
	440509	BE410132	Hs.134202	gb:QV2-PT0012-020500-186-a08 PT0012 Homo ESTs, Weakly similar to T17279 hypotheti	3.9 3.9
30	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
	449658 429876	AI964033 AB028977	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEX	3.8
	410330	AW023630	Hs.225974 Hs.159425	KIAA1054 protein ESTs	3.8
35	431369	8E184455	Hs.251754	secretory leukocyte protease inhibitor (	3.8 3.8
	437659	AB007944	Hs.5737	KIAA0475 gene product	3.8
	438171 418394	AW976507 AF132818	Hs.293515 Hs.84728	ESTS	3.8
	405588	74 152010	113.04726	Kruppel-like factor 5 (intestinal) NM_000299:Homo sapiens plakophilin 1 (ec	3.8 3.8
40	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	3.8
	426716	NM_006379	Hs.171921	sema domain, immunoglobutin domain (lg),	3.8
	438202 404606	AW169287	Hs.22588	ESTs Target Exon	3.8
	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	3.8 3.8
45	407604	AW191962	Hs.288061	collagen, type Vill, alpha 2	3.6
	416498 430868	U33632 W93178	Hs.79351	potassium channel, subfamily K, member 1	3.7
	457008	AA410446	Hs.5232 Hs.112011	HSPC125 protein ESTs, Weakly similar to unknown (H.sapie	3.7 3.7
<b>60</b>	458660	AI299739	Hs.99601	hypothetical protein FLI12553	3.7
50	408732	AL117490	Hs.47225	Ras-associated protein Rap1	3.7
	436281 413493	AW411194 BE144444	Hs.85195	myeloid leukemia factor 1	3.7
	418407	AL044818	Hs.84928	gb:MR0-HT0168-141199-002-f09 HT0168 Homo nuclear transcription factor Y, beta	3.7 3.7
<i>E E</i>	445797	A1253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.7
55	457121	A1743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	3.6
	417620 421952	R02530 AA300900	Hs.191198	ESTs	3.6
	454247	AJ243950	Hs.98849 Hs.46735	ESTs, Moderately similar to AF161511 1 H deafness locus associated putative guani	3.6 3.6
60	431662	AA513406	Hs.152307	ESTs	3.6
60	426908	AW815163	Hs.172851	arginase, type II	3.6
	438519 415606	AI186033 W70022	Hs.147025	ESTs, Wealdy similar to C57785 zinc fing	3.6
	444859	AW449137	Hs.157487	gb:zd51e10.r1 Soares_fetal_heart_NbHH19W ESTs	3.6 3.6
	414631	AW970130	Hs.65406	ESTS	3.6
65	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	3.5
	437073 427287	A1885608 NM_014903	Hs.94122	ESTs	3.5
	415927	AL120168	Hs.78919	KIAAUSJ8 protein Kell blood group precursor (McLeod pheno	3.5 3.5
70	450235	AA007512	Hs.17538	ESTs	3.5 3.5
70	447263	AW965667	Hs.322406	hypothetical protein FLJ14494	3.5
	419440 427254	A8020689 AL121523	Hs.90419 Hs.97774	KIAA0882 protein ESTs	3.5
	434348	8E393191	Hs.181795	putative b,b-carotene-9',10'-dioxygenase	3.5 3.5
75	441264	AA927170	Hs.23290	ESTs	3.5
13	433629	R13140	Hs.13359	ESTS	3.5
	446494 441585	AA463276 AI760755	Hs.288906 Hs.202383	WW Domain-Containing Gene ESTs	3.5
	438704	AI435060	Hs.32825	ESTs	3.5 3.4
80	445279	R41900	Hs.22245	ESTs	3.4
	415114 449561	D60468 A1022240	Hs.94181 Hs.17924	ESTs ESTs, Moderately similar to ALU1_HUMAN A	3.4
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC3) yeast	3.4 3.4
	416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26S subu	3.4

	441134	W29092	Hs.346950	moliulus assistation auto bit. The manufact d	
	427176	AW381569	Hs.40334	ceflutar retinoic acid-binding protein 1 ESTs	3.4 3.4
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.4
_	450928	AI744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	3.4
5	457012	R41480	Hs.302754	ESTs	3.3
	405354	Total	14- 010010	CX000321:gi[6671579 sef[NP_031518.1] ari	3.3
	408855 418525	T83061 AW450369	Hs.319946 Hs.86937	Homo septens mRNA for KtAA1727 protein, ESTs	3.3
	420174	AIB24144	Hs.23912	ESTs	3.3 3.3
10	437124	AA554458	Hs.279860	KIAA0666 protein	3.3
	419211	BE270817	Hs_37617	ESTs, Wealthy similar to AS3933 myosin I	3.3
	424335	AW021508	Hs.28170	ESTs	3.3
	453344 428065	BE349075 AI634046	Hs.44571 Hs.157313	ESTs SET	3.3
15	417248	AA329449	Hs.247302	ESTs twisted gastrulation	3.3 3.3
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.3
	411393	AW797437	Hs.69771	8-factor, properdin	3.3
	406976	M60299		gb:Human alpha-1 collagen type II gene,	3.3
20	441071 414327	D79550 BE408145	Hs.7149 Hs.185254	Homo sapiens cDNA: FLJ21950 fis, clone H	3.3
20	433703	AA210863	Hs.183234 Hs.3532	ESTs, Wealdy similar to T24435 hypotheti nemo-like kinase	3.3
	418880	N87353	Hs.89421	CBF1 Interacting corepressor	3.3 3.3
	445947	AW612084	Hs.298494	ESTs	3.3
25	437334	AL353947	Hs.283780	hypothetical protein DKF2p761N1814	3.3
23	434795 400127	BE620794	Hs.4147	translocating chain-associating membrane	3.2
	414602	AW630088	Hs.76550	Eos Control Homo sepiens mRNA; cDNA DKFZp564B1264 (f	3.2
	402429	***************************************	113.10000	Target Exon	3.2 3.2
20	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.2
30	427699	AW965076	Hs.180378	hypothetical protein 669	3.2
	403442 419272	AACC2004	LI- 00000	Target Exon	3.2
	456614	AA663904 AV653110	Hs.89862 Hs.106650	TNFRSF1A-associated via death domain hypothetical protein FLJ20533	3.2
	407581	R48402	Hs.173508	P3ECSL	3.2 3.2
35	412633	AF001691	Hs.74304	periplakin	3.2
	433328	AW298159	Hs.23644	ESTs. Weakly similar to S65824 reverse t	3.2
	449294 442799	AI651786	Hs.195045	ESTs	3.1
	434045	AI564739 AI065133	Hs.68505 Hs.152316	ESTs hypothetical protein PRQ0971	3.1
40	409403	AA668224	Hs.6634	Homo sapiens cONA: FLJ22547 fis, clone H	3.1 3.1
	420033	D59502	Hs.292590	ESTs	3.1
	422137	AJ236885	Hs.112180	zinc finger protein 148 (pHZ-52)	3.1
	444760	A1796296	Hs.208062	ESTs	3.1
45	403488 411359	H86088	Hs.22635	ENSP00000201948:KARYOPHERIN BETA2B HOMOL . ESTs	3.1
	443037	AW500305	Hs.8906	syntaxin 7	3.1 3.1
	407127	R45970	Hs.236349	EST	3.1
	416851	AW963951	Hs.85618	ESTs	3.1
50	416838	D84109	Hs.80248	RNA-binding protein gene with multiple s	3.1
50	443030 410389	R68048 AW954049	Hs.9238 Hs.8177	hypothetical protein FLJ23516 ESTs, Weakly similar to PIHUB6 salivary	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1 3.1
	433582	BE548749	Hs. 148016	ESTs	3.1
55	431128	AI203545	Hs.296169	S-phase response (cyclin-related)	3.1
23	420411 459584	AI581085	Hs.2467B	sphingosine-1-phosphatase	3.1
	449883	AI910884 AI004464	Hs.346429 Hs.344156	ESTs gb:ot56e06.s1 Soares_testis_NHT Homo sap	3.1
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	3.1 3.1
60	410786	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	3.1
60	418207	C14685	Hs.34772	ESTs	3.0
	420521 425890	A1915734 H24530	Hs.87298	ESTs	3.0
	416749		Hs.273294 2000 Hs.79732	hypothetical protein FLJ20069 fibulin 1	3.0
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.0 3.0
65	407173	T64349		gb:yc10d08.s1 Stratagene tung (937210) H	3.0
	415672	N53097	Hs.193579	ESTs	3.0
	448583 429043	NM_015239 AI824977	Hs.21542	KIAA1035 protein	3.0
	404091	P00243/1	Hs.145319	ESTs Target Exon	3.0
70	406085			Target Exon	3.0 3.0
	438825	BE327427	Hs.79953	ESTs	3.0
	457441	BE467737	Hs.146125	ESTs	3.0
	403512 416866	AA297356	He DOSSA	C3000579*:gi 12643308 sp Q9Y4K1 AIM1_HUM	3.0
75	439877	M39685	Hs.80324 Hs.250700	serine/threonine protein phosphatase cat tryptase beta 1	3.0
	441984	AB037763	Hs.8059	synaptotagmin IV	3.0 3.0
	436765	AB028952	Hs.5307	synaptopodin	3.0
	445071	AI280246	Hs.149504	ESTs	3.0
80	404333 422907	AI879263	Hs.77273	C7001735°:gi 7768636 db  BAA95483.1  (AB	3.0
	413266	BE300352	na.//2/3	Human glucose transporter pseudogene gb:600944231F1 NIH_MGC_17 Homo sapiens c	3.0
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	3.0 3.0
	415337	Z44881	Hs.9012	ESTs, Wealdy similar to S26650 DNA-bindi	3.0

	445044	44440400			
	415044	AA419108	Hs.77840	annexin A4	2.9
	403469	44400		Target Exon	2.9
	416928	AA190573	Hs.85902	ESTs, Weakly similar to MCHU calmodulin	2.9
5	430195	AW969308	Hs.188594	ESTs	2.9
3	458544	A1631036	Hs.196843	ESTs .	29
	440667	BE076969	Hs.7337	hypothetical protein FLJ 10936	29
	424641	AB001106	Hs.151413	glia maturation factor, bela	2.9
	428820	AA436187	Hs.172631	integrin, elpha M (complement component	2.9
10	405403	*******		Target Exon	29
10	452197	AW023595	Hs.232048	ESTa	29
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp762O2215 (1	29
	423479	NM_014328	Hs.129208	death-associated protein kinase 2	29
	404559			Target Exon	2.9
15	406270			Target Exon	2.9
15	422190	H17399	Hs.11506	Human clone 23589 mRNA sequence	2.9
	431300	AA502346		gb::ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	29
	420286	A1796395	Hs.111377	ESTs	2.9
	422964	AW439476	Hs.256895	ESTs	29
20	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	29
20	428595	AB037795	Hs.186547	KIAA1374 protein	2.9
	402198			NM_024323:Horno sapiens hypothetical prot	29
	416246	U47413	Hs.79101	cyclin G1	2.9
	427593	AK001132	Hs.179752	Homo sapiens cDNA FLJ 10270 fis, clone HE	2.9
25	446351	AW444551	Hs.35380	x 001 protein	2.9
25	440432	AI239637	Hs.202653	ESTs, Weakly similar to T14267 Xin prote	2.9
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	2.8
	400965			C11002190":glj12737279 ref XP_012163.1	2.8
	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	2.8
20	458793	N80159	Hs.121849	microtubule-associated proteins 1A/1B (i	2.8
30	406810	U82275	Hs.94498	teukocyte immunoglobulin-like receptor,	2.8
	445577	N40596	Hs.137054	cytoplasmic polyadenylation element bind	2.8
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	2.8
	418745	AW882645	Hs.88044	sprouty (Orosophila) homolog 1 (antagoni	2.8
25	433095	AK001092	Hs.302480	Homo sapiens cONA FLJ 10230 fis, clone HE	2.8
35	425580	L11144	Hs.1907	galanin	28
	416233	AA176633		gb:zp13g01.s1 Stratagene fetal retina 93	2.8
	438219	AI916151	Hs.257194	ESTs .	2.8
	404661			C9000306*:gij12737280 ref XP_006682.2  k	28
40	435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	28
40	423665	BE167153	Hs.24380	ESTs	2.8
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	2.8
	401783			NM_003771*:Homo sepiens keratin, hair, a	2.8
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	2.8
45	447271	AL041747	Hs.170261	EST6	2.8
45	438913	AJ380429	Hs.172445	ESTs	2.8
	441962	AW972542	Hs.289008	Horno sapiens cDNA: FLJ21814 fis, clone H	2.8
	444385	BE278964	Hs.11085	CGI-111 protein	2.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.8
FΛ	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	2.8
50	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	2.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.8
	439556	AI623752	Hs.163603	ESTs	2.8
	405474			NM_001093*:Homo sapiens acetyl-Coenzyme	28
55	426208	Al370379	Hs.132216	ESTs	2.8
55	419461	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	28
	428501	AL041162	Hs.98587	ESTs	2.8
	413427	U31120	Hs.845	interleukin 13	2.8
	433109	N58907	Hs.162430	EST	28
60	427974	BE093023	Hs.188767	ESTs	2.8
60	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.8
	453994	BE180964	Hs.165590	ribosomal protein S13	2.8
	459171	AW967801	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	2.8
	404845			C22000163":gij10242166jgbjAAG15318.1jAF2	2.8
65	408182	AA047854		gb:z149g04.r1 Soares retina N2b4HR Homo	2.8
65	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	2.7
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.7
	432815	Z30045	Hs.293676	ESTs	2.7
	404035			Target Exon	2.7
70	418157	W99382	Hs.283709	lipopolysaccharide specific response-7 p	2.7
70	426403	NM_000361	Hs.2030	thrombomodulin	2.7
	439659	AW970780	Hs.59483	Homo sapiens cDNA FLJ14471 fis, clone MA	2.7
	443932	AW888222	Hs.9973	tensin	2.7
	444930	BE185536	Hs.301183		2.7
75	419269	AA235838		gb:zs41b04.s1 Soares_NhHMPu_S1 Homo sapi	2.7
75	416004	D11880	Hs.299254		2.7
	430371	D87466	Hs.240112		2.7
	449117	AW449310	Hs.210262		27
	451007	H38108	Hs.32759	ESTs	2.7
00	421202	AF193339	Hs.102506		2.7
80	406308			NM_025192:Homo saptens hypothetical prot	2.7
	413208	BE071799		gb:RC0-BT0522-071299-011-b10 BT0522 Homo	27
	421420	AI024236	Hs.123296	ESTs, Weakly similar to PEC1_HUMAN PLATE	2.7
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	2.7
				·	

	452351	AA025647		gb:zeB5d01_r1 Scares_letal_heart_NbHH19W	2.7
	410538 448072	AW753115 AI459306	Hs.24908	gb:PM0-CT0248-131099-001-h12 CT0248 Homo ESTs	2.7
	420912	AW853156	Hs.90787	ESTS	2.7 2.7
5	453830	AA534296	Hs.20953	ESTS	2.7
	457791	AW117431	Hs.191906	ESTs	2.7
	417735	AA188175	Hs.82506	KIAA1254 protein	2.7
	411773 417076	NM_006799 AW973454	Hs.72026	protease, serine, 21 (testisin)	2.7
10	436476	AA326108	Hs.238442 Hs.33829	ESTs, Moderately similar to ALU7_HUMAN A bHLH protein DEC2	2.7
	440945	AW505345	Hs.7540	f-box and leucine-rich repeat protein 3A	2.7 2.7
	425826	U97698		mucin 6, gastric	27
	422795	AB033109	Hs.120866	KIAA1283 protein	2.7
16	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo saplens	2.7
15	414272	AI651603	Hs.46988	ESTs	2.7
	418047 421089	R37633 AB037771	Hs.4847 Hs.101799	ESTs KIAA1350 protein	2.7
	419763	AI039691	Hs.127486	ESTs	2.7 2.7
	459265	AJ003616		gb:AJ003816 Selected chromosome 21 cDNA	27
20	410970	AW812151		gb:RC5-ST0178-081099-011-A06 ST0178 Homo	2.7
	401925	N98378		sialyltransferase 1 (beta-galactoside al	2.7
	418504 433789	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	2.6
	418308	AA220977 AA215738	Hs.182514	gb:zr01a08.r1 Stratagene NT2 neuronal pr ESTs, Wealdy similar to A46010 X-limked	26 26
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO	26
	406299			Target Exon	2.6
	422963	M79141	Hs.13234	ESTs	2.6
	441244	BE612935	Hs.184052	PP1201 protein	2.6
30	439954 405088	AL046748	Hs.6790	DnaJ (Hsp40) homolog, subfamily 8, membe	2.6
50	404741			Target Exon Target Exon	2.6
	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.6 2.6
	439103	AF085959	Hs.38705	ESTs	26
26	437241	AL137318	Hs.306450	Homo sapiens mRNA: cDNA DKFZp434L171 (fr	2.6
35	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	2.6
	457394 427229	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.6
	414630	A1799751 BE410857	Hs.5635 Hs.16064	ESTs gb:601301177F1 NIH_MGC_21 Homo sapiens c	2.6
	406744	AA554082	Hs.279860	turnor protein, translationally-controlle	2.6 2.6
40	443984	AJ424415	Hs.143719	ESTs	26
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	2.6
	421709	AA159394	Hs.107056	CEO-6 protein	2.6
	426747	AA535210	Hs.171995	kalikrein 3, (prostate specific antigen	2.6
45	439480 419567	AL038511 AW339890	Hs.125316 Hs.128187	ESTs, Wealdy similar to S33990 finger pr ESTs	2.6
	421922	AW295043	Hs.109590	genethonin 1	2.6 2.6
	421859	AA356620	Hs.108947	KIAA0050 gene product	2.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.6
50	444843	AA400172		gb:zu69e01.r1 Soares_testis_NHT Homo sap	2.6
30	416729 439238	U46165	Hs.1027	Ras-related associated with diabetes	2.6
	4391B3	N47305 AW970600	Hs.302161 Hs.303261	ESTs ESTs	2.6
	408739	W01556	Hs.238797	ESTs, Moderately similar to 138022 hypot	2.6 2.6
	412061	AA833763	Hs.330211	ESTs	2.6
55	432114	AL036021	Hs.8934	EST\$	2.6
	425337	AA355442	Hs.169054	ESTs	2.6
	424299 448871	AK000377	Hs.82294	homolog of mouse C2PA	2.6
	414516	BE616709 Al307802	Hs.159265 Hs.135560	kruppel-related zinc finger protein hcKr ESTs, Weakly similar to T43458 hypotheti	2.6 2.6
60	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	26
	410429	AA310600	Hs.63657	peptide:N-glycanase similar to yeast PNG	2.6
	449251	AW151660	Hs.31444	ESTs	2.6
	436546	AW023329	Hs.132743	EST8	2.6
65	450546 437255	AA010200 R58970	Hs.175551	ESTs ESTs	2.6
03	409041	AB033025	Hs.9887 Hs.50081	Hypothetical protein, XP 051860 (KIAA119	2.6 2.6
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	2.5
	413341	H78472	Hs. 191325	ESTs, Weakly similar to T18967 hypotheti	2.5
70	423763	R98203	Hs.132724		2.5
70	413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo	2.5
	415590 406215	T74068	Hs.170081	gb:ye81f07.r1 Soares infant brain 1NIB H	2.5
	453938	AF082569	Hs.36794	Target Exon  D-type cyclin-interacting protein 1	2.5
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	2.5 2.5
75	442097	AW015799	Hs.128474		25
	456650	AA620501	Hs.106773	ESTs, Weakly similar to T42689 hypotheti	2.5
	413231	D87461	Hs.75244	BCL2-like 2	2.5
	457 <b>2</b> 97 444942	AW968188	LL 202007	gb:EST380383 MAGE resequences, MAGJ Homo	25
80	425764	AW293458 AW996009	Hs.283807 Hs.112572	chromosome 11 open reading frame 16 Homo sepiens cDNA FLJ14130 fis, clone MA	25
	435712	AA694607	Hs.176956		2.5 2.5
	436624	T64297		faity acid binding protein 1, liver	2.5
	443155	R54485	Hs.23772	ESTs	2.5
				216	

	425907	AA365752	Hs.155965	ESTs	2.5
	414759	AW295157	Hs.47587	ESTs	2.5
	414699	AI815523	Hs.76930	symuclein, alpha (non A4 component of am	2.5
5	411426 404492	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	25
•	425153	AW023193	Hs.27046	C8000067":gi 10432400 emb CAC10290.1  (A ESTs	25 25
	426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/Hs) box polypep	25
	434803	AW974640	Hs.303413	ESTs	2.5
10	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.5
10	433069 428054	X76732 AI948688	Hs.3164 Hs.266619	nucleobindin 2 ESTs	2.5
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	25 25
	456972	AI054347	Hs.2017	ribosomal protein L38	25
	431405	Al470895	Hs.334895	ribosomal protein L10a	2.5
15	427982	NM_016156	Hs.181326	KIAA1073 protein	2.5
	412831 437114	AA121352 AA836641	Hs.143314 Hs.163085	ESTs ESTs	25
	426157	AA370977	Hs.345728	STAT induced STAT inhibitor 3	2.5 2.5
••	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	25
20	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	2.5
	453572	AA382590	Hs.46366	KIAA0948 protein	2.5
	TABLE 23	<b>B</b> :			
25	Pkey:		ue Eos probes	et identifier number	
	CAT numb	er: Geni	duster numb	er er	
	Accession	: Gent	pank accessio	n numbers	
	Pkey	CAT Number	Accession		
30	408182	104479_1		AA057506 AA053841	•
	409856	1156268_1	AW502082	AW502979 AW502807 AW501876	
	410509	1206699_1		AW752404 H43469	
	410538 410786	1207341_1		AW753113 R45779	NAS.48A
35	410788	1221063_1 1228131_1		AW803280 AW803275 AW803415 AW803343 AW8 AW812186 AW812166	\$03422
	411426	1245515_1		AW845993 AW845989	
	411906	1265204_1	AW875765	H50294 AW875444	
	412636	13165_1			723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413
40			AW849074	AW997139 AW799304 AW799309 BE077020 BE07	77017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985
70			AW607238	AW177700 AW377699 RE082626 RE082606 RE082606	0253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 2507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516
			AW265328	AW847678 AW847688 AW365151 AW365148 AW3	365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145
			BE001925	BE182166 BE144243 BE001923 AI951766 AI434511	8 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488
45					1128 AA337270 AA340777 AW384371 AA852212 RS8704 AW366566 AW364859
43			AA025851	AA025852 AA455100 AA719958 AW352220 AW996	5245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690
					H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 34 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592
					8 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181
50			BE 167165	N84767 H27408 H30146 AI190590 C03378 AI55440	03 Al205263 AA 128470 Al392926 AF 139065 AW370813 AW370827 AW798417
50			AW798780	AW798883 AW798569 R33557 AA149190 C03029	AW177783 AA088866 AW370829 AA247685 BE002273 AJ760816 AJ439101 AW879451
			A17009637	VAA51923 A1340326 A1590975 148793 A1568096 A11 A1417643 A1306664 A1696960 A16689003 A14400666	142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 5 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383
			Al270345	M417012 M300334 M300003 M300032 AVI 13033 M021347 AW166807 AW105614 AI346078 AA5523	300 W95070 Al494069 Al911702 AA149191 AA026864 Al830049 Al887258 AW780435
			Al910434	N819984 AI858282 AI078449 AI025932 AI860584 AI	N635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892
55			T87181 AA	.782066 AW243815 AW150038 AW268383 AW0046	533 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182
	•				362 Al498487 Al348053 Al783914 H44405 AW799118 AA128330 AA515500 AA918281
	413208	1353610 1		905927 AA022701 W38382 R20795 T77861 AW860 BE071804 BE071798	0878
	413266	1356260_1		BE299274 BE075351 BE297444	
60	413282	1358147_1		BE078276 BE078163 BE078277 BE078279 BE0781	158
	413493	1373555_1	BÉ 144444		
	415606 415666	1540470_1 1543492_1	W70022 R	35201 F12763 T74725 H63485 Z45782 H61126	
	416233	158010_1		)8673 H72694 F20990 R08580 AW961842 AA309418	
65	419269	183444_1		BE180775	
	419386	184356_1	AA236867	AA237066 AA354236 AW957759 H08961	
	425826	25682_1	U97698 AV	N815264 AI791966 AI732669 AAS88236 AI521662 A	AIB04760 AI955717 AW292169 AI468227 AI420483 AA603459 AI868225 AI919551
	431300 433789	331217_1 37421_1		BE159863 AF091029 AA701227	•
70	433921	377350_1		A1114549 R36464 R36465	
	436624	4237_5			T53219 T48785 T64166 AA706930 R29813 T55913 T56518 T64679 R29666 M10617
		_	A1768596	AA101894 W90338 A1742193 AW752206 AA099433	3 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121
	444545		AW842284		
75	444843 445797	62260_1		AA400146 AV651691	
, ,	447135	650943_1 70963_1		Al366014 R34822 NS16579 AW059603	
	449901	818599_1	AI574072		
	450928	851593_1	AI744417	R91614 H77365	
80	452351	91233_1		R45716 AW753786	•
50	455040 456235	1250028_1 168686_1		5 AW851934 AW852096 AW852274 AA832266 H67452	
	457297	313764_1		AA632266 A67432 3 AA468196 AA468269 AA468298	
	459265	966590_1		AJ003654 AJ003617	

TABLE 23C: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. 5 Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Strand: Nt_position: Pkey Strand Nt position 10 7770576 7534110 173043-173564 71055-71259 400965 Minus 401507 Ptus 4388746 7249190 401600 27363-27518,28727-28891,29526-29731 Minus 139369-139827, 140509-140591, 140834-140990, 141496-141657, 141757-141882, 142063-142283 138252-138469, 140239-140364, 140437-140598, 141037-141193, 141925-142007, 142787-143230 401783 Phrs Minus 15 402198 8576116 Plus 402364 9454515 54983-55240,56507-56785,56982-57365 Minus 402429 9796372 7210003 Minus 57622-57793,59282-59402,59624-59827 174560-175270 403442 Plus 9929739 9966615 Minus Minus 4831-7707 12450-12753 403469 20 403488 7656757 7710561 403512 114487-114610 403890 83165-83350 Plus 404036 404091 65247-67529,112537-114863 7584554 Minus 82121-83229 137948-138024,138111-138300 25 404333 404492 9802821 Minus 8123400 Minus 138612-138803 73499-73651,89575-89739 8748893 9212936 9797073 404559 404606 Minus Minus 22310-23269 33374-33675,33769-34008 404661 Plus 30 143025-143467 47174-47326.52928-53146.53312-53602 404741 8574139 Plus 404845 7958980 Minus 405088 8072518 2642452 Minus 405354 Plus 52213-53089 6850244 8439781 405403 37491-37670,40951-41031 35 405474 Plus 172005-172175 405586 38810-39017 5002511 405670 4662655 4589984 Plus 96543-96870 405674 Plus 68302-68429 18665-18843 310-432 406085 9123888 Ptus 40 406215 7342161 Plus 7534217 5686278 406270 13136-13591 406299 Minus 35655-36119 406308 9211532 358408-358651 45 TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrio/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 7.5° percentile amongst various glioblastoma tumors. The "average" normal adult tissue lavel was set to the 85° percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was exclusived. 50 before the ratio was evaluated. Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title UnigenetD: 55 Unigene Title: R1: Ratio of 75th percentile tumor to 85th percentile normal body tissue UnigenelD Hs.2868 Pkey 431917 Unigene Title peripheral myelin protein 2 protein kinase C binding protein 2 SRY (sex determining region Y)-box 2 D16181 75.2 74.6 60 427343 455601 AI880044 Hs.176977 A1368680 Hs.816 428321 AI699994 Hs.2868 peripheral myelin protein 2 412719 AW016610 Hs.129911 70.7 449494 415817 AW237014 Homo sapiens cDNA: FLJ23075 fis. clone L Hs.315369 66.3 64.3 Homo sapiens CDNA: FLUXBY7a ns, cone L protein tyrosine phosphatase, receptor-t solute carrier family 1 (gliat high affi delta (Drosophila)-like 3 Homo sapiens mRNA: cDNA DKFZp761C1712 (I NK-2 (Drosophila) homolog B 65 U88967 BE242870 Hs.78867 Hs.75379 413472 60.1 52.3 456759 435147 BE259150 Hs.127792 AL133731 Hs.4774 Hs.159623 425842 412733 AI587490 40.1 39.0 70 NA-2 (Urosopraja) nominog 8 KIAA0080 protein synaptosomal-associated protein, 25kD SRY (sax determining region Y)-box 11 Homo sapiens mRNA; cDNA DKFZp761J1324 (I fibroblast growth factor 1 (acidic) catenin (cadherin-associated protein), d AA984472 Hs.74554 Hs.84389 418375 NM_003081 38.7 37.2 1123752 453392 Hs.32964

Homo sapiens cDNA FLJ20099 fls, clone CO

myelin-associated oligodendrocyte basic

hypothetical protein FLJ12015 ESTs

achaete-scute complex (Orosophila) homol

36.8 32.8

31 B

30.9

30.4

30.2

28.3

26.9 25.9

423849

413333 416829

431941 436878

426325

425057

446711

439415

430838

75

80

AL157425

M74028 AB013805

AK000106 BE465204

D28114

FASS 38

N46664

M85835

AAB26434

AF169692

Hs.133315

Hs.75297

Hs.80220

Hs.272227

Hs.4744B

Hs. 1619

Hs.12450

Hs.12825

Hs.169395

Hs.12827

Hs.169309

FSTs

ESTS

protocadherin 9

	447004	414400000			
	447004 424581	AW296968 M62062	Hs.157539 Hs.150917	ESTs	25.3
	452744	AI267652	Hs.30504	catenin (cadherin-associated protein), a Homo sapiens mRNA; cDNA DKFZp434E082 (fr	24.8 24.8
_	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.3
5	453642	Al370936	Hs.34074	dipentidylpeptidase VI	24.3
	424140 450133	Z48051 AW969769	Hs.141308 Hs.105201	myelin oligodendrocyte głycoprotein ESTs	24.2
	408562	A1436323	Hs.31141	Homo saplens mRNA for KIAA1568 protein,	24.2 23.3
••	448672	AI955511	Hs.225106	ESTs	22.7
10	435708	Al362949	Hs.75169	ESTs .	22.0
	407034 407168	U84540 R45175	1- 117103	gb:Human dystrobrevin isoform DTN-3 (DTN	21.9
	431019	NM_005249	Hs.117183 Hs.2714	ESTs forkhead box G1B	21.7 21.5
	409049	Al423132	Hs.146343	ESTs	21.4
15	433896	AW294729	Hs.274461	EŞTS	21.1
	445041	T64183	Hs.282982	solute carrier	21.0
	418738 444378	AW388633 R41339	Hs.6682 Hs.12569	solute cerrier family 7, (cetionic emino ESTs	20.4
	411305	BE241596	Hs.69547	myelin basic protein	20.0 19.9
20	437414	AW894071	Hs.48448	hypothetical protein OKFZp547C176	19.8
	441016	AW138653	Hs.25845	ESTs	19.6
	440435 438209	AL042201 AL120659	Hs.21273 Hs.6111	transcription factor NYD-sp10	18.5
	452461	N78223	Hs.108106	aryi-hydrocarbon receptor nuclear transi transcription factor	18.4 18.1
25	409395	U46745	Hs.54435	dystrobrevin, alpha	18.1
	417183	R52089	Hs.172717	ESTs	18.0
	409638 428392	AW450420 H10233	Hs.21335 Hs.2265	ESTs	18.0
	449611	AJ970394	Hs.197075	secretory gramule, neuroendocrine protei ESTs	18.0 17.0
30	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	16.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9
	444471 421659	AB020684 NM_014459	Hs.11217	KIAA0877 protein protocadherin 17	16.8
	431725	X65724	Hs.106511 Hs.2839	Nome disease (pseudoglioma)	16.7 15.6
35	429276	AF056085	Hs.198612	G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
	441440 449433	AI807981 AI672096	Hs.30495	ESTs	15.7
	421264	AL039123	Hs.9012 Hs.103042	ESTs, Weakly similar to S26650 DNA-bindi microtubule-associated protein 18	15.7 15.5
40	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885	Hs.117183	ESTs	15.1
	424945	AI221919	Hs.173438	hypothetical protein FLJ 10582	14.9
	447414 426269	D82343 H15302	Hs.18551 Hs.168950	neuroblastoma (nerve tissue) protein Homo sapiens mRNA; cDNA DKF2p566A1046 (I	14.9
45	416857	AA188775	Hs.292453	ESTs	14.8 14.7
	419721	NM_001650	Hs.288650	aqueporin 4	14.6
	411078	AJ222020	Hs.182364	CocoaCrisp	14.4
	453924 409389	R49295 AB007979	Hs.24886 Hs.301281	ESTs Homo sapiens mRNA, chromosome 1 specific	14.4
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	14.3 14.1
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266 412986	N59006	Hs.26133	ESTs	14.0
	424790	X81120 AL119344	Hs.75110 Hs.13326	cannabinoid receptor 1 (brain) ESTs, Wealdy similar to 2004399A chromos	14.0
55	439239	AI031540	Hs.235331	ESTs	14.0 14.0
	441497	R51064	Hs.23172	ESTs	14.0
	445495	BE622641	Hs.38489	ESTs, Weakly similar to (38022 hypotheti	14.0
	414245 429900	BE148072 AA460421	Hs.75850 Hs.30875	WAS protein family, member 1 ESTs	13.7
60	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6 13.6
	449605	AW138581	Hs.198416	ESTs	13.6
	452526 420547	W38537	Hs.280740	hypothetical protein MGC3040	13.6
	441350	AF155140 AB020690	Hs.98738 Hs.7782	gonadotropin-regulated testicular RNA he paraneoplastic antigen MA2	13.3
65	420077	AW512260	Hs.87767	ESTs	13.3 13.2
	424120	T80579	Hs.290270	ESTs	13.2
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	13.2
	423361 428409	AW170055 AW117207	Hs.47628 Hs.98523	ESTs ESTs	13.1
70	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	12.9 12.6
	451621	A1879148	Hs.26770	fatty acid binding protein 7, brain	12.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
	436954 430691	AA740151 C14187	Hs.130425 Hs.103538	ESTs ESTs	12.4
75	433551	AI985544	Hs.12450	protocadherin 9	12.4 12.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	12.2
	427540	R12014	Hs.20976	ESTs .	12.1
	435624 415849	AF218942 R20529	Hs.24889	formin 2	12.1
80	428845	AL157579	Hs.6806 Hs.153610	ESTs KIAA0751 gene product	12.1 11.9
	442671	AI005668	Hs.134779	EST	11.9
	444396	T65213	Hs.4257	ESTs	11.8
	452752	AW044058	Hs.33578	KIAA0820 protein	11.8

				•	
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
•	428976	AL037824	Hs.194695	ras homolog gene family, member I	11.6
5	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	11,6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	11.6
	414214	D49958	Hs.75819	glycoprotein M6A	11.5
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11,5
10	405238			_	11.4
10	420362	U79734	Hs.97206	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs.169309	myelin-essociated oligodendrocyte basic	11,4
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
	451952	AL120173	Hs.301663	ESTs	11.3
15	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-Q-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTS	11.3
	429918	AW873986	Hs.119383	ESTs	11.3
	443912	R37257	Hs.184780	ESTs	11.3
20	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092	AA814043	Hs.88045	ESTA	
	408081	AW451597	Hs.167409	ESTs	11.2 11.2
	411642	NM_014932	Hs.71132	neuroligin 1	
	415170	R44386	Hs.164578	ESTs	10.9
25	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.9
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein.	10.8
	423853	AB011537	Hs.133466	stit (Drosophila) homotog 1	10.8
	400293	N51002	Hs.306480		10.7
30	447773	AI423930	Hs.36790	Homo sapiena mRNA; cDNA DKFZp761E2112 (1	10.7
	448321	NM_005883	Hs.20912	ESTs, Weakly similar to putative p150 (H	10.7
	448533	AL119710	Hs.21365	adenomatous polyposis coli like nucleosome assembly protein 1-like 3	10.5
	440684	AI253123	Hs.127356		10.5
	444017	U04840	Hs.214	ESTs. Highly similar to S21424 nestin [H	10.3
35	438380	T06430	Hs.6194	neuro-oncological ventral antigen 1	10.3
	440471	AA886146	Hs.307944	chondroitin sutfate proteoglycan BEHAB/b ESTs	10.3
	413063	AL035737	Hs.75184		10.2
	439978	BE139460	Hs.124673	chitinase 3-like 1 (cartilage glycoprote	10.1
	448902	Z45998	Hs.22543	Homo sapiens cDNA FLJ11477 fis, clone HE	10.1
40	424932	R14070	Hs.315369	Homo saplens mRNA; cDNA DKFZp76111912 (I	10.1
	431721	AB032996	Hs.268044	Homo sapiens cDNA: FLJ23075 fis, clone L	9.9
	419088	AI538323	Hs.52620	KIAA1170 protein	9.9
	420602	AF060877		integrin, beta 8	9.8
	436511	AA721252	Hs.99236	regulator of G-protein signalling 20	9.8
45	414696	AF002020	Hs.291502	ESTs	9.8
1.5	449539	W80363	Hs.76918	Niemann-Pick disease, type C1	9.7
	412959	D87458	Hs.58445	ESTs	9.7
	412811	H06382	Hs.75090	KIAA0282 protein	9.6
	449300	AI656959	Hs.21400	ESTs	9.6
50	426344	H41821	Hs.222165	ESTs	9.6
•	419271	N34901	Hs.322469	transcriptional activator of the c-fos p	9.5
	419078		Hs.238532	ESTs	9.5
	451516	M93119	Hs.89584	insulinoma-associated 1	9.4
	422656	AI800515	Hs. 12024	ESTs	9.4
55	449318	AI870435	Hs.1569	LIM homeobox protein 2	9.3
55	414175	AW236021 Al308876	Hs.78531	Homo sapiens, Similar to RIKEN cONA 5730	9.3
	415279	F04237	Hs.103849	hypothetical protein DKFZp761D112	9.3
	428784	Y12851	Hs.1447	glial fibrillary acidic protein	9.2
	429903	AL134197	Hs.193470	purinergic receptor P2X, ligand-gated to	9.2
60	424541	AB001106	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
	417435	NM_005181	Hs.151413	glia maturation factor, beta	9.1
	449448	D60730	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	408508	AI806109	Hs.57471	ESTs	9.1
	452785	AL359942	Hs.135736	KIAA1580 protein	9.0
65	448986	H42169	Hs.296434	erythroid differentiation and denucleati	9.0
05	447072		Hs.18653	hypothetical protein FLJ14627	8.9
	433800	D61594 Al034361	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	408926		Hs.135150	lung type-I cell membrane-associated gly	8.9
		AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
70	449625 400292	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
, ,		AA250737	Hs.72472	ESTs .	8.7
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	8.7
	420345 429927	AW295230	Hs.25231	ESTS	8.7
		NM_001115	Hs.2522	adenylate cyclase 8 (brain)	8.7
75	437528	N59646 AD002276	Hs.169745	crumbs (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs_25954	interleukin 13 receptor, alpha 2	8.6
	400780	A A D 4 4 2 2 2	11- 4		8.6
	434891	AA814309	Hs. 123583	ESTs	8.6
80	449277	AA001064	Hs.172976	ESTs	8.6
55	415709	AA649850	Hs.278558	ESTs	8.5
	439947	A8006627	Hs.6788	astrotación	8.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	8.4

	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	8.4
	452785	R61362	Hs.106642	ESTs. Weakly similar to T09052 hypotheti	8.4
	415798 426271	R87548 AF026547	Hs.78854	ATPase, Na+/K+ transporting, beta 2 poly	8.3
5	408947	AL080093	Hs.169047 Hs.49117	chondroitin sulfate proteoglycan 3 (neur	8.3
•	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp564N1662 (I Homo sapiens mRNA; cDNA DKFZp761D191 (tr	8.3
	433447	U29195	Hs.3281	neuronal pentraxin ()	8.3 8.3
	431467	N71831	Hs.258398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	8.3
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
10	414300	AJ304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
15	429007	080642		gb:HUM092E098 Human fetal brain (TFujiwa	8.1
13	442710 425048	AI015631	Hs.23210	ESTs	8,1
	429149	H05468 AW193360	Hs.164502 Hs.197962	ESTs	8.1
	445740	T78281	Hs.13226	ESTs, Wealtly similar to 138022 hypotheti Homo sapiens clone 25181 mRNA sequence	8.0
	418771	AAB07881	Hs.25329	ESTs	8.0
20	422728	AW937826	Hs.103262	ESTs, Wealdy similar to ZN91_HUMAN ZINC	7.9 7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neuroliain	7.9
	455384	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
25	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
25	435501	AW051819	Hs.129908	KIAA0591 protein	7.8
	423500	AI633559	Hs.310359	ESTs	7.8
	450625 415314	AW970107	U- 5400	gb:EST382188 MAGE resequences, MAGK Homo	7.8
	420036	N88802 R60336	Hs.5422	glycoprotein M6B	7.7
30	427687	AW003867	Hs.52792 Hs.1570	Homo sapiens mRNA; cDNA DKFZp586I1823 (I	7.7
-	449328	AI962493	Hs.197647	histamine receptor H1 ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.7 7.7
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
35	438779	NM_003787	Hs.6414	nucleolar protein 4	7.6
	433532	AW975357		gb:EST387475 MAGE resequences, MAGN Homo	7,6
	448555	AI536697	Hs.159863	ESTs .	7.5
	439662	H97552	Hs.269060	ESTs .	7.5
40	448543	AW897741	Hs.21380	Homo sepiens mRNA; cDNA DKFZp586P1124 (f	7.5
40	410099	AA081630	Hs.169387	KIAA0036 gene product	7.5
	431592 409731	R69016 AA125985	Hs.213194	hypothetical protein MGC10895	7,4
	405819	AA 123303	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	407886	AW969688	Hs.100826	ESTs	7.4
45	437416	AL359605	Hs.283851	Homo sapiens mRNA; cDNA DKF2p547G036 (fr	7.4
	437698	R61837	Hs.7990	ESTs. Moderately similar to 184505 catci	7.4 7.4
	408604	D51408	Hs.21925	ESTs	7.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
60	447499	AW262580	Hs.147674	protocadherin beta 16	7.3
50	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.2
	410037	AB020725	Hs.58009	KIAA0918 protein	7.2
	419318 424051	AW969742	Hs.291005	ESTs	7.2
55	442026	AL110203 AI243749	Hs.138411 Hs.8074	Homo sapiens mRNA; cDNA OKFZp586J1922 (f	7.2
	448243	AW369771	Hs.52620	brain-specific anglogenesis inhibitor 3 Integrin, beta 8	7.2
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	7.2
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	7.2 7.2
<b>~</b> ^	407182	AA312551	Hs.230157	ESTs	7.1
60	415293	R49462	Hs.106541	ESTs	7.1
	422764	AI767727	Hs.47522	ESTs .	7.1
	451592	AI805416	Hs.213897	ESTs	7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0
65	415734 434149	NM_014747 Z43829	Hs.78748	KIAA0237 gene product	7.0
V.	436726	AA324975	Hs.19574 Hs.128993	hypothetical protein MGC5469 ESTs. Wealdy similar to T00079 hypotheti	7.0
	417632	R20855	Hs.5422	glycoprotein M68	7.0
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	7.0
	435267	N23797	Hs.110114	ESTs	6.9 6.9
70	437117	AL049256	Hs.122593	ESTs	6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
	445745	AB007924	Hs.13245	KIAA0455 gene product	6.9
75	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.9
, ,	428588	F12101	Hs. 185701	Homo sapiens mRNA full length insert cDN	6.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	6.8
	447342 443297	Al199268 Al049864	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.7
	443992	AI049864 AW022228	Hs.133029 Hs.322922	ESTs ESTs	6.7
80	453096	AW294631	Hs.11325	ESTs ESTs	6.7
-	453857	AL080235	Hs.35861	DKFZP586E1621 protein	6.7 6.7
	443761	AI525743	Hs.160603	EST\$	6.6
	429509	AF002246	Hs.210863	cell adhesion molecule with homology to	6.6
				••	

	125055	411000000		-1 1	
	435056 453431	AW023337 AF094754	Hs.5422 Hs.32973	glycoprotein M68 glycine receptor, beta	6.5
	444190	AI878918	Hs. 10526	cysteine and glycine-rich protein 2	6.5 6.5
_	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.5
5	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805	L10333	Hs.99947	reficulon 1	6.4
	429125 435256	AA446854 AF193766	Hs.271004 Hs.13872	ESTs, Wealthy similar to 138022 hypotheti cytokine-like protein C17	6.4
	407866	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.4 6.3
10	440700	AW952281	Hs.296184	guarine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
	445102 452401	AW204610 NM_007115	Hs.22270 Hs.29352	ESTS	6.2
15	435538	AB011540	Hs.4930	turnor necrosis factor, alpha-induced pro low density lipoprotein receptor-related	8.2 6.2
	410102	AW248508	Hs.279727	Homo saplens cDNA FLJ14035 fis, clone HE	6.2
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
20	419347 424997	C15944 AL138167	Hs.90005 Hs.96920	superiorcervical ganglia, neural specifi ESTs	6.1
~~	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1 6.1
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	6.1
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.1
25	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
23	425517 427457	AF121179 AW779105	Hs.164682	gb:AF121179 Homo sepiens liver (Chang L- ESTs	6.0
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GC81 Homo saplens	6.0 6.0
	444170	AW613879	Hs.102408	ESTs	6.0
30	457183	H91882	Hs.118569	DVI-binding protein IDAX (inhibition of	6.0
30	448999 454048	AF179274	Hs.22791	transmembrane protein with EGF-like and ESTs	6.0
	439772	H05626 AL365406	Hs.6921 Hs.10268	Homo sapiens mRNA full length insert cON	6.0 5.9
	448944	AB014505	Hs.22599	strophin-1 interacting protein 1; activi	5.9
25	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
35	415486	H12214	Hs.13284	ESTs, Wealthy similar to 2109260A B cell	5.9
	438993 447350	AA828995 AI375572	Hs.172634	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9 5.9
40	447101	N72185	Hs.44189	ESTs	5.9
40	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.9
	438461 418064	AW075485 BE387287	Hs.286049 Hs.83384	phosphoserine aminotransferase S100 calcium-binding protein, beta (neur	5.9
	437035	AI571514	Hs.133022	ESTs	5.8 5.7
45	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Hamo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218 445828	AF070641 F05802	Hs.10684 Hs.81907	Homo sapians clone 24421 mRNA sequence ESTs	5.7
	447198	D81523	Hs.283435	ESTs	5.7 5.7
50	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7
	443672 412155	AA323362 R38167	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	5.6
	435718	R06569	Hs.12449 Hs.269534	Homo sapiens transmembrane protein HTMP1 ESTs	5.6 5.6
55	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996 422411	AW514021 AW749443	Hs.245510	ESTs	5.6
	438328	Al492261	Hs.22511 Hs.32450	EST8 ESTs	5.6 5.6
60	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	5.5
	418677 400859	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
	413625	AW451103	Hs.71371	ESTs	5.5
65	421863	AI962677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.5 5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702 452055	AI879064	Hs.54618	ESTs	5.5
	430979	AJ377431 AJ479755	Hs.141693 Hs.129010	hypothetical protein MGC10858 ESTs	5.5
70	412709	AL022327	Hs.74518	KIAA0027 protein	5.5 5.5
	439920	H05430	Hs.288433	neurotrindn	5.5
	424343	AW956360	Hs.4748	adenylata cyclase activating polypeptide	5.4
	407846 419235	AA426202 AW470411	Hs.40403 Hs.288433	Cbp/p300-interacting transactivator, wit	5.4
75	418030	BE207573	Hs.83321	neurotrimin neuromedin 8	5.4 5.4
-	410330	AW023630	Hs.46786	ESTs	5.4 5.4
	410781	A1375672	Hs.165028	ESTs	5.4
	420658 421308	AW965215	Hs.336656		5.4
80	443740	AA687322 R56434	Hs.192843 Hs.21062	leucine zipper protein FKSG14 ESTs	5.4
	426457	AW894667	Hs.169965		5.4 5.4
	450375	AA009647	Hs.8850	8 disintegrin and metalloproteinase doma	5.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4

	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.4
	424432	AB037821	Hs.146858	protocadherin 10	5.4
	429250 443785	H56585 AW449952	Hs.198308	tryptophan rich basic protein	5.4
5	435282	R91913	Hs.190125 Hs.272104	basic-helix-loop-helix-PAS protein	5.4
_	404584	10.513	113.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4 5.3
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	5.3
• •	424001	W67883	Hs.137476	paternally expressed 10	5.3
10	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	5.3
	426625	T78300	Hs.300642	serologically defined colon cancer antig	5.3
	428137	AA421792	Hs_170999	EST8	5.3
	428679 438176	AA431765 AW138970	Hs.122113	gb:zw80c03.s1 Scares_testis_NHT Homo sap	5.3
15	440138	AB033023	Hs.318127	ESTs hypothetical protein FLJ 10201	5.3
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3 5.3
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	5.3
	435244	N77221	Hs.187824	ESTs	5.3
20	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
20	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	5.3
	430437 414825	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fs, clone PL	5.3
	453941	X06370 U39817	Hs.77432 Hs.36820	epidermal growth factor receptor (avian Bloom syndrome	5.2
25	424998	U58515	Hs.154138	chitinase 3-like 2	5.2 5.2
	423419	R55336	Hs.23539	ESTs	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	5.2
30	408206	AF041853	Hs.43670	kinesin family member 3A	5.2
30	421013 429443	M52397	Hs.1345	mutated in colorectal cancers	5.2
	434367	AB028967 AB020700	Hs.202687 Hs.3830	potassium voltage-gated channel, Shal-re	5.2
	444861	R46789	Hs.76118	KIAA0893 protein ubiquitin carboxyl-terminal esterase L1	5.2
	446142	AI754693	Hs.145968	ESTs	5.2 5.2
35	448816	AB033052	Hs.22151	KIAA1226 protein	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	5.2
	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
40	416737 424800	AF154335	Hs.79691	LIM domain protein	5.2
40	443695	AL035588 AW204099	Hs.153203 Hs.337720	MyoD family inhibitor	5.2
	415257	F03016	Hs.27513	ESTs, Wealdy similar to AF126780 1 retin ESTs	5.2 - 5.2
	433929	AJ375499	Hs.27379	ESTs	5.1
4-	415651	AI207162	Hs.3815	stathmin-like-protein RB3	5.1
45	451027	AW519204	Hs.40808	ESTs	5.1
	409172	Z99399	Hs.118145	ESTs	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	429172 437268	AA447417 AJ754847	Hs.285491	ESTs	5.1
50	451270	AW341392	Hs.227571 Hs.235795	regulator of G-protein signalling 4 ESTs	5.1
••	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (f	5.1 5.1
	420560	AW207748	Hs.59115	ESTs	5.1
	418097	R45137	Hs.21868	ESTs	5.1
55	442910	Al365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.1
23	434849	AW292765	Hs.8053	ESTS	5.1
	413554 414217	AA319146 AI309298	Hs.75426	secretogranin II (chromogranin C)	5.1
	412068	S72043	Hs.279898 Hs.73133	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1
	413627	BE182082	Hs.246973	metallothionein 3 (growth inhibitory fac ESTs	5.0 5.0
60	418661	NM_001949	Hs.1189	E2F transcription factor 3	5.0
	422438	AA445925	Hs.270896	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
65	435087 452097	AW975241 AB002364	Hs.23567 Hs.27916	ESTs	5.0
0.0	410434	AF051152	Hs.63668	a disintegrin-like and metalloprotease ( toll-like receptor 2	5.0
	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	4.9 4.9
	407808	AA663559	Hs.279789	histone deacetylase 3	4.9
20	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	4.9
70	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.9
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
	447112	H17800	Hs.7154	ESTs	4.9
	449574 453652	F05048 AW009640	Hs.175373 Hs.28368	ESTS	4.9
75	423869	BE409301	Hs.134012	ESTs, Moderately similar to S65657 alpha C1q-related factor	4.9
_	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4,9 4.9
	449176	AI633545	Hs.198072	ESTs	4.9
	448451	AW015994		gb:Ul-H-BIOp-abh-g-09-0-Ul.s1 NCI_CGAP_S	4.8
80	402604				4.8
30	436039	AW023323	Hs.121070		4.8
	448769 423678	N66037 AW963357	Hs.38173 Hs.7847	ESTs ESTs	4.8
	439451	AF086270	Hs.278554	helerochromatin-like protein 1	4.8
					4.8

	425870	R13406	Hs.56782	ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
	413409	Al638418	Hs.78580	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	4.8
5	413823 417246	AA825721	Hs.246973	ESTS	4.8
,	420900	A1760098 AL045633	Hs.21411 Hs.44269	ESTs ESTs	4.6
	424153	AA451737	Hs.141496	MAGE-like 2	4.8 4.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
10	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
10	454030 424458	AW021429 M29273	Hs.231980 Hs.1780	ESTs	4.8
	444119	R41231	Hs.184261	myelin associated glycoprotein ESTs, Wealdy similar to T26686 hypothe6	4.8 4.8
	407792	A)077715	Hs.39384	putative secreted ligand homologous to f	4.8
16	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
15	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956 435060	AI374651 AI422719	Hs.22542 Hs.233349	ESTs ESTs, Wealdy similar to fork head like p	4.7 4.7
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
20	422222	Al699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733 449353	AW298410 AA001220	Hs.21475 Hs.271369	ESTs ESTs	4.7
	452022	AW072330	Hs.293875	ESTS	4.7 4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
25	404541				4.7
	428189 409125	AA424030 R17268	Hs.46627 Hs.259873	ESTs	4.7
	458435	AI418718	Hs.144121	exonal transport of synaptic vesicles ESTs, Wealdy similar to T46916 hypotheti	4.7 4.6
••	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.6
30	413492	D87470	Hs.75400	KIAA0280 protein	4.6
	419629	A8020695	Hs.91662	KIAA0888 protein	4.6
	407638 438140	AJ404672 W87355	Hs.334483 Hs.269587	hypothetical protein FLI23571	4.6
	439169	AI912122	Hs.41095	ESTs ESTs	4.6
35	443150	AI034467	Hs.34650	ESTs	4.6 4.8
	451073	AJ758905	Hs.206063	ESTS	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
	452106 451407	A141031 AA131376	Hs.21342 Hs.326401	ESTs fibroblast growth factor 12B	4.6
40	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6 4.6
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	4.6
	437204	AL110216	Hs.12285	ESTs, Weakly similar to ISS214 salivary	4.6
	431117	AF003522	Hs.250500	delta (Orosophila)-like 1	4.5
45	422175 407889	N79885 R34556	Hs.6382 Hs.30800	ESTs, Highly similar to T00391 hypotheti	4.5
	419343	AA456245	Hs.85603	ESTs, Weakly similar to S65657 alpha-1C- down-regulated by Ctnnb1, a	4.5 4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4,5
	429399	AA452244	Hs.16727	ESTa	4.5
50	450149 453118	AW969781 AW195849	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
50	443455	AB001025	Hs.252757 Hs.9349	ESTs ryanodine receptor 3	4.5 4.4
	442613	AI004002	Hs.130522	Ky channel-interacting protein 1	4.4
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
55	416209 418845	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
"	435202	AA852985 AI971313	Hs.89232 Hs.170204	chromobox homolog 5 (Drosophila HP1 alph KIAA0551 protein	4.4
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4 4.4
	451254	AI571016	Hs.172967	ESTs	4.4
60	439039	AI656707	Hs.48713	ESTs	4.4
50	439979 441607	AW600291 NM_005010	Hs.6823 Hs.7912	hypothetical protein FLJ10430 neuronal cell adhesion molecule	4.4
	424983	AI742434	Hs.169911	ESTs	4.4 4.4
	410611	AW954134	Hs.20924	KIAA1628 protein	4.4
65	402605			•	4,4
05	409248 442222	AB033035 Al061301	Hs.\$1965	KIAA1209 protein	4.4
	454027	R40192	Hs.164773 Hs.21527	ESTs Human DNA sequence from clone GS1-115M3	4.4
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	4.4 4.4
70	442832	AW206560	Hs.253569	EST ₅	4.4
70	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279 427194	AW959861 AA399018	Hs.290943 Hs.250835	ESTs ESTs	4.3
	419723	AL120193	Hs.92614	longevity assurance (LAG1, S. cerevisiae	4.3 4.3
76	445810	AW265700	Hs.155660	ESTs	4.3 4.3
75	409734	BE161664	Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Wealtly similar to PIHUBB salivary	4.3
	411571 433024	AA122393 AA573847	Hs.70811 Hs.26549	hypothetical protein FLJ20516	4.3
00	453202	AW085781	Hs.26270	KIAA1708 protein hypothetical protein FLJ11588	4.3 4.3
80	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	4.3 4.3
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.3
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3
	444600	R41398	Hs. <b>6</b> 996	ESTs	4.3

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	454042	H22570	Hs.172572	hypothetical protein FLJ20093	4.3
	441899	AI372588	Hs.8022	TU3A protein	4.3
	425256	8E297611	Hs.155392	collapsin response mediator protein 1	4,3
5	410358 430291	AW975168 AV660345	Hs.13337 Hs.238126	ESTs, Wealthy similar to unnamed protein CGI-49 protein	4.2 4.2
•	433597	AA708205	Hs.100343	ESTs	4.2
	444127	N63620	Hs.13281	ESTs	4.2
	448507 413589	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (I	4.2
10	408577	AW452631 H50572	Hs.313803 Hs.19515	ESTs, Highly similar to AF157833 1 noncl ESTs, Highly similar to NRG3_HUMAN PRO-N	4.2 4.2
. •	409719	AI769160	Hs.108681	Homo sapiens brain turnor associated prot	4.2
	428536	AJ143139	Hs.2288	visinin-like 1	4.2
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
15	432865 447138	AI753709 AI439112	Hs.152484 Hs.93828	ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to 2109260A B cell	4.2 4.2
	450648	AJ703366	Hs.26766	ESTs	4.2
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2
	421686 452776	AB011156 AA194540	Hs.106794 Hs.13522	KIAA0584 protein	4.2
20	436421	AI678031	Hs.122813	ESTs, Wealdy similar to I38022 hypotheti ESTs, Wealdy similar to ZN22_HUMAN ZINC	4.2 4.2
	423858	AL137326	Hs.133483	Homo sepiens mRNA; cDNA DKFZp43480650 (f	4.2
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.2
	437380 432328	AL359577 AI572739	Hs.112198 Hs.195471	Homo sapiens mRNA; cDNA DKFZp547M073 (tr 6-phosphofructo-2-kinase/fructose-2,6-bi	4.2 4.1
25	439607	BE540565	Hs.159460	ESTs	4.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, done Y7	4.1
	446936	H10207	Hs.47314	ESTs	4.1
	424240 412446	AB023185 AI768015	Hs.143535 Hs.92127	calcium/calmodufin-dependent protein kin ESTs	4.1 4.1
30	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.1
	419683 426071	AA248897 AW138057	Hs.48784	ESTs	4.1
	428743	AL080060	Hs.163835 Hs.301549	ESTs Homo sagiens mRNA; cONA DKFZpS64H172 (fr	4.1 4.1
35	432809	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039 425905	A1922988 AB032959	Hs.172510 Hs.318584	ESTS	4.1 4.1
	457561	AA331517	Hs.286055	novel C3HC4 type Zinc finger (ring finge chimerin (chimaerin) 2	4.1
40	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433932	AW954599	Hs.169330	neuronal protein	4.1
	436637 439231	AJ783529 AW581935	Hs.26766 Hs.141480	ESTs Horno sapiens mRNA; cDNA DKFZp434N079 (fr	4,1
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4,1 4,1
45	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968	heparan suffate (glucosamine) 3-O-sulfot	4.1
	410486 413916	AW235094 N49813	Hs.69233 Hs.75615	zinc finger protein apolipoprotein C-II	4.0 4.0
	438703	AI803373	Hs.31599	ESTs	4.0
50	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	405771 418841	NM_002332	Hs.89137	low density Epoprotein-related protein	4.0 4.0
	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.0
**	424176	AL137273	Hs.142307	hypothetical protein	4.0
55	425773 427304	N21279	Hs.237749	ESTs	4.0
	428882	AA761526 AA436915	Hs.163853 Hs.131748	ESTs ESTs, Moderately similar to ALU7_HUMAN A	4.0 4.0
	452834	AJ638627	Hs.105685	KIAA1688 protein	4.0
60	453745	AA952989	Hs.63908	hypothetical protein MGC14726	4.0
50	405239 413801	U89281 M62246	Hs.11958 Hs.35406	oxidative 3 alpha hydroxysteroid dehydro ESTs, Highly similar to unnamed protein	4.0 4.0
	429698	AI685086	Hs.26339	ESTs, Weathly similar to S21348 probable	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
65	439199 439450	R40373 R51613	Hs.26299 Hs.125304	ESTs	4.0
05	446782	AI653048	Hs.144006		4.0 4.0
	419687	AI638859	Hs.227699		3.9
	402408				3.9
70	453362 414219	H14988 W20010	Hs. 107375 Hs. 75823	ESTs AU.1-fused gene from chromosome 1q	3.9 3.9
	420578	AAB13546	Hs.99034	GTP-binding protein Rho?	3.9
	425010	T16837	Hs.4241	ESTa	3.9
	444230	H95537 AW292779	Hs.146067		3.9
75	441736 418951	F07809	Hs.169799 Hs.89506	ESTs paired box gene 6 (ani/idla, keratitis)	3.9
. •	406311			have now Reise a feminist unional	39 39
	408460	AA054726	Hs.285574		3.9
	410658	AW105231 AIB15523	Hs.192035		3.9
80	414699 418849	AW474547	Hs.76930 Hs.53565	synuclein, alpha (non A4 component of am Homo sapiens PIG-M mRNA for mannosyltran	3.9 3.9
-	429477	AI275514	Hs.6658	ESTs	3.9
	433766	AA609234	Hs.112669		3.9
	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	3.9

	447004	D41364	Lie CADE	F. C. T. C.	
	447891 450221	R41754 AA328102	Hs.6496 Hs.24641	ESTs	3.9
	404283	70-020102	113.24041	cytoskeleton associated protein 2	3.9 3.9
_	453919	AW959912	Hs.7076	KIAA1705 protein	19
5	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.9
	412754	AW160375	Hs.74565	armyloid beta (A4) precursor-like protein	3.9
	445314	AI689948	Hs.65489	Homo sepiens cDNA: FLJ21517 fs, done C	3.9
	435652 407378	N32388 AA299264	Hs.334370 Hs.57776	uncharacterized hypothalamus protein HBE	39
10	438054	AA776626	Hs.62183	ESTs, Moderately similar to (38022 hypot ESTs	19 19
	438420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157648	Hs.153506	ESTs	3.9
	432590	A1609273	Hs.110783	ESTs	3.9
15	453331	A1240665	Hs.8895	ESTs	3.9
13	410227 424635	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	451489	AA420687 NM_005503	Hs.115455 Hs.26468	Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	447247	AW369351	Hs.287955	amyloid beta (A4) precursor protein-bind Homo sapians cDNA FLJ13090 lis, clone NT	3.8 3.8
	448302	A1480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
20	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	3.8
	417355	D13168	Hs.82002	endothelin receptor type B	3.8
	446727	AB011095	Hs.16032	KIAA0523 protein	3.8
	424340 423346	AA339036 AI267677	Hs.7033	ESTs	3.8
25	412788	AA120960	Hs.127416 Hs.198416	synaptojanin 1 ESTs	3.8
	404593	***************************************	14.130410	5013	3.8 3.8
	416856	N27833	Hs.269028	ESTs. Wealty similar to 138022 hypotheti	3.8
	429896	AA460367	Hs.224223	ESTs, Moderately similar to 138022 hypot	3.8
20	439619	AW975998	Hs.58595	ESTs, Wealdy similar to I38022 hypotheti	3.8
30	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
	440322 447761	AA879430 AF061573	Un 10400	gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	452453	Al902519	Hs.19492	protocadharin 8 gb:QV-BT009-101198-051 8T009 Homo sapien	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8 3.8
3 <i>5</i>	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22468 fis, clone H	3.8
	447028	AI973128	Hs.167257	brain link protein-1	3.8
	449458 445888	A1805078	Hs.208261	ESTs	3.8
40	407385	AF070564 AA610150	Hs.13415 Hs.272072	Homo sapiens clone 24571 mRNA sequence ESTs, Weakly similar to 136022 hypotheti	3.8
	428841	AI418430	Hs.104935	ESTs	3.8 3.8
	430643	AW970065	Hs.287425	MEGF10 protein	3.8
	422263	AA307639	Hs.129908	KIAA0591 protein	3.8
45	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-ti	3.8
43	439236	8E160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN !	3.8
	441928 441797	A1370188 A1936933	Hs.211454 Hs.214635	ESTs ESTs	3.8
	414922	000723	Hs.77631	glycine cleavage system protein H (amino	3.7 3.7
	425588	F07396	Hs.46751	ESTs	3.7
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to 138022 hypotheti	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682 425741	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
	418211	AF052152 BE244748	Hs.159412 Hs.247474	Homo sapiens clone 24528 mRNA sequence . hypothetical protein FLJ21032	3.7
55	440080	AW051597	Hs.143707	ESTs	3.7 3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.7
	409234	AI879419	Hs.27206	ESTs	3.7
60	420489	AA815089	Hs.193513	ESTs	3.7
00	426890 438849	AA393167 W28948	Hs.41294 Hs.10762	ESTs ESTs	3.7
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.7
	448796	AA147829	Hs.301431	endothetial zinc finger protein induced	3.7 3.7
10	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.7
65	459518	AJ937419	Hs.294069	Homo sapiens cDNA FLJ 13384 fis, clone PL	3.7
	434444	AJ765276	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL135740	Hs.102447	TSC-22-like	3.7
	410555 421637	U92649 AF035290	Hs.64311 Hs.106300	a disintegrin and metalloproteinase doma	3.7
70	418522	AA605038	Hs.7149	Homo sapiens clone 23556 mRNA sequence Homo sapiens cDNA: FLJ21950 fis, clone H	3.7
	420807	AA280627	Hs.57846	ESTs	3.7 3.7
	449961	AW265634	Hs.133100		3.7
	422634	NM_016010		CGI-62 protein	3.7
75	421030	AW161357	Hs.101174		3.7
, 5	427099	AB032953	Hs.173560		3.7
	452355 440483	N54926 A1200836	Hs.29202 Hs.150386	G protein-coupled receptor 34 ESTs	3.7
	429597	NM_003816		a disintegrin and metalloproteinase doma	3.7
00	423756	AA828125	7 78	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7 3.6
80	425187	AW014488	Hs.22509	ESTs	3.6
	434859	BE255080	Hs.299315		3.6
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.6
	445729	H21066	Hs.13223	Homo saplens mRNA full length insert cON	3.6

	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	25
	429239	AA448419	Hs.45209	ESTs	3.6 3.6
	419086	NM_000216	Hs.89591	Kaltmann syndrome 1 sequence	3.6
5	446659	AJ335361	Hs.226376	ESTs	3.6
,	426757 418819	AW205640 AA228776	Hs.158206 Hs.191721	ESTs ESTs	3.6
	458332	AI000341	Hs.220491	ESTs	3.6 3.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.6
10	410343	AA084273	Hs.76561	ESTs, Weakly similar to \$47072 finger pr	3.6
10	410507 422977	AA355288 AA631498	Hs.40834	transitional epithelia response protein	3.6
	425305	AA363025	Ha.155572	gbmp83h04.s1 NCI_CGAP_Thy1 Homo sapiens Human clone 23801 mRNA sequence	3.6
	428002	AA418703	14.10072	gbzv98c03.s1 Soares_NhHMPu_S1 Homo sapi	3.6 3.6
16	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	3.6
15	430530	AA480870	Hs.47660	ESTs	3.6
	436425 438078	AI913146 AI016377	Hs.318725 Hs.131693	CGI-72 protein	3.6
	442927	AI024347	Hs.131519	ESTs ESTs	3.6 3.6
20	446242	N66336	Hs.7360	ESTs	3.6
20	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.6
	450474 452198	AW872844	Hs.201919	ESTs	3.6
	455800	A1097560 R22479	Hs.61210 Hs.167073	ESTs, Wealdy similar to I38022 hypotheti Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
	436443	AW138211	Hs.128746	ESTs	3.6 3.6
25	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.6
	456038	AA203285	Hs.294141	ESTs, Wealtly similar to alternatively sp	3.6
	408902 442950	AW014859 AJ500417	Hs.5510 Hs.46764	ESTs	3.6
	423905	AW579960	Hs.135150	ESTs lung type-I cell membrane-associated gly	3.6
30	425478	AB007953	Hs.268840	ESTs	3.6 3.6
	453884	AA355925	Hs.35232	KIAA0186 gene product	3.6
	404721 408453	A12C0020	11- 45400		3.6
	440553	AJ369838 AA889416	Hs.45127 Hs.295362	chondroitin sulfate proteoglycan 5 (neur Homo sapiens cDNA FLJ14459 fis, clone HE	3.6
35	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	3.5 3.5
	413999	N46124	Hs.34460	ESTs	3.5
	421458	NM_003654	Hs.104576	carbohydrate (keratan sutfate Gal-6) sul	3.5
	425017 435958	AL119305 H98180	Hs.288405	ESTS	3.5
40	415101	R45531	Hs.117975 Hs.144534	ESTs ESTs	3.5
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.5 3.5
	430290	A1734110	Hs. 136355	ESTS	3.5
	416836	D54745	Hs.80247	cholecystokinin	3.5
45	414821 419412	M63835 AW161058	Hs.77424 Hs.90297	Fc tragment of IgG, high affinity Ia, re synuclein, beta	3.5
-	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 ffs, clone L	3.5 3.5
	452689	F33868	Hs.284176	transferrin	3.5
	416661	AA834543	Hs.79440	IGF-II mRNA-binding protein 3	3.5
50	427491 428037	R43279 N47474	Hs.22574 Hs.89230	ESTs. Wealdy similar to 138022 hypotheti	3.5
-	444584	Al168422	ns.03230	polassium intermediate/small conductance gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.5 3.5
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.5
55	412659 429077	AW753865 AB028983	Hs.74376 Hs.2352	offactomedin related ER localized protei	3.5
	436887	AW953157	Hs.193235	adenylate cyclase 2 (brain) hypothetical protein DKFZp547D155	3.5 3.5
	450784	AW246803	Hs.47289	ESTs	3.5 3.5
	446827	AW451243	Hs.157069	ESTs	3.5
60	436434 412777	N50465 Al335773	Hs.92927 Hs.270123	putative 47 kDa protein	3.5
00	438476	AA326108	Hs.33829	ESTs bHLH protein DEC2	3.5
	408601	U47928	Hs.86122	protein A	3.5 3.4
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	3.4
65	448425 418727	A1500359	Hs.233401	ESTs	3.4
03	451729	AA227609 AW160725	Hs.94834 Hs.312469	ESTs ESTs	3.4
	435910	AI084152	Hs.21782	ESTS, Wealdy similar to ALU7_HUMAN ALU S	3.4 3.4
	434577	R37316	Hs.179769	Homo sepiens cDNA: FLJ22487 fis, clone H	3.4
70	41459B	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.4
70	439627 413293	BE621702 ALD47483	Hs.29076	hypothetical protein FLJ21841	3.4
	423992	AW898292	Hs.302498 Hs.137206	GTP-binding protein homotogous to Saccha Homo sapiens mRNA; cDNA DKFZp564H1663 (f	3.4
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.4 3.4
75	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.4
13	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.4
	435061 452291	AI651474 AF015592	Hs.163944 Hs.28853	ESTS CDC7 (not) divining much 2 S associati	3.4
	449714	AB033015	Hs.23941	CDC7 (cell division cycle 7. S. cerevisi KIAA1189 protein	3.4 3.4
00	443392	AI055821	Hs.293420	ESTs	3.4
80	410082	AA081594	Hs.158311	Musashi (Orosophila) homolog 1	3.4
	445337 408493	NM_013280 BE206854	Hs.12523 Hs.46039	fibronectin leucine rich transmembrane p phosphoglycerate mutase 2 (muscle)	3.4
	432731	R31178	Hs.287820	phosphogrycerate mutase 2 (muscle) fibronectin 1	3.4 3.4
					3.4

	440750				
	448758 432613	AB018311	Hs.21917	KIAA0768 protein	3.4
	434164	AW081698 AW207019	Hs.80712 Hs.148135	KIAA0202 protein	3.4
	425294	AF033827	Hs.155553	serine/threonine kinase 33 HNK-1 sulfotransferase	3.4
5	410108	AA081659	Hs.318775	OSBP-related protein 6	3.4 3.4
	406815	AA833930	Hs.288036	TRNA isopentanyipyrophosphate transferas	3.4
	402855			and the same of th	3.3
	422170	A1791949	Hs.112432	anti-Multerian hormone	3.3
10	445034	AW293376	Hs.143659	ESTs	3.3
10	424378	W28020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593 404819	R88872	Hs.4964	DKFZP586J1624 protein	3.3
	436607	AW681783	Hs.211061	ESTs	3.3
15	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.3
	452693	T79153	Hs.48589	zinc finger protein 228	3.3 3.3
	454996	AW850180		gb:IL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400615 (f	3.3
20	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZpS86F1822 (f	3.3
	421192 426695	AAB33718 AW118191	Hs.204529 Hs.112729	KIAA1806 protein	3.3
	438885	A1886558	Hs.184987	ESTs ESTs	3.3
25	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3 3.3
	452103	R42764	Hs.339654	ESTs, Wealty similar to 138022 hypotheti	3.3
	453590	AF150278	Hs.33578	KIAA0820 protein	3.3
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.3
30	457285	A1038858	Hs.130522	Kv channel-interacting protein 1	3.3
50	436045	AB037723	Hs.5028	DKFZP56400423 protein	3.3
	437470 448520	AL390147 AB002367	Hs.134742 Hs.21355	hypothetical protein DKFZp5470065	3.3
	436480	AJ271643	Hs.87469	doublecortin and CaM kinase-like t putative acid-sensing ion channel	3.3
	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3 3.3
35	443898	AW804296	Hs.9950	Sec61 gamma	13
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3
	445953	AI612775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
40	414683	S78298	Hs.76888	hypothetical protein MGC12702	3.3
40	428484 420649	AF104032	Hs.184601 Hs.124704	solute carrier family 7 (cationic amino	3.3
	419498	AI866964 AL036591	Hs.20887	ESTs, Moderately similar to \$65657 alpha hypothetical protein FLJ 10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3 3.3
	436556	AI384997	Hs.7572	ESTs	3.3 3.2
45	424369	R87622	Hs.26714	KIAA1831 protein	3.2
	457065	AI476318	Hs.192480	ESTs	3.2
	440210	AW674562	Hs.125296	ESTs	3.2
	444513 434353	AL120214 AA630863	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
50	414430	AI346201	Hs.131375 Hs.76118	ESTs, Moderately similar to ALUB_HUMAN !	3.2
00	439924	A1985897	Hs.125293	ubiquitin carboxyl-terminal esterase L1 ESTs	3.2 3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	3.2
66	415115	AA214228	Hs.127751	hypothetical protein	3.2
55	407878	D87468	Hs.40888	activity-regulated cyloskeleton-associat	3.2
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437762 438944	178028 AA302517	Hs.154679 Hs.92732	synaptotagmin I	3.2
	450313	AI038989	Hs.332633	KIAA1444 protein Bardet-Biedl syndrome 2	3.2
60	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2 3.2
	410953	AW811766	Hs.334858	hypothetical protein MGC12250	3.2
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin tyrosine ligase-like 1	3.2
65	429496	AA453800	Hs.192793	ESTs	3.2
05	430099 434928	AW194988 AW015595	Hs.20537	hypothetical protein FLJ13942	3.2
	435532	AW291488	Hs.4267 Hs.117305	Homo sapiens clones 24714 and 24715 mRNA Homo sapiens, clone IMAGE:3682908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
<b>30</b>	439274	AF086092	Hs.48372	ESTS	3.2 3.2
70	440847	AA907511	Hs.130178	ESTs	3.2
	447750	AI422234	Hs.143434	contactin 1	3.2
	455350	AW901809	44. 8000	gb:QV0-NN1020-170400-195-h02 NN1020 Homo	3.2
	430890	X54232	Hs.2699	glypican 1	3.2
75	420568 410768	F09247 AF038185	Hs.247735	protocadherin alpha 10	3.2
	427450		Hs.66187 Hs.178121	Homo sapiens clone 23700 mRNA sequence K/AA0626 gene product	3.2
	430456	AA314998	Hs.241503		3.2 3.2
	430181	AF065314	Hs.234785		3.2 3.2
<b>0</b> Λ	418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.2
80	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (	3.2
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.2
	424899 436277	AL119387 R88520	Hs.119062 Hs.120917	ESTs ESTs	3.2
	-50211	100020	rs. (2031/	Ca19	3.2

	451455	A1937227	Hs.8821	hepcidin antimicrobial peptide	3.2
	445078	AI869975	Hs.4775	junctophilin 3	3.2
	447746 435458	AW015920 F11872	Hs.161359 Hs.4892	ESTs Homo sapiens clone 24841 mRNA sequence	3.2 3.2
5	427729	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	3.2
	417417	F05745	Hs.89512	ATPase, Ca→ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
	439570 432527	T79925 AW975028	Hs.269165 Hs.102754	ESTs, Wealdy similar to ALU1_HUMAN ALU S ESTs	3.1 3.1
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	3.1
	421988	AW450481	Hs.161333	ESTS	3.1
	426509 408786	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
	433494	AA773187 AB029396	Hs.294027 Hs.3353	ESTs beta-1,3-glucuronyltransferase 1 (glucur	3.1 3.1
15	412723	AA648459	Hs.335951	hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439456 428832	A1752409 AA578229	Hs.109314 Hs.324239	hypothetical protein FLJ20980 ESTs, Moderately similar to ZN91_HUMAN Z	31
	452780	BE171598	Hs.13522	ESTs, Wealdy similar to 138022 hypotheti	31 31
20	438192	A1859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	31
	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.1
	403053 404299	R58624	Hs.2186	eukaryotic translation elongation factor	3.1 3.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
25	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1
	449101 453240	AA205847 AI969564	Hs.23016 Hs.166254	G protein-coupled receptor hypothetical protein DKFZp566I133	3.1 3.1
	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
30	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864 414706	AI720078 AW340125	Hs.291997	ESTs, Weakly similar to A47582 8-cell gr	3.1
	436315	BE390513	Hs.76989 Hs.27935	KtAA0097 gene product hypothetical protein MGC4837	3.1 3.1
25	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.1
35	425683	AB037813	Hs.159200	hypothetical protein OKFZp762K222	3.1
	410126 435312	BE169274 AJ243396	Hs.169387 Hs.4865	KIAA0036 gene product voltage-gated sodium channel beta-3 subu	3.1
	425491	AA883316	Hs.255221	ESTs	3.1 3.1
40	456273	AF154846	Hs.1148	zinc finger protein	3.1
40	412140 445255	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.1
	432154	NM_014841 AI701523	Hs.12477 Hs.112577	synaptosomal-associated protein, 91 kDa ESTs	3.1 3.1
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.1
45	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.1
45	448616 429281	AF035621 AA830856	Hs.21611 Hs.29808	kinesin family member 3C	3.0
	443906	AA348031	Hs.7913	Homo sapiens cDNA: FLJ21122 fis, clone C ESTs	3.0 3.0
	417318	AW953937	Hs.12891	ESTS	3.0
50	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
50	444153 408790	AK001610 AW580227	Hs.10414 Hs.47860	hypothetical protein FLJ10748 neurotrophic tyrosine kinase, receptor,	3.0 3.0
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
55	422758 421633	AF152329 AF121860	Hs.284180 Hs.106260	protocadherin gamma subfamily C, 3	3.0
•	428361	NM_015905	Hs.183858	sorting nexin 10 transcriptional Intermediary factor 1	3.0 3.0
	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.0
	416805 419518	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.0
60	422709	U79289 AA315331	Hs.90798 Hs.153485	Human clone 23695 mRNA sequence ESTs	3.0 3.0
	423135	N67655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	3.0
	426617 427386	W58006 AW836261	Hs.266258 Hs.337717	endonuclease G-like 1 ESTs	3.0
65	429859	NM_007050		protein tyrosine phosphatase, receptor t	3.0 3.0
	435071	D60683	Hs.35495	ESTs	3.0
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (	3.0
	436211 436936	AK001581 AL134451	Hs.334828 Hs.197478	hypothetical protein FLJ10719; KIAA1794 ESTs	3.0 3.0
70	445855	BE247129	Hs.145569		3.0
	452294	AJ871925	Hs.117895		3.0
	433980 430228	AA137152 AW950939	Hs.286049 Hs.6382		3.0
	451026	AN930939 AA013218	Hs.157492	ESTs, Highly similar to T00391 hypotheti cer-d4 (mouse) homotog	3.0 3.0
75	435232	NM_001262		cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.0
	425782 416586	U66468 D44643	Hs.159525 Hs.14144		3.0
00	416874	H98752	Hs.42568	secreted modular calcium-binding protein ESTs	3.0 3.0
80	410386	W26187	Hs.3327	Homo sepiens cDNA: FLJ22219 fis, clone H	3.0
	411411 424066	AA345241 700348	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	404048	Z99348	Hs.112461	ESTs, Wealdy similar to 138022 hypotheti	3.0 3.0
	-			***	5.0

	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.0
	418196 434131	AI745649 AI858275	Hs.26549	KIAA1708 protein	3.0
5	441255	R06350	Hs.143659 Hs.171635	ESTs ESTs	3.0 2.9
-	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.9
	453905	NM_002314	Hs.36566	LIM domain kinase 1	2.9
	416602 431173	NM_006159 AW971198	Hs.79389 Hs.294068	nel (chicken)-like 2	2.9
10	425599	AW366745	Hs.214140	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S	29 29
	436401	AI087958	Hs.29088	ESTs	29
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
	451558 412490	NM_001089 AW803564	Hs.26630 Hs.288850	ATP-binding cassette, sub-family A (ABC1 Homo sepiens cDNA: FLJ22528 fis, clone H	29
15	433149	BE257672	Hs.42949	hypothetical protein HES6	2.9 2.9
	434811	AW971205	Hs.114280	ESTs	29
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	29
	452092 453496	BE245374 AA442103	Hs.27842 Hs.33084	hypothetical protein FLJ11210 solute carrier family 2 (facilitated gtu	29 29
20	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	29
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651 441707	AW405731 R42637	Hs.18498 Hs.21963	Homo sapiens cDNA FLJ12277 fis, clone MA	29
	435741	A1240668	Hs.113099	hypothetical protein OKFZp761B0514 ESTs	29 29
25	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypotheti	2.9
	422939	AW394055	Hs.98427	ESTs, Wealthy similar to 138022 hypotheti	2.9
	439376 439935	AA883521 \$75105	Hs.222064 Hs.301676	ESTs glutamate receptor, lonotropic, kainate	29 29
	437267	AW511443	Hs.258110	ESTs	29
30	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	29
	400250 400992				2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9 2.9
3.5	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	29
35	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9
	423751 426910	AW235633 AA470023	Hs.46525 Hs.190089	ESTs ESTs, Moderately similar to ALU1_HUMAN A	29
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	29 29
40	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.9
40	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9
	428500 421641	AI815395 AI638184	Hs.184641 Hs.106334	fatty acid desaturase 2 Homo sapiens clone 23836 mRNA sequence	2.9 2.9
	421141	AW117261	Hs.125914	ESTs	2.9
15	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
45	456723 436456	Z43902 AW292677	Hs.4748 Hs.248122	adenylate cyclase activating polypeptide	2.9
	421483	NM_003388	Hs.104717	G profein-coupled receptor 24 hypothetical protein MGC11333	2.9 2.9
	412190	R16180	Hs.274461	ESTs	2.9
50	446131	NM_000929	Hs.290	phospholipase A2, group V	2.9
50	441668 437387	AI611973 AI198874	Hs.127525 Hs.28847	ESTs AD026 protein	2.9 2.9
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cONA DKFZp761I1224 (f	2.9
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
55	429084 447067	AJ001443 R42098	Hs.195614 Hs.21964	splicing factor 3b, subunit 3, 130kD ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9 2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
	424126 408739	AA335635	Hs.96917	ESTs	2.9
60	447422	W01556 BE618703	Hs.238797 Hs.98258	ESTs, Moderately similar to 138022 hypot orthopedia (Drosphila) homolog	2.9 2.9
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.9
	446997	AA383439	Hs.16758	Spir-1 protein	29
	433573 408447	AF234887 AK002089	Hs.57652 Hs.45080	cadherin, EGF LAG seven-pass G-type rece Homo sapiens cDNA FLJ11227 fis, clone PL	2.9 2.9
65	419586	AI088485	Hs.144759		2.8
	417022	NM_014737	Hs.80905	Ras association (RalGOS/AF-6) domain fam	2.8
	408432 420320	AW195262 AB002361	Hs.96633	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sepiens	2.8
	425241	AA324624	Hs.155247	KIAA0363 protein aldolase C, fructose-bisphosphate	2.8 2.8
70	428870	AA431682	Hs.134832		2.8
	424415	NM_001975			2.8
	409185 411555	AW961601 AF113537	Hs.252406 Hs.70669	hypothetical protein FLJ12296 similar to HMP19 protein	28
~-	426847	\$78723	Hs.298623		2.8 2.8
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	28
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.8
	424572 444670	M19650 H\$8373	Hs.150741 Hs.332938		2.8
00	411089	AA456454	Hs.183418		2.8 2.8
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	2.8
	440637 408554	AW900115 AA836381	Hs.7309 Hs.315111	Homo sapiens clone 23741 mRNA sequence nuclear receptor co-repressor/HDAC3 como	2.8
	403056	R58824	Hs.2186	eukaryotic translation elongation factor	2.8 2.6
			-		2.0

	423449	A1407000	Un 22067	ECT-	
	424188	AJ497900 AW954552	Hs.33067 Hs.142634	ESTs zinc finger protein	2.8 2.8
	429006	AA443143	Hs.50929	hypothetical protein FLJ 13842	2.6 2.8
_	434981	AW182577	Hs.293077	ESTs	2.8
5	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	2.8
	442748	AI016713	Hs.135787	ESTs	2.8
	443312	N52025	Hs.46616	ESTs	2.8
	450940	AJ744943	Hs.143209	ESTs, Weakly similar to I38022 hypotheti	2.8
10	452738	AL133800	Hs.7088	hypothetical protein MGC12435 .	2.6
10	409182	AA064970	Hs.118145	ESTs .	2.8
	439793 432683	AA018825 AW995441	Hs.7934 Hs.10475	Kruppel-like factor 4 (gut) ESTs	2.8
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	2.8 2.8
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	2.8
15	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	2.8
	434276	AF123659	Hs.93605	feucine zipper, putative tumor suppresso	28
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.8
20	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	28
20	428180 409348	AI129767	Hs.182974	guanine nucleotide binding protein (G pr	2.8
	409887	Al401535 AL137534	Hs.146090 Hs.56876	ESTs Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8 2.8
	457211	AW972565	Hs.32399	ESTs, Wealdy similar to S51797 vasodilat	2.8
	430039	BE253012	Hs.153400	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.8
25	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	2.8
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	2.8
	434008	AA740878	Hs.112982	ESTa	2.8
	446776	AW293417	Hs.156455	ESTs .	2.8
30	408838 422565	AI669535	Hs.40369 Hs.118400	ESTs	2.8
30	447397	BE259035 BE247676	Hs.18442	singed (Drosophila)-like (sea urchin fas E-1 enzyme	2.8
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.8 2.8
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fls, clone PL	2.8
~-	446377	AW014022	Hs.170953	ESTs	2.8
35	458924	BE242158	Hs.24427	DKFZP566O1646 protein	28
	447710	AJ420523	Hs.328241	ESTs .	2.8
	404049				28
	416913 426400	AW934714	14. 100743	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8
40	413264	M78361 W26456	Hs.169743 Hs.134757	Homo sapiens clone 25121 neuronal olfact hypothetical protein FLJ20033	28
. •	458997	AW937420	Hs.69662	ESTs	2.8 2.7
	422854	AA318323	. 4.45644	gb:EST20390 Retina II Homo sepiens cONA	2.7
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
45	452023	AB032999	Hs.27566	KIAA1173 protein	27
45	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
	452438	BE514230	Hs.29595	JM4 protein	2.7
	435408 418791	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	2.7
	438821	AA935633 AA826425	Hs.194628 Hs.291829	ESTs ESTs	2.7
50	423454	NM_016240	Hs. 128856	CSR1 protein	2.7 2.7
	442091	AW770493	Hs.182874	guanine nucleotide binding protein (G pr	2.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.7
	412436	AA665089		gb:nu76d01.s1 NCI_CGAP_AN1 Homo sapiens	2.7
55	432821	BE170702	Hs.279005	solute cerrier family 21 (organic anion	2.7
25	416404 441364	AA180138	Hs.107924	ESTs	2.7
	450202	AW450466 AW969756	Hs.126830 Hs.34145	ESTs, Wealthy similar to YO38_YEAST HYPOT	2.7
	426304	AA374532	Hs.124673	ESTs, Wealdy similar to B49647 GTP-bindi Homo sapiens cDNA FLJ11477 fis, clone HE	2.7 2.7
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	27
60	449701	AW952323	Hs.129908	KIAA0591 protein	27
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.7
	410318	AA084050	Hs.269259	ESTs, Wealty similar to S23650 retroviru	2.7
	414603	R58394	Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	2.7
65	416096 420896	H18577 AW149342	Hs.88974 Hs.24444	cytochrome b-245, beta polypeptide (chro	2.7
	424856	AA347746	Hs.9521	Homo sapiens cDNA: FLJ22165 fis, clone H ESTs, Wealdy similar to ZN43_HUMAN ZINC	2.7
	436304	AA339622	Hs.108887	ESTs	2.7 2.7
	441027	AJ911412	Hs.126444	ESTs	2.7
70	452545	N31940	Hs.14434	ESTs, Weakly similar to I38022 hypotheti	2.7
70	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	448560	BE613183	Hs.23213	ESTs	2.7
	426807	AA385315	Hs.156682		27
	425825 440351	AI929508 AF030933	Hs.159590 Hs.7179		2.7
75	425390	AP030333 AI092634	Hs.156114	RAD1 (S. pombe) homolog protein tyrosine phosphalase, non-recept	2.7
	427624	AA406245	Hs.24895	ESTs	27 27
	426413	AA377823	1000	gb:EST90805 Synovial sarcoma Homo saplen	2.7
	422491	AA338548	Hs.117546	neuronatin	2.7
80	424560	AA158727	Hs.150555		27
οU	432415	T16971	Hs.289014		2.7
	414865	AA157155	Hs.274414		2.7
	415827 445568	H17462 H00918	Hs.23079 Hs.268744	ESTs KIAA1796 protein	2.7
			110.200144	restrict popular	2.7

#### Hs. 239706 GR82-essociated binding protein 1 Hs. 2316 SRY (sex determining region Y)-box 9 (ca Hs. 270270 ESTs, Weakly similar to 2109260A 8 cell 433315 R96754 NM_000346 447959 A1452784 BE383808 426420 Hs 322430 NDRG family, member 4 5 436899 AA764852 Hs.291567 AA383343 CDC14 (cell division cycle 14, S. cerevi 444100 Hs.22116 2.7 2.7 ESTs alpha2.8-sialytransferase 426501 AW043782 Hs.293616 U91641 449092 Hs.22985 427311 AB020672 Hs.175411 KIAA0865 protein 10 BE005771 hypothetical protein FtJ22490 453313 Hs.153746 404029 27 27 416289 W26333 Hs.337438 439108 AW163034 synaptogyrin 3 ribosomal protein L36 Hs 6467 AI955289 Y07847 418746 Hs.300759 15 412046 Hs.73088 RAS-related on chromsome 22 435040 A1932350 Hs.152825 EST8 contactin associated protein 1 453083 U87223 Hs.31622 Hs.16332 428167 AA770021 ESTs 420028 443715 Hs.8786 Hs.9700 AB014680 carbohydrate (N-acetylglucosamine-6-0) s 20 cyclin E1 general transcription factor IIH, polype matrix metalloproteinase 9 (gelatinase B adenosine A1 receptor POM (POM121 rat homolog) and ZP3 fusion AI583187 421247 424687 BE391727 J05070 Hs.102910 Hs.151738 AB004662 AW449774 415056 Hs.77867 451697 Hs 296380 25 AW445023 AJ479755 433701 Hs.15155 457358 Hs.129010 **ESTs** 26 26 430347 NM_002039 AB037807 Hs.239706 GRB2-associated binding protein 1 418027 Hs.83293 Hs.24944 hypothetical protein ESTs, Weakly similar to 2109260A B cell 440491 R35252 30 Hs.16365 Hs.250726 425171 AW732240 **ESTs** 26 459335 AW298545 EST ESTs, Weakly similar to 834323 GTP-bindi KIAA1394 protein 425402 AI215881 Hs.24970 Hs.32156 453169 AB037815 ESTs KIAA1716 protein 433647 AA603367 Hs.222294 35 Al907735 450414 Hs.21446 446233 415446 Hs.25205 F08898 Hs.66075 **ESTs** AA250970 Hs.251946 poly(A)-binding protein, cytoplasmic 1-l 26 KIA0193 gene product zinc finger protein 179 D83777 Hs.75137 Hs.189482 413012 40 BE297851 428671 427158 408988 Hs.166231 Hs.49476 AA935603 ESTa AL119844 Homo sapiens clone TUA8 Cri-du-chat regi 459516 AI049662 Hs.246858 402693 45 408039 AA131424 **ESTs** Hs.50340 Hs.154116 Hs.21213 AW961489 AW897586 422896 **ESTs** 423130 ESTs Hs.109590 Hs.46736 Hs.190598 Hs.92374 438796 W67821 genethonin 1 hypothetical protein FLJ23476 R88518 50 440192 AA872282 419708 AK000753 hypothetical protein 449436 AA860329 Hs.279307 hypothetical protein DKFZp434l2117 436870 AW204219 Hs.155560 catnexio 448424 401324 AW009892 55 414136 AA812434 AA992805 Hs.119023 SMC2 (structural maintenance of chromoso 433943 Hs.44865 Hs.219907 lymphoid enhancer-binding factor 1 ESTs, Moderately similar to Transforming H97428 F09092 428001 429139 Hs.66087 60 BE252922 Hs.123119 423073 MAD (mothers against decapentaplegic, Dr phosphoinositol 3-phosphate-binding prot ESTs, Moderately similar to S65657 alpha Hs.86149 Hs.152299 448956 AW372914 444001 AI095087 adenytate kinase 5 Homo sapiens clone 25012 mRNA sequence 412049 N53437 Hs.18268 441783 BE313412 Hs.7961 65 Homo sapens clone 25012 mRNA sequence peanut (Drosophia)-Rise 2 ESTs, Weakly similar to T34549 probable ESTs, Weakly similar to T34549 probable esting weakly similar to T34522 hypotheti neuro-oncological ventral antigen 2 ESTs 425287 432149 R88249 AW614326 Hs.155524 26 Hs.157022 AW084176 AF083898 452234 Hs.223296 Hs.33021 Hs.271863 453478 AA714835 418962 70 hypothetical protein RG083M05.2 HSPC065 protein Ksp37 protein Hs.21145 Hs.11614 418858 AW961605 443257 AJ334040 428748 444984 AW593206 Hs.98785 Hs.132898 H15474 fatty acid desaturase 1 T32982 AF153815 433404 Hs.102720 ESTs potassium inwardly-rectifying channel, s homo sapiens chromosome 19, cosmid R2837 protein fyrosine phosphatase, receptor 1 Homo sapiens cDNA FLJ11723 fis, clone HE RAB7, member RAS oncogene family-like 1 poursients. 75 434779 Hs.50151 420582 452856 BE047878 AF034799 Hs.99093 Hs.30881 Hs.196008 436440 AJ471862 438527 AI969251 Hs.115325 80 433216 AF217412 neuroligin 3 Hs.47320

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435380

428966

439653

AA679001 AF059214

AW021103

Hs.192221

Hs.194687

Hs.6631

cholesterol 25-hydroxylase

hypothetical protein FLJ20373

	419304	Al271326	Hs.145101	ESTs, Weathy similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.6
	448548 435370	R13209 AJ964074	Hs.21413 Hs.225838	solute carrier family 12, (potassium-chi	26
5	408875	NM_015434	Hs.48604	ESTs DKFZP4348168 protein	2.6 2.5
-	457005	AJ007421	Hs.172597	sal (Orosophila)-like 3	2.5
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	2.5
	438549 427951	8E386801 AI826125	Hs.21858 Hs.43546	trinucleotide repeat containing 3 ESTs	2.5 2.5
10	411800	N39342	Hs.103042	microtubule-essociated protein 1B	2.5
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451422	AB002336 AA351647	Hs.26395	erythrocyte membrane protein band 4.1-5	2.5
	430713 428826	AL048842	Hs.2642 Hs.194019	eukaryotic translation elongation factor attractin	2.5 2.5
15	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	25
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.5
	429550 438662	AW293055 AA223599	Hs.119357 Hs.6351	ESTs cteavage and polyadenylation specific fa	2.5 2.5
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.5
20	427513	AI476318	Hs.192480	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	435923 417123	BE301930 BE326521	Hs.5010 Hs.159450	Homo sapiens clone 24572 mRNA sequence ESTs	2.5 2.5
~-	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.5
25	412980	AI815750	Hs.20977	hypothetical protein MGC3129 similar to	2.5
	427209 424327	H06509 AA431707	Hs.92423 Hs.31209	KIAA1566 protein ESTs	2.5
	436340	R42246	Hs.21606	ESTS	2.5 2.5
20	450650	T65617	Hs.101257	hypothetical protein MGC3295	2.5
30	439444	A1277652	Hs.54578	ESTs, Weakly similar to 138022 hypotheti	2.5
	400777 439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.5 2.5
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.5
25	450385	AI531024	Hs.24948	synuclein, alpha interacting protein (sy	25
35	432558 400860	R97268	Hs.177269	ESTs	2.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.5 2.5
	416063	BE047699	Hs.93454	ESTs	2.5
40	414998	NM_002543	Hs.77729	cooldised low density lipoprotein (lectin	2.5
70	452823 417791	AB012124 AW965339	Hs.30696 Hs.111471	transcription factor-like 5 (basic helix ESTs	25 25
	418079	R40058	Hs.6911	ESTs	2.5
	408495	W68796	Hs.237731	ESTs	2.5
45	442104 437370	L20971 AL359567	Hs. 188	phosphodiesterase 4B, cAMP-specific (dun	2.5
7.5	429803	W81489	Hs.161962 Hs.223025	Homo sapiens mRNA; cDNA DKFZp547D023 (fr RAB31, member RAS oncogene family	2.5 2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.5
50	408955 415261	BE315170 T40928	Hs.8087 Hs.8346	NAG-5 protein ESTs	2.5
-	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.5 2.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.5
	418388 421002	R72332 AF116030	Hs.29258	Homo sapiens cDNA FLJ11364 fls, clone HE	2.5
55	423244	AL039379	Hs.100932 Hs.209602	transcription factor 17 ESTs, Wealtly similar to ubiquitous TPR m	2.5 2.5
	423553	AA405635	Hs.96854	ESTs, Wealdy similar to DYLX_HUMAN CYTOP	2.5
	427981	AWZ93165	Hs.143134	ESTs	2.5
	428301 428508	AW628666 BE252383	Hs.98440 Hs.184668	ESTs, Weakly similar to 138022 hypotheti SBBI31 protein	25
60	428858	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.5 2.5
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	2.5
	432427 435347	AL037630 AW014873	Hs.6638	Homo sapiens cONA FLJ11602 fis, clone HE	2.5
	437949	U78519	Hs.116963 Hs.41654	ESTs ESTs, Weakly similar to A46010 X-linked	2.5 2.5
65	438208	ALD41224	Hs.65379	ESTs	2.5
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	2.5
	441523 441805	AW514263 AA285136	Hs.301771 Hs.301914		2.5
	442337	AJ371029	Hs.129257		2.5 2.5
70	442789	AW904361	Hs.131191	ESTs. Weakly similar to ALU7_HUMAN ALU S	2.5
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.5
	449086 459583	AI628357 AI907673	Hs.208037	ESTs gb:lL-BT152-080399-004 BT152 Homo sapien	2.5
76				Base or reconditioned by 195 units 25this	2.5
75	TABLE 2				
	Pkey:			set identifier number	
	CAT nun Accessio		ne cluster num nbank accessio		
٥٨				······································	
80	Pkey	CAT Numbe			
	408432 412225	1058667_1 1284108_1	AW195262 AW902042	! R27868 AW811262 ! N77591	
	412436	129439_1		AA135130 AA484059 AA102419 AW877765	
				•	
				333	

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	416120	1571266_1	H45739 H515	13 H19779		
	416871	1626761_1	H98716 N907			
	416913	163001_1	AW934714 BE	161007 BE162500 AW749902 AW7	49864 BE162498 BE161005 AA1	90449 AW513465 BE161006 BE162499
5	422864 422949	222336_1 223184_1		1145 R15289 AA451945 AA476690 6456 AA319377 AW961532 T48452		31 081821
	422977	223410_1				059 AA570223 AA574389 AA582438 A1745346 AW964510 AA319642
		-	AW853758 H	56414		
	423756	231725_1		834883 AA330555		
10	425168 425517	247552_1 252729_1		3929 AA351636 H78818 AA477084 163336 AA369833	Z28957 H80194	•
10	426413	266650_1		162736 AA358827 V954494 A1022688		
	428002	285602_1		418711 BE071915 BE071920 BE07	1912	
	428679	294049_1	AA431765 AA	432015		
15	428858	296453_1		Y237453 BE327496 N47347 N56961	7	
13	429007 429163	298301_1 300543_1		3145 AL119015 AW904500 V974271 AA592975 AA447312		
	433532	368950 1		A598607 AA742735		
	436190	41555_1	AK001059 AA			
20	437034	431713_1		808575 AW976668		•
20	438458	457837_1		A807807 D29548		
	438993 439566	467651_1 47387_1		\834879 Al926361 77884 W72711		
	440322	491966_1			0484 RE070397 BE070395 BE07	0201 BE070198 BE070404 BE070270 BE070400
25	444584	611496_1	AJ168422 D8			
25	447197	711623_1	R36075 AI36			
	448451 450625	764066_1 84032_1		39898 AW000978 AI598202 AI5217 A513951 AA010406	U6	
	452453	918300_1		02518 AI902516		
	454996	1248640_1	AW850180 A			
30	455350	1283853_1	AW901809 A	<b>W901787</b> AW901795 AW901792 AV	V901744 AW901753 AW901807 A	W901798
	TABLE 24	^				
	Pkey:	-	ique number com	esponding to an Eos probeset		
	Ref.	Se	quence source. T	he 7 digit numbers in this column an	e Genbank Identifier (GI) numbers	. "Dunham, et al." refers to the publication entitled "The DNA
35		sec	quence of human	chromosome 22° Dunham, et al. (19	99) Nature 402:489-495.	,,,,,,,,
	Strand:	Ind		from which exons were predicted.		
	Nt_positio	n, mg	icates nucleotote	positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position		
40	400777	8131663	Plus	70745-71121		
	400780	8131663	Minus	118372-118619		
	400859 400860	9757499 9757499	Minus	91888-92018,98131-98294,99474-	99570	
	400992	8096828	Minus Plus	151830-152104,152649-152744 140390-140822		
45	401324	9863791	Plus	234057-234174		
	402408	9796239	Minus	110326-110491		
	402604 402605	9909420	Plus	20393-20767		
	402693	9909420 8569863	Minus Minus	47680-47973 82366-82515		
50	402855	9662953	Minus	59763-59909		
	404029	7671252	Plus	108716-111112		
	404048	3688074	Minus	54421-56808		
	404049 404283	3688074 2276311	Minus Minus	75765-78155 99460-99564		,
55	404299	5738652	Minus	3826-4025		
	404541	8318559	Plus	103456-103664		
	404584	9857511	Plus	138651-139153		
	404593 404721	9944086 9856648	Minus Minus	74922-75788 173763-174294		
60	404819	4678240	Plus		16859 16941,17075 17170,17287	,17389-17529,18261-18357,18443-18578
	405238	7249119	Minus	51728-51836		,11303-11325,10201-10331,10-43-10310
	405771	7018349	Plus	91191-91254,91510-91589		
	405819 406311	4007557	Plus	2830-2967		
65	400311	9211559	Minus	137114-139033		
	TABLE 2	SA: ABOUT	202 GENES UP-	REGULATED IN GLIOBLASTOMA (	COMPARED TO NORMAL ADULT	CENTRAL NERVOUS SYSTEM (CNS)
	7 able 25/	Nists about 1	202 genes up-reg	ulated in glioblastoma compared to r	normal adult central nervous system	m (CNS). These were selected from 59680 probesets on the
70	ofioblasto	ma level was	set to the 75° ner	an man me rado or "everage" grobias Centile amonost vorinus dichlastom:	oma to "average" normal aduli CA	4S tissues was greater than or equal to 2.0. The "average" dult CNS tissue level was set to the 95" percentile amongst various
	non-maile	mant tissues.	In order to remov	e gene-specific background levels o	non-specific hybridization, the 10	P percentile value amongst various non-malignant tissues was
	subtracte	d from both th	e numerator and	the denominator before the ratio was	evaluated.	
	Pkey:			et identifier number		
75	ExAccn: Unigenet		xemplar Accessio nigene number	n number, Genbank accession numb	DET .	
	Unigene		nigene gene tide			
	RI:			itile turnor to 95% percentile normal a	dult nervous system tissue	
	Oke-				=	
80	Pkey 452461	ExAcca N78223	UnigenelD Hs.108106	Unigene Title transcription factor		R1 20.1
	436895	AF037335	Hs.5338	carbonic anhydrase XII		15.2
	453941	U39817	Hs.36820	Bloom syndrome		14.2
	443247	BE614387	Hs.333893	c-Myc target JPO1		12.4

	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.0
	447342 422163	AI199268 AF027208	Hs.19322 Hs.112360	Homo sapiens, Similar to RIKEN cDNA 2010	11.7
_	439451	AF086270	Hs.278554	prominin (mouse)-like 1 heterochromatin-like protein 1	11.4 11.2
5	424800	ALD35588	Hs.153203	MyoD family inhibitor	10.2
	416111 444190	AA033813 AI878918	Hs.79018 Hs.10526	chromatin assembly factor 1, subunit A (	10.0
	412140	AA219691	Hs.73625	cysteine and glycine-rich protein 2 RAB6 interacting, kinesin-like (rabkines	9.9 9.9
10	449340	AW235786	Hs.195359	hypothetical protein MGC10954	9.8
10	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	9.4
	439978 411411	BE139460 AA345241	Hs.124673 Hs.55960	Homo sapiens cDNA FLJ11477 ffs, ctone HE ESTs, Weakly similar to KIAA1330 protein	8.9 8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.2
15	420092	AA814043	Hs.88045	ESTs	7.9 ·
13	422631 453392	BE218919 U23752	Hs.118793 Hs.32964	hypothetical protein FLJ10688	7.9
	438527	A#969251	Hs.115325	SRY (sex determining region Y)-box 11 RAB7, member RAS oncogene family-like 1	7.9 7.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.8
20	418661 440684	NM_001949 AI253123	Hs.1189	E2F transcription factor 3	7.8
	429643	AA455889	Hs.127356 Hs.167279	ESTs, Highly similar to S21424 nestin [H FYVE-finger-containing Rab5 effector pro	7.8 7.7
	409638	AW450420	Hs.21335	ESTS	7.5
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	7.5
25	456759 412777	BE259150 Al335773	Hs.127792 Hs.270123	delta (Drosophila)-like 3 ESTs	7.5 7.4
	436607	AW661783	Hs.211061	ESTs	7.3
	432058 417061	AW665996 AI675944	Hs.130729	ESTs. Weakly similar to ALU1_HUMAN ALU S	7.3
	428976	AL037824	Hs.188691 Hs.194695	Homo sepiens cDNA FLJ12033 fis, clone HE ras homolog gene family, member I	7.3 7.2
30	433244	AB040943	Hs.271285	KIAA1510 protein	7.1
	436726	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypotheti	7.1
	408432 434164	AW195262 AW207019	Hs.148135	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens serine/threonine kinase 33	7.1 7.0
26	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	7.0
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to 138598 zinc fing	7.0
	432656 431117	NM_000246 AF003522	Hs.3076 Hs.250500	MHC class II transactivator delta (Drosophila)-like 1	6.8
	453387	AI990741	Hs.252809	ESTs	6.8 6.8
40	418821	AA436002	Hs.183161	ESTs	6.6
40	437034 411252	AA742643 AB018549	Hs.69328	gb:ny91c01.s1 NCt_CGAP_GC81 Homo sapiens MD-2 protein	8.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.5 6.4
	452953	AJ932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	6.3
45	433532 420311	AW975367 AW445044	Hs.38207	gb:ES7387475 MAGE resequences, MAGN Homo Human DNA sequence from clone RP4-530(15	6.3
	418097	R45137	Hs.21868	ESTs	6.3 6.2
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	6.2
	435256 449448	AF193766 D60730	Hs.13872 Hs.57471	cytokine-like protein C17 ESTs	6.1
50	403790	000,00	113.51 47 1	2518	6.1 6.0
	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	420674 435542	NM_000055 AA687376	Hs.1327 Hs.269533	butyryicholinesterase ESTs	6.0
	418216	AA662240	Hs.283099	AF15q14 protein	5.9 5.8
55	439086	AF085947		gb:Homo sepiens full length insert cDNA	5.8
	408037 412225	AW271720 AW902042	Hs.42233	hypothetical protein FLJ10300 gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7 5.7
60	435005 429149	U80743	Hs.306094	trinucleotide repeat containing 12	5.7
UU	429149	AW193360 AJ272141	Hs.197962 Hs.83484	ESTs, Wealdy similar to 138022 hypotheti SRY (sex determining region Y)-box 4	5.7 5.6
	405558		. 4.55	over from accession with to Bross 1 Loom 2	5.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
65	442547 413063	AA306997 AL035737	Hs.217484 Hs.75184	ESTs, Wealtly similar to ALU1_HUMAN ALU S chitinase 3-like 1 (cartilage glycoprole	5.6 5.5
	420560	AW207748	Hs.59115	ESTs	5.5
	408096	BE250162	Hs.83765	dihydrofolate reductase	5.5
	443539 426318	AI076182 AA375125	Hs.134074 Hs.147112	ESTs, Moderately similar to ALU6_HUMAN A Homo sapiens cDNA: FLJ22322 fis, clone H	5.4
70	429115	AA446728	Hs.289020		5.4 5.3
	453900	AW003582	Hs.226414	ESTs. Weakly similar to ALUS_HUMAN ALU S	5.3
	444168 432789	AW379879 D26351	Hs.3104	gb:RC1-HT0256-081199-011-f01 HT0256 Hamp KIAA0042 gene product	5.3
7.	437036	AI571514	Hs.133022	ESTs	5.3 5.2
75	421247	BE391727	Hs.102910	general transcription factor IIH, polype	5.2
	441523 451106	AW514263 BE382701	Hs.301771	ESTs, Weskly similar to ALUF_HUMAN !!!!	5.2
	457211	AW972565	Hs.25960 Hs.32399	v-myc avian myelocytomatosis viral relat ESTs, Wealdy similar to S51797 vasodilat	5.1 5.1
80	454157	AW162906	Hs.312481	ESTs. Weakly similar to S66668 hydrogen	5.1
οU	423343 425292	AA324643 NM_005824	Hs.246106		5.1
	406679	AA070788	Hs.155545	37 kDa leucine-rich repeat (LRR) protein gb:zm66b07.r1 Stratagene neuroepithelium	5.1 5.1
	442671	AI005668	Hs.134779		5.1
				226	

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	433001	AF217513	Hs.279905	done HQ0310 PRO0310p1	5.0
	418819	AA228776	Hs.191721	ESTs	5.0
	432946	U60899	Hs.279854	mannosidase, alpha, class 28, member 1	4.9
5	420730	NM_002691	Hs.99890	polymerase (DNA directed), delta 1, cata	4.9
,	441217	A#922183	Hs.213246	ESTs	4.9
	453385	AW296101	Hs.252806	ESTs	4.8
	418203 450813	X54942	Hs.83758	CDC28 protein kinase 2	4.7
	444006	AI739625	Hs.203376	ESTs	4.7
10		8E395085	Hs.10086	type i transmembrane protein Fn14	4.7
10	412530	AA766268	Hs.266273	hypothetical protein FLI 13346	4.7
	431070 429786	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
		AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (tr	4.7
	405771 457065	AJ476318	U- 400400	Fox	4.6
15	436190	AK001059	Hs.192480	ESTs	4.6
13	400859	VV001023		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	435267	N23797	te- 450554	F07-	4.6
	443454	AI057494	Hs.110114 Hs.133421	ESTs .	4.6
	452811	AA937079		ESTs	4.5
20	437267	AW511443	Hs.118983	hypothetical protein FLJ12150	4.5
LU	435020	AW505076	Hs.258110	ESTs	4.5
	454269	AI961060	Hs.301855 Hs.129908	DiGeorge syndrome critical region gene 8	4.5
	422106	D84239	Hs.111732	KIAA0591 protein	4.5
	422765	AW409701	Hs.1578	Fc fragment of IgG binding protein baculoviral IAP repeat-containing 5 (sur	4.5
25	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125	16.100023		4.5
	417308	H80720	Hs.81892	gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens KIAA0101 gene product	4.5
	422170	A1791949	Hs.112432	anti-Mullerian hormone	4.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.4
30	406568	AF088886	Hs.11590	cathepsin F	4.4
	426812	AF 105365	Hs.172613	solute carrier family 12 (polassium/chio	4.4
	402516		. 4.172010	double desires restely 12 (postassionisticate)	4.4
	432865	AI753709	Hs.152484	ESTs, Wealdy similar to I38022 hypotheti	4.4 4.4
	413625	AW451103	Hs.71371	ESTs	4.4
35	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	4.3
40	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	441020	W79283	Hs.35962	ESTs	4.3
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3
45	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	405701				4.3
	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2
50	433323	AA805132	Hs.30701	ESTs	4.2
50	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4,1
	441269	AW015206	Hs.178784	ESTs	4,1
55	418727	AA227609	Hs.94834	ESTs	4.1
22	433006	8E242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	4,1
	430786	AA486144	Hs.31293	ESTs	4.1
	445372	N36417	Hs.144928	ESTs	4.1
60	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.0
VV	457465	AW301344	Hs.122908	ONA replication factor	4.0
	422094 442029	AF129535	Hs.272027	F-box only protein 5	4.0
	442029 459321	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
	421308	AW044477	Hs.299538	ESTs	4.0
65	420567	AA687322 AK000812	Hs.192843	leucine zipper protein FKSG14	4.0
05	447004	AW296968	Hs.98874	similar to proline-rich protein 48	4.0
	448295	AU381911	Hs.157539	ESTs	4.0
	439699	AF086534	Hs.334859	KIAA1814 protein	3.9
	440704	M69241	Hs.187561 Hs.162	ESTs, Moderately similar to ALU1_HUMAN A	3.9
70	453096	AW294631		Insufin-like growth factor binding prote	3.9
. •	457026	AA397620	Hs.11325 Hs.48692	ESTs ESTs	. 3.9
	404642		15.40032	E018	3.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	3.9
75	437718	AI927288	Hs.196779	ESTs	3.9
	438490	AW593272	Hs.301299	ESTS	3.9
	429919	AA460692	Hs.278945	hypothelical protein FLJ23024	3.9
	413604	R51767		gbryg73g11.r1 Soares Infant brain 1NIB H	3.9
••	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
80	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.9
	449300	AI656959	Hs.222165	ESTs	3.9
	452203	X57522	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8 3.8
	425769	U72513	Hs. 159486	Human RPL13-2 pseudogene mRNA, complete	3.8 3.8
					3.0

	404295				3.8
	410361	BE391804	Hs.62661	guanylate trinding protein 1, interferon-	3.8
	428728	NM_016625	Hs.191381	hypothetical protein	3.8
5	409142 430172	AL136877 AA468591	Hs.50758 Hs.161889	SMC4 (structural maintanance of chromoso ESTs	3.8
_	447499	AW262580	Hs.147674	protocadherin beta 16	3.8 3.8
	405884			providentification for	3.8
	437236	AW137B17	Hs.244353	ESTs	3.7
10	418883 444143	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
	425529	AW747996 NM_014656	Hs.160999 Hs.158282	ESTs, Moderately similar to A56194 throm KIAA0040 gene product	3.7
	425502	R98895	Hs.125823	ESTs	3.7 3.7
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
15	402424	145.4500			3.7
13	429469 434072	M64590 H70854	Hs.27 Hs.283059	glycine dehydrogenase (decarboxylating;	3.7
	414872	U82010	Hs.77513	Homo sapiens PRO1082 mRNA, complete cds COX10 (yeast) homolog, cytochrome c oxid	3.7 3.7
	426071	AW138057	Hs.163835	ESTs	3.7
20	419078	M93119	Hs.89584	insulinoma-associated 1	3.7
20	428037 416547	N47474	Hs.89230	potassium intermediate/small conductance	3.7
	436899	H62914 AA764852	Hs.268946 Hs.291567	ESTs. Wealtly similar to PC4259 ferritin ESTs	3.7
	436722	AW975977	110.251001	gb:EST388086 MAGE resequences, MAGN Homo	3.6 3.6
25	440652	AJ216751	Hs.143977	ESTs	3.6
25	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6
	452103 409048	R42764 H59990	Hs.339654 Hs.37699	ESTs, Wealdy similar to 138022 hypotheti ESTs	3.6
	439546	AF088056	113.31033	gb:Homo sapiens full length insert cONA	3.6 3.6
20	443544	AJ076315	Hs.16359	ESTs	3.6
30	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
	435889 420301	AJ249107 AA767526	Hs.269901	ESTs	3.6
-	438078	AI016377	Hs.22030 Hs.131693	paired box gene 5 (B-cell lineage specif ESTs	3.6
25	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6 3.6
35	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	3.5
	424085 446291	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.5
	432281	BE397753 AK001239	Hs.14623 Hs.274263	interferon, gamma-inducible protein 30 hypothetical protein FLJ 10377	3.5
	436123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5 3.5
40	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo	3.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	3.5
	435065 435632	BE084391 AW291488	Hs.117305	gb:RC4-BT0310-110300-015-b08-BT0310 Horno	3.5
	447101	N72185	Hs.44189	Homo sapiens, clone IMAGE:3682908, mRNA ESTs	3.5 3.5
45	410530	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	3.5
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.5
	453616 439743	NM_003462 AL389956	Hs.33846 Hs.283858	dynein, axonemal, light intermediate pol	3.5
	453884	AA355925	Hs.36232	Homo sapiens mRNA full length insert cDN KIAA0186 gene product	3.5 3.5
50	424954	NM_000546	Hs.1846	turnor protein p53 (Li-Fraumeni syndrome)	3.5
	420721	AA927802	Hs.159471	ZAP3 protein	3.5
	426764 420649	AA732524 AI866964	Hs.151464 Hs.124704	ESTs, Wealdy similar to ALUC_HUMAN !!!!	3.4
	448831	AL080123	Hs.22182	ESTs, Moderately similar to S65657 alpha zinc finger protein 23 (KOX 16)	3.4 3.4
55	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604				3.4
	442407 414300	AW469584 Al304870	Hs.32353	mitogen-activated protein kinase kinase	3.4
	444670	H58373	Hs.188680 Hs.332938	ESTs hypothetical protein MGC5370	3.4
60	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4 3.4
	452211	Af985513	Hs.233420	ESTs	3.4
	414416 449961	AW409985	Hs.76084	hypothetical protein MGC2721	3.4
	413257	AW265634 8E075035	Hs.133100	ESTs gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4
65	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.4 3.4
	417404	NM_007350	Hs.82101	plackstrin homology-like domain, family	3.4
	422848	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.4
	446189 437385	HB5224 AA757055	Hs.214013 Hs.164060	ESTs ESTs	3.4
70	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 atpha	3.4 3.4
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.4
	455778	BE088748		gb:CM2-8T0693-210300-123-d09 BT0693 Homo	3.3
	417546 412471	M65569	Hs.18845	ESTs	3.3
75	454631	M63193 AW811324	Hs.73946	endothelial cell growth factor 1 (plate) gb:ll.3-ST0141-131099-017-A02 ST0141 Homo	3.3
	454294	AB000734	Hs.50640	JAK binding protein	3.3 3.3
	457131	AC002310	Hs.301463	Human Chromosome 18 BAC clone CIT987SK-A	3.3 3.3
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
80	449676 436211	AW380579 AK001581	Hs.209657 Hs.334828	ESTs hypothetical protein FLJ 10719, KIAA1794	3.3
	453746	AL120611	113,334020	gb:DKFZp761H119_r1 761 (synonym: hamy2)	3.3
	452799	A1948829	Hs.213786	ESTs	3.3 3.3
	435380	AA579001	Hs.192221	EST ₅	3.3

	400746	Marne	11- 2052	and all and a second a second and a second a	
	426746 453362	J03626 H14988	Hs.2057 Hs.107375	undine monophosphate synthetase (orotat	33
	456473	AI202788	Hs.25682	ESTS	3.3
_	416426	AA180256	Hs.210473	Homo sapiens mRNA for KIAA1863 protein, Homo sapiens cDNA FLJ14872 fs, clone PL	3.3
5	445777	AI580371	Hs.145384	ESTs	3.3 3.3
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299				3.3
10	404108				3.3
10	425189	H16622		gb:ym26c07.r1 Soares infant brain 1NIB H	3.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.3
	450193 427725	AI916071 U66839	Hs.15607 Hs.180533	Homo sapiens Fanconi anemia complementat	3.2
	424051	AL110203	Hs.138411	mitogen-activated protein kinase kinase	3.2
15	418968	NM 000078	Hs.89538	Homo seplens mRNA; cDNA DKFZp586J1922 (f	3.2
	449248	M33782	Hs.23391	chotesteryl ester transfer protein, plas Homo sepiens, Similar to transcription (	3.2
	439416	W58294	Hs.56254	ESTs	3.2 3.2
	401596	AA172106	Hs.110950	Rag C protein	3.2 3.2
	408380	AF123050	Hs.44532	diubiquitin	3.2
20	450325	Al935962	Hs.26289	ESTA	3.2
	428730	AA625947	Hs.25750	ESTs	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2
25	442710 435232	AI015631 NM_001262	Hs.23210	ESTs	3.2
23	430970	AI018210	Hs.4854 Hs.144083	cyclin-dependent kinase inhibitor 2C (p1	3.2
	416192	NM_005036	Hs.998	ESTs	3.2
	446676	H09380	Hs.300965	peroxisome proliferative activated recep ESTs	3.2
	451459	AJ797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2 3.2
30	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
	413840	AI301558	Hs.146381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	12
	432593	AW301003	Hs.51483	ESTs. Wealdy similar to hypothetical pro	3.2
35	458786	AI457098	Hs.280848	ESTs	3.2
33	455909	BE156417	Hs.278798	ESTs .	3.2
	419311 439710	AA689591		gb:nv66a12s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	434559	AF086543 AF147315		gb:Homo sapiens full length insert cDNA	3.2
	455800	R22479	Hs.167073	gb:Homo saplens full length insert cDNA Homo saplens cDNA FLJ 13047 fis, clone NT	3.1
40	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1 3.1
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
46	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.1
45	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo saplen	3.1
	447959	AJ452784	Hs.270270	ESTs, Wealthy similar to 2109260A B cett	3.1
50	404589 421764	AI681535	Hs.148135		3.1
	419986	AI345455	Hs.78915	serine/threonine kinase 33 GA-binding protein transcription factor.	3.1
	416941	BE000150	Hs.48778	niban protein	3.1
	414761	AU077228	Hs.77256	enhancer of zeste (Orosophila) homolog 2	3.1 3.1
~ ~	449611	AI970394	Hs.197075	ESTs	3.1
55	434746	AA648368	Hs.295368	ESTs	3.1
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum armyloid A1	3.1
	417642 452472	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
60	452472	AW957300 NM 000929	Hs.294142	ESTs, Wealthy similar to C55663 oligodend	3.1
-	440052	NM_000929 AI633744	Hs.290 Hs.195648	phospholipase A2, group V ESTs. Wealth similar to (2002) benethed	3.1
	426531	AA381071	110.133040	ESTs, Wealdy similar to 138022 hypotheti gb:EST94100 Activated T-cells XII Homo s	3.1 3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
	406267			process with a such action for a factor	3.1
65	447039	AV661798	Hs.282915	ESTs	3.1
	404802				3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
	419314	AW971924	Hs.87280	ESTs	3.0
70	435894 432140	A1076667 AK000404	Hs.188011	ESTs	3.0
, ,	443426	AF098158	Hs.272688	hypothetical protein FLJ20397	3.0
	425202	AW962282	Hs.9329 Hs.152049	chromosome 20 open reading frame 1 ESTs, Weakly similar to I38022 hypotheti	3.0
	407047	X65965	14.102073	gb:H.sapiens SQD-2 gene for manganese su	3.0
~-	418241	M26682	Hs.1149	UM domain only 1 (rhombotin 1)	3.0
75	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse	3.0 3.0
	412950	BE018581	Hs.245342	hypothetical protein FLJ14642	3.0
	428670	AA431682	Hs.134832	ESTs	3.0
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0
80	437756	AA767537	Hs.197096	ESTs	3.0
00	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.0
	402374 443885	AL135225 H91806	Hs.301865	dopachrome tautomerase (dopachrome detta	3.0
	434008	AA740878	Hs.15284 Hs.112982	ESTs ESTs	3.0
	-5-1000		110.112302	EQ13	3.0

	452568	AA805634	Hs.300870	Maria anciera - Data - Data Duritz-Cattinato H.	••
	414239	AI288330	Hs.182330	Homo sapiens mRNA; cDNA DKFZp547M072 (fr ESTs	3.0 3.0
	421013	M62397	Hs.1345	Mutated in cotoractal cancers	3.0
-	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.0
5	410276	AI554545	Hs.68301	ESTs	3.0
	433865	N29862	Hs.44104	ESTs	3.0
	406028 401626				3.0
	415949	H10562	Hs.21691	ESTa	3.0
10	418583	AA604379	Hs.86211	hypothetical protein	3.0 3.0
	417933	X02308	Hs.82962	frymklylate synthetase	3.0
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.0
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.0
15	427940	AA417812	Hs.38775	ESTs	29
13	455060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	29
	421988 448775	AW450481 AB025237	Hs.161333 Hs.388	ESTs	2.9
	438598	AI805943	Hs.326067	nudix (nucleoside diphosphate linked moi hypothetical protein MGC5178	2.9 2.9
	429612	AF062649	Hs.252587	pituitary turnor-transforming 1	2.9
20	451189	AA016019	Hs.40905	ESTs	29
	401558				2.9
	426207	BE390657	Hs.30026	HSPC182 protein	29
	404721				2.9
25	401384 417288	Al984792	Hs.108812	hypothetical protein FLJ22004	29
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit.	2.9 2.9
	435928	H84345	Hs.183961	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF115721 67	29
20	428242	H55709	Hs.2250	teukemia inhibitory factor (cholinergic	2.9
30	439972	Al348100	Hs.124662	ESTs	2.9
	433112	AA973801	Hs.144553	ESTs, Weakly similar to unnamed protein	2.9
	423751 406748	AW235633 AW339106	Hs.46525 Hs.217493	ESTs	2.9
	422154	179045	Hs.126927	annexin A2 ESTs	2.9
35	405588	*******	***********	2013	2.9 2.9
	440911	AA909538	Hs.143562	ESTs	29
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066	ESTs	29
40	410114	AW590540	Hs.271280	EST8	2.9
70	419217 415849	AA504571 R20529	Hs.6806	gb:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens	2.9
	448140	AF146761	Hs.20450	ESTs BCM-like membrane protein precursor	29
	453331	AI240665	Hs.8895	ESTs	2.9 2.9
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	29
45	438380	T06430	Hs.6194	chendroitin sulfate proteoglycan BEHAB/b	29
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTS	2.9
	452291 415446	AF015592 F08898	Hs.28853 Hs.66075	CDC7 (cell division cycle 7, S. cerevisi	2.8
50	439518	W76326	115.00075	ESTs gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.8 2.8
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.8
	419451	AJ907117	Hs.90535	syntaxin binding protein 2	2.8
55	448789 424126	BE539108	Hs.22051	hypothetical protein MGC15548	2.8
55	458695	AA335635 AV660159	Hs.96917 Hs.282284	ESTS Missister similar to 120000 to a site of	2.8
	418973	AA233056	Hs.191518	ESTs, Wealdy similar to I38022 hypotheti ESTs	2.8 2.8
	440471	AA886146	Hs.307944	ESTs	2.8
<i>c</i> ^	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
60	433647	AA603367	Hs.222294	ESTs	2.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.8
	421723 434964	AA620400 A1638850	Hs.300717 Hs.130746	sodium channel, voltage-gated, type III,	2.8
	432022	AL162042	Hs.272348	ESTs Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
65	400517	AF242388	Hs.149585	lengsin	2.8 2.8
	433023	AW864793	Hs.87409	thrombospondin 1	2.8
	448734	8E614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	406736	AI254733	Hs.182426	ribosomal protein S2	2.8
70	409207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	2.8
, 0	440196 403961	N72847	Hs.125221	EST8	2.8
	425193	. AW965689	Hs.22509	ESTs	28
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.8 2.8
75	440483	AI200836	Hs.150386	ESTs	2.8
75	412391	AW947710		gb:RCD-MT0004-130300-011-e07 MT0004 Homo	2.8
	448769	N66037	Hs.38173	ESTs	2.8
	411632 438221	AW854829 AI798853	He 199994	gb:QV2-CT0261-201099-011-01 CT0261 Homo	2.8
	457578	AA578027	Hs.122224	ESTs, Westly similar to ALU5_HUMAN ALU S gb:n/20h01.s1 NCI_CGAP_HSC1 Homo sapiens	2.8
80	455510	AA422029	Hs.143640	ESTs, Wealthy similar to hyperpolarizatio	2.8 2.8
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	28
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.8
	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	2.8

	439662	H97552	Hs.269060	ESTs .	2.8
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.8
	414747 414598	U30872 A1094221	Hs.77204 Hs.135150	centromere protein F (350/400kD, mitosin	2.8
5	447752	M73700	Hs.105938	lung type-I cell membrane-associated gly lactotransferrin	2.8 2.8
	408761	AA057264	Hs.238936	ESTs, Wealdy similar to (defline not ava	2.8
	453350 456629	AI917771 AW891965	Hs.61790	hypothetical protein FLJ23338	2.7
	439538	AA837323	Hs.279789 Hs.164047	histone deacetylase 3 ESTs	2.7 2.7
10	458814	A1498957	Hs.170861	ESTs, Wealty similar to Z195_HUMAN ZINC	27
	456029	BE255990	Hs.218329	hypothetical protein	2.7
	451129 456412	BE072881 AW749617	Hs.280776	gb:RC2-870548-200300-012-e09 BT0548 Homo tankyrase, TRF 1-interacting ankyrin-rela	27
	453536	AA137000	Hs.62578	ESTs	27 27
15	438378	AW970529 U44060	Hs.88434	hypothetical protein FLJ21816	2.7
	425745 446322	N23033	Hs.14427 Hs.155814	Homo sapiens cDNA: FLJ21800 fis, clone H ESTs	27
	451592	AI805416	Hs.213897	ESTA	27 27
20	429466	M85835	Hs.12827	ESTs	27
20	429747 455514	M87507 AVV983871	Hs.2490	gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.7 2.7
	444207	AJ565004	Hs.79572	cathepsin D (lysosomal asparty) protease	2.7
25	427421 449655	AA402414 Al021987	Hs.3059 Hs.59970	coatomer protein complex, subunit beta ESTs	2.7
	422648	D86983	Hs.118893	Melanoma associated gene	2.7 2.7
	428494	AA233439	Hs.184634	hypothetical protein FLJ 20005	2.7
	406895 453255	X60648 AA278167	Hs.172550 Hs.19215	potypyrimidine tract binding protein (he Homo sapiens, clone IMAGE:3605822, mRNA	2.7
30	427348	NM_014137	Hs.177258	PRO0650 protein	2.7 2.7
	435370	AI964074	Hs.225838	ESTs	2.7
	407862 411874	BE548267 AA096106	Hs.50724 Hs.20403	Homo seplens cDNA FLJ10934 fis, clone OV ESTs	2.7
~ -	421192	AA833718	Hs.204529	KIAA1806 protein	2.7 2.7
35	435899	W89093	Hs.189914	ESTs	2.7
	414603 453462	R58394 AL037291	Hs.25119 Hs.236605	ESTs, Weakly similar to YEXO_YEAST HYPOT	2.7
	436554	AI985810	Hs.301173	ESTs, Moderately similar to ALU4_HUMAN A ESTs	2.7 2.7
40	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7
40	403881 431779	AW971178	Hs.268571	apolipoprotein C-I	2.7
	404984	,,,,,,,,,,,	113-200371	epospoprotein C1	2.7 2.7
	448275	BES14434	Hs.20830	kinesin-like 2	27
45	445839 411927	8E091926 8E274009	Hs.16244 Hs.772	mitotic spindle coiled-coil related prot glycogen synthese 1 (muscle)	27
-,-	404756	565, 4003	149.772	Ritcolless shim teet a (Listenses)	2.7 2.7
	447072	D61594	Hs.17279	tyrosylprotein suffotransferase 1	2.7
	422176 439627	H80977 BE621702	Hs.29076	gb:yu89a11.s1 Soares fetal liver spleen hypothetical protein FLJ21841	2.7
50	436532	AA721522		gb:nv54h12r1 NCI_CGAP_Ew1 Homo sapiens	2.7 2.7
	412833 457245	AW950547	Hs.298262	ribosomal protein S19	2.7
	446881	A1745498 A1696519	Hs.204579 Hs.14427	ESTs Homo sapiens cONA: FLJ21800 fis, clone H	2.7 2.7
<i>E E</i>	453263	R91778	Hs.99369	ESTs	2.7
55	459385 438764	BE380047 AA824524	11. 020450	gb:601159362F2 NIH_MGC_53 Homo sapiens c	2.7
	429285	AI971081	Hs.336452 Hs.20432	ESTs ESTs, Wealdy similar to I38022 hypotheti	2.7 2.7
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	2.7
60	430037 449892	BE409649 N73608	Hs.227789 Hs.50309	mitogen-activated protein kinase-activat	2.7
-	454201	AB023191	Hs.44131	ESTs KIAA0974 protein	2.7 2.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ 13164	27
_	427954 400371	J03060 U80740	Hs.247551	metaxin 1	2.7
65	452449	AW068658	Hs.20943	ESTs	2.7 2.7
	431114	AA492400	Hs.291015	ESTs	2.7
	417088 447674	M54915 BE270640	Hs.81170 Hs.19192	pim-1 oncogene	2.7
~^	403680	02270040	113,13134	cyclin-dependent kinase 2	2.7 2.7
70	454679	AWB13110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.7
	411968 422240	Al207410 R60594	Hs.69280 Hs.29002	Horno sapiens, clone IMAGE:3636299, mRNA, KIAA1706 protein	2.6
	424368	AB037766	Hs.146085	KIAA1345 protein	2.6 2.6
75	405808	. ====		·	2.6
15	419700 435972	AF084935 W95088	Hs.92357 Hs.114198	galactokinase 1 ESTs	2.6
	453568	870782	Hs.557	adrenergic, alpha-1D-, receptor	2.6 2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
80	444156 428209	AW500059 AA424197	Hs.85437 Hs.98947	ESTs. Highly similar to AF219140 1 gastr	2.6
	437640	AA764893	Hs.272155	ESTs, Wealthy similar to S33496 trypsin [ ESTs, Wealthy similar to I38022 hypotheti	2.6 2.6
	453948	AI970797	Hs.64859	ESTs	2.6
	415402	AA164587	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	2.6
				340	

	425202	101000			
	425397	J04088	Hs.156346	topoisomerase (DNA) II atpha (170kD)	26
	418228	AA962181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	401324				26
5	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	2.6
3	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.6
	457244	AA581385	Hs.162473	ESTs, Wealthy similar to I38022 hypotheti	2.6
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	2.6
	433933	AI754389	Hs.133494	Homo sapiens clone TCCCIA00164 mRNA sequ	26
10	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
10	434206	AW136973	Hs.288516	ESTs, Weakly simitar to S69890 mitagen i	2.6
	400992				2.6
	455530	AW984744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	26
	436139	AA765786	Hs.120936	ESTs	26
	448330	AL038449	Hs.207163	EST ₅	26
15	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	2.6
	433430	AI863735	Hs.186755	ESTs	26
	436693	AW973223	Hs.303197	B-cell CLL/lymphorna 7C	2.6
	429482	AF076974	Hs.203952	transformation/transcription domain-asso	2.6
20	432715	AA247152	Hs.200483	ESTs, Wealty similar to KIAA1074 protein	26
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	26
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	2.6
	414835	AA156720	Hs.185342	ESTs	2.6
~-	424489	T48851	Hs.149250	O-siglec precursor,	2.6
25	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797			Garage Control of the	26
	434573	AW372340	Hs.159717	ESTs	26
	418841	NM 002332	Hs.89137	low density lipoprotein-related protein	
	415785	R82419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6
30	450608	AA010365	Hs.193229	ESTs	2.6
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.6
	432268	BE311856	Hs.274230	3-phosphoadenosine 5-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	26
	427343	AJ880044	Hs.176977	protein kinase C binding protein 2	26
35	420917	AW135716	Hs.117330	ESTs	26
	414399	L47345	Hs.155202		2.6
	446089	AI860021	Hs.270651	transcription elongation factor 8 (SIII)	2.6
	440829	AF136407	Hs.7446	ESTs, Moderately similar to A47582 B-cel	2.6
	408475	AA315514	Hs.47986	chromosome 6 open reading frame 5	2.6
40	450946	AA374569	Hs.127698	hypothetical protein MGC10940	2.6
	421462	AF016495	Hs.104624	ESTs, Moderately similar to 2109260A B c	2.6
	434846	AW295389		aquaporin 9	2.6
	422887		Hs.119768	ESTs	2.6
	417435	A1751848	Hs.49215	ESTs	2.6
45		NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
73	437389 408981	AL359587	Hs.271586	hypothetical protein DKFZp762M115	2.5
	432180	AW500797	Hs.49427	Gem-interacting protein	25
	418079	Y18418	Hs.272822	RuvB (E coll homolog)-like 1	2.5
	437820	R40058	Hs.6911	ESTs	2.5
50	439685	AA769062	Hs.323836	ESTs, Wealdy similar to atternatively sp	2.5
50	425681	AW956781	Hs.293937	ESTs, Wealthy similar to FXD2_HUMAN FORKH	2.5
	435177	AB018297	Hs.159183	KIAA0754 protein	2.5
		AI018174	Hs.42936	ESTs	2.5
	437323 422114	AA371145 AW194851	Hs.226627	leptin receptor	2.5
55			Hs.111801	arsenate resistance protein ARS2	2.5
J J	448478 426623	AI523218 AA382826	Hs.203456	ESTs	2.5
			Hs.132793	ESTs	2.5
	448764 458385	AI568607	Hs.182112	ESTs	2.5
	403726	AIQ51489 N28939	Hs.246214	ESTs	2.5
60	444888	AI651039	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
	456179		Hs.148559	ESTs	2.5
	424840	H75490	Hs.271930	ESTs	2.5
	406273	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	25
	418054	NM_000919 NM_002318	Hs.83920	peptidytglycine alpha-amidating monooxyg	2.5
65	445936		Hs.83354	lysyl oxidase-like 2	2.5
05	454967	BE543594 AW848276	Hs.61478	hypothetical protein FLJ22329	2.5
				gb:IL3-CT0214-150200-074-E06 CT0214 Homo	2.5
	442303 456583	AA989289	Hs.129169	ESTs	25
	434263	AF179897 N34895	Hs.104105	Meis (mouse) homolog 2	2.5
70			Hs.44648	ESTs	2.5
, ,	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	2.5
	406038	Y14443	Hs.88219	zinc finger protein 200	2.5
	413495	Y12395	Hs.315177	interferon-related developmental regulat	2.5
75	423098	AA321980	Hs.204682	ESTs	2.5
, ,	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	2.5
	439841	AF038961	Hs.6710	mannose-P-dolichol utilization defect 1	2.5
	453828	AW970960	Hs.293821	ESTs	2.5
	445034	AW293376	Hs.143659	ESTs	2.5
80	449620	BE407797	Hs.23794	checkpoint with forkhead and ring finger	2.5
00	406876	AJ382286	Hs.180842	ribosomal protein L13	2.5
	412370	AW946614		gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.5
	430357	AW976789	Hs.165607	ESTs	2.5

	414853	U31116	Hs.77501	conseines had 1270 to destruction	
	416097	8E387371	Hs.118964	sarcoglycan, beta (43kD dystrophin-assoc hypothetical protein FL/20085	2.5
	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	25 25
_	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.5
5	445223	AW291553	Hs.254983	ESTs	25
	423926	X03833	Hs.1722	interleukin 1, alpha	25
	410165	BE56022B	Hs.71869	apoptosis-associated speck-like protein	2.5
	406474				2.5
10	433908	AW298141	Hs.157975	EST ₅	2.5
10	439755	AW748482	Hs.77873	B7 homotog 3	25
	437528	N\$9646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	ESTs	2.5
	415346 419337	243108	11- 0000000	gb:HSC13E071 normalized infant brain cDN	2.5
15	444606	AW291112 R09478	Hs.209978	ESTS	2.5
13	430061	AB037817	Hs.16041 Hs.230188	ESTs NIAA1396 protein	2.5
	413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
	411955	BE467339	Hs.280115	ESTs	2.5
	409278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5 2.5
20	403142		. 5.52, 00	analysissa-horrorrid contract society t	2.5 2.5
	401714				2.5
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	25
	416505	H66470	Hs.16004	ESTs	2.5
25	431518	AA743462	Hs.165337	ESTs	2.5
25	448623	BE613468	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti	2.5
	428301	AW628666	Hs.98440	ESTs, Wealdy similar to 138022 hypotheti	2.5
	404366				25
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HE	2.5
30	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
30	402856	AW939659		gb:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	24
	436805	AA731533	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
35	<b>453</b> 496 <b>453</b> 853	AA442103 AL040600	Hs.33084	solute carrier family 2 (facilitated glu	24
55	407909	AW103986	Hs.188083	ESTS	2.4
	454630	BE142075		gb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	2.4
	451026	AA013218	Hs.157492	gb:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4
	420779	L12398	Hs.99922	cer-d4 (mouse) homolog	2.4
40	438322	AA804170	Hs.221349	dopamine receptor D4 ESTs	2.4
	455908	BE158306	14.661443	gb:QV0-HT0367-150200-114-h04 HT0367 Homo	2.4
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4
	440773	AA352702	Hs.332541	Homo sepiens, Similar to RIKEN cDNA 2700	2.4 2.4
	450823	T81223	Hs.22011	complement-c1g tumor necrosis factor-ref	2.4
45	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.4
	451802	AI817711	Hs.209374	ESTs	2.4
	419417	R92491	Hs.39429	ESTs	2.4
60	407094	AF000574	Hs.22405	leukocyte immunoglobutin-like receptor,	24
50	423567	BE252949	Hs.69331	hypothesical protein FLJ13633	2.4
	427501	AI369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2.4
	435845	AA732297	Hs.113928	ESTs	2.4
55	431584	AW295121	Hs.266263	Homo sapiens cDNA FLJ14115 fis, done MA	2.4
55	440614	AA781530	Hs.127236	hypothetical protein FLJ 12879	2,4
	423721 452125	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotrophi	2.4
	452125 419508	BE312642 AW997938	Hs.28077 Hs.90786	GOP-mannose pyrophosphorylase B	24
	453446	BE299996	F13.0U/00	ATP-binding cassette, sub-family C (CFTR	2.4
60	419792	AA250890	Hs.190037	gb:500944574F1 NIH_MGC_17 Homo sepiens c ESTs	2.4
	452786	R61362	Hs.106642	ESTs. Weakly similar to T09052 hypotheti	2.4 2.4
	410447	AW816134	1.0.100012	gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	24
~-	402408			barkaman kuman abasana in	2.4
65	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.4
	414625	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403048			•	2.4
	432088	AA525454		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo sapiens	2.4
70	431592	AL021331	Hs.267749	unc93 (C.elegans) homolog A	24
70	455023	AW850907		gb:IL3-CT0220-310100-065-H11 CT0220 Homo	24
	426249	F05422	Hs.168352	nucleoporin-like protein 1	2.4
	448795	AI797713	Hs.156471	ESTs	24
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
75	414252	AA346483	Hs.126191	ESTs	2.4
, 5	417918	AA209205	Hs.163754	hypothetical protein FLJ 12606	24
	427550	BE242818	Hs.179606	nuclear RNA helicase, DECO variant of OE	24
	404020	A A 420202	U- 40400	Ch. L 200 L.A	2.4
	407846 417222	AA426202 AI525424	Hs.40403	Cbp/p300-interacting transactivator, wit	2,4
80	443639	BE269042	Hs.42053 Hs.9661	hypothetical protein MGC2383	2.4
	452706	AW449390	Hs.257150	protessome (prosome, macropain) subunit,	2.4
	401676	A11-71303V	113.237 130	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	428882	AA435915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
					2.4

		-			
	436277	R88520	Hs.120917	ESTs	2.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
	405353				2.4
-	409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithetium	2.4
5	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
	407889	R34556	Hs.30800	ESTs, Wealty similar to \$65657 alpha-1C-	2.4
	453335	AW857376	Hs.169238	fucosyftransferase 3 (galactoside 3(4)-L	24
	450621	AW297288	Hs.55918	hypothetical protein FL/11354	
	419652	AL157485	Hs.91973		24
10	421151	BE174431		hypothetical protein	24
			Hs.63386	EST ₈	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALUZ_HUMAN A	2.4
	405288				24
16	453527	R49570	Hs.180236	EST8	2.4
15	429875	A3091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	2.4
	436360	AI962796	Hs.136754	ESTs	24
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.4
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	24
	449539	W80363	Hs.58446	ESTs	24
20	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	
	404584		. 0.200110	hyddhydrau scannard with OEWS	24
	454276	AW294996	Hs.255374	COT.	2.4
	423746	AW361817		ESTs	2.4
			Hs.132370	NADPH coddase 1	24
25	415558	AA885143	Hs.125719	ESTs	2.4
23	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	24
	406953	L36847		gb:Human (clone p17/90) rearranged iduro	2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4
	451031	AJ360187	Hs.4254	ESTs	2.4
~ ~	455302	AW997641		gb:RC6-BN0052-170200-011-D05 BN0052 Homo	2.4
30	449063	AJ627352	Hs.236547	Homo sapiens, clone IMAGE:2905978, mRNA	2.4
	401048				
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
	425848	BE242709	Hs.159637		2.4
	449086	A1628357		valyl-tRNA synthetase 2	2.4
35			Hs.208037	ESTs	2.4
"	415238	R37780	Hs.21422	ESTs	2.4
	448337	AW206453	Hs.3782	ESTs	24
	416991	N36389	Hs.141296	KIAA0226 gene product	2.3
	412600	L28824	Hs.74101	spleen tyrosine kinase	2.3
••	418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
40	440769	BE561793	Hs.21446	KIAA1716 protein	2.3
	450437	X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	
	406739	AI566709	Hs.182426	ribosomal protein S2	2.3
	418506	AA084248	Hs.85339		2.3
45	410286	AI739159		G protein-coupled receptor 39	2.3
73			Hs.61898	DKFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	ESTs	2.3
	405605				2.3
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
50	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	2.3
50	445828	F05802	Hs.81907	ESTs .	2.3
	457195	AB011099	Hs.196647	KIAA0527 protein	23
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA	2.3
	423198	M81933	Hs.1634	cell division cycle 25A	2.3
	457730	AW753613		gb:RC1-CT0268-060100-013-e01 CT0268 Homo	
55	412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	2.3
-	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.3
	446288	AW189209	Hs.149708	ESTs	2.3
	436954	AA740151	Hs.130425		2.3
	411658	AW855598	FIS. 130423	EST8	2.3
60	404240	VI103223Q		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
55		Uncoo4		-b	2.3
	456094	H95091		gb:yw57a09.r1 Soares_placenta_8to9weeks_	2.3
	416951	AA190926	Hs.190785	ESTs, Moderately similar to \$65657 alpha	2.3
	406737	AJ356586		gb:qy15h09.x1 NCI_CGAP_Brn23 Homo sapien	2.3
C F	458453	AI097452	Hs.135095	ESTs	2.3
65	452330	AI879127	Hs.191979	KIAA1733 protein	2.3
	408523	AW833259	Hs.314287	ESTs	2.3
	455470	AW947992		gb:PM0-MT0011-240300-001-c09 MT0011 Homo	2.3
	436323	R17697	Hs.140963	ESTs. Weakly similar to (38022 hypothet)	2.3
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	
70	416171	H23896	Hs.125790		2.3
	419134	T89863		leucine-rich repeat-containing 2	2.3
	445933		Hs.221771	ESTs	2.3
	422089	AV655733	Hs.293860	spinster-like protein	23
		AA523172	Hs.103135	ESTs. Weakly similar to SFR4_HUMAN SPLIC	2.3
75	449911	A1262106	Hs.12653	ESTs	2.3
13	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.3
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.3
	423491	AA191765	Hs.129673	eukaryotic translation initiation factor	2.3
00	407182	AA312551	Hs.230157	ESTs .	2.3
80	411448	AA178955	Hs.271439	ESTs, Weakly similar to 138022 hypotheti	
-	438644	AJ126162	Hs.129037	ESTs. Westly saleate to 130022 hypotheti	2.3
	432691	U29725			2.3
			Hs.3080	mitogen-activated protein kinase 7	2.3
	452198	AI097560	Hs.61210	ESTs, Wealty similar to I38022 hypotheti	2.3
				A . A	

	411125	AA151647	Hs.68877	exteches h 245 whole extensists	
	404054	221131947	12.00017	cytochrome b-245, alpha polypeptide	2.3 2.3
	430458	AA479300	Hs.225706	ESTs, Wealdy similar to 138022 hypotheti	2.3
_	440210	AW874562	Hs.125296	ESTS	2.3
5	445727	AB011095	Hs.16032	KIAA0523 protein	2.3
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	23
	438379	N23018	Hs.171391	C-terminal binding protein 2	23
	449919	A1674685	Hs.200141	ESTs	23
10	415293 441126	R49462 NM_000429	Hs.106541	ESTs	2.3
10	408203	AA053137	Hs.323715	methionine adenosyltransterase I, alpha	23
	434941	AW073202	Hs.42390 Hs.334825	nasopharyngeal carcinoma susceptibility Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
	450748	AI733093	Hs.130016	ESTS	23
	404185		. 4	2010	23 23
15	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
	451370	AJ791929	Hs.300782	ESTs	2.3
	400034				2.3
	407723	AW071161	Hs.252873	ESTs .	23
20	431320	AW969474	Hs.183070	ESTs	2.3
20	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	23
	419225 444656	U70073 AI277924	Hs.145199	gb:HSU70073 Human Homo sapiens cDNA clon ESTs	23
	405741	14511354	16,143133	CQ13	23
25	400917				23 23
	432567	AA736777	Hs.293770	ESTs .	23
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	23
	450514	AC005785	Hs.25059	A kinase (PRKA) anchor protein 8	2.3
20	418400	BE243026	Hs.301989	KIAA0246 protein	2.3
30	444019	BE173977	Hs.10098	putative nucleolar RNA helicase	2.3
	406326	1154400			2.3
	412077	NS1107	Hs.47199	ESTs, Weakly similar to FLJ00004 protein	23
	427647 414528	W19744 AA148950	Hs.180059 Hs.188836	Homo sapiens cONA FLJ20653 fis, clone KA	23
35	414854	BE546797	Hs.51483	ESTs ESTs, Weakly similar to hypothetical pro	2.3
	420352	BE258835	113.51465	gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.3
	439467	AW292275	Hs.158365	ESTs	2.3 2.3
	402627				2.3
40	451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	23
40	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.3
	423869	BE409301	Hs.134012	C1q-related factor	2.3
	405915				2.3
	431503	NM_012129	Hs.258576	claudin 12	2.3
45	423306	W88562	Hs. 108198	ESTs	2.3
73	443232 433064	AF161521 D79991	Hs.9081	phenylalanyi-tRNA synthetase beta-subuni	2.3
	434437	AJ912566	Hs.30002 Hs.187813	SH3-containing protein SH3GLB2; KIAA1848	2.3
	435191	BE407866	Hs.170253	ESTs hypothetical protein FLJ23282	23
	420006	H14429	Hs.94300	serologically defined colon cancer antig	23 23
50	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3
	403166			,, ,	2.3
	422119	A1277829	Hs.111862	KIAA0590 gene product	2.3
	403751				23
55	426451	A1908165	Hs.169946	GATA-binding protein 3	23
ور	427413 409091	BE547647 AW970386	Hs.177781	hypothetical protein MGC5618	23
	440491	R35252	Hs.269423	ESTs Worlds similar to 21000004 0 and	2.3
	427722	AK000123	Hs.24944 Hs.180479	ESTs, Wealdy similar to 2109260A B cell hypothetical protein FLJ20116	2.3
	405747		1.0.100715		23 23
60	438210	AA780519	Hs.311601	EST	2.3
	404652				2.3
	423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	22
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.2
65	444424 434031	AJ654684	Hs.196377	ESTs	2.2
05	427650	BE384165	Hs.23723	pseudouridytate synthase 1	2.2
	435220	AW501245 D50030	Hs.252259 Hs.104	ribosomal protein S3	2.2
	438279	AAB05166	Hs.154762	HGF activator HIV-1 rev binding protein 2	2.2
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
70	429961	BE246829	Hs.226770	DKFZP566C0424 protein	2.2 2.2
	442065	AI831229	Hs.128417	hypothetical protein FLJ14009	2.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.2
	420538	AL117455	Hs.275438	histone deacetylase 7A	2.2
75	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
13	443753	AW387578	Hs.134749	ESTs	22
	423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	2.2
	446572 412247	AV659151 AE022375	Hs.282961	ESTs	2.2
_	412247 421040	AF022375 AA715026	Hs.73793 Hs.135280	vascular endothelial growth factor	2.2
80	426212	871824	Hs.167988	ESTs neural cell adhesion molecule 1	2.2
	455584	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	22
	406851	AA609784	Hs.180255	major histocompatibility complex, class	2.2 2.2
	444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	2.2

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	419575 418672	U43431 L44284	Hs.91175 Hs.159743	topoisomerase (DNA) III alpha ESTs	
	456261	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0694 protein	
5	415737	AA167626	Hs.118743	ESTs	
,	447554 405159	Al391598	Hs.38119	ESTs, Weakly similar to ALU1_HUMAN ALU S	
	442177	AW561820	Hs.211413	ESTS	
	446139 458339	H77395 AW976853	Hs.39749 Hs.172843	ESTs ESTs	
0	401876	A11370033	118.172040		
_	439566	AF086387		gb:Homo sapiens full length insert cDNA	
	425079	H09963	Hs.2257	vitronectin (senum spreading factor, som	
	441837 430644	AA361743 AB015419	Hs.179881 Hs.247710	core-binding factor, beta subunit preproprolactin-releasing peptide	
5	431474	AL133990	Hs.190642	ESTs	
	407739	NM_002285	Hs.38070	hymphoid nuclear protein related to AF4	
	424244 438057	AV647184 AW294544	Hs.143601 Hs.125785	hypothetical protein hCLA-iso ESTs, Wealdy similar to CORB MOUSE CORNI	
^	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	
)	422385	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	
	404170 406902	M32074		gb:Human retinoic acid receptor gamma 2	
	437902	AA770599	Hs.144055	ESTs	
5	401012	AIZOSEA	U- 200024	CCT-	
•	446502 442554	A1302654 AW467376	Hs.208024 Hs.129640	ESTs ESTs	
	443021	AA368546	Hs.8904	lg superfamily protein	
	421141 443070	AW117261	H\$.125914	ESTS	
0	446566	BE388662 H95741	Hs.8984 Hs.17914	Homo sapiens chromosome 14 BAC 98L12 membrane-spanning 4-domains, subfamily A	
	427695	R88483	Hs.172862	ESTS	
	426503	AA380153	U. neceno	gb:EST93093 Skin tumor I Homo sapiens cD	
	431468 416185	AW248431 AW975861	Hs.256526 Hs.47367	nuclear prelamin A recognition factor KIAA1785 protein	
5	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	
	402064 413335	AI613318	Hs.48442	ESTs	
	408212	AA297567	Hs.43728	hypothetical protein	
^	406169				
0	451099 407335	R52795 AA631047	Hs.25954	interteukin 13 receptor, alpha 2	
	409715	W42591	Hs.158761 Hs.23892	Homo sapiens cDNA FLJ13054 fis, clone NT ESTs	
	431921	N48466	Hs.58879	ESTs	
5	443823	8E089782	Hs.9877	hypothetical protein	
•	432458 419726	AI968598 U50330	Hs.78768 Hs.1274	malignant cell expression-enhanced gene/ bone morphogenetic protein 1	
	423178	AI033140	Hs.124983	Home sapiens mRNA; cDNA DKFZp564C142 (fr	
	451089	AA903705 AJ825905	Hs.4190	Home sapiens cDNA: FLJ23269 fs, clone C	
0	415216 442242	AV647908	Hs.193211 Hs.90424	Homo sapiens cDNA FLJ11421 fis, clone HE Homo sapiens cDNA: FLJ23285 fis, clone H	
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	
	406660 443378	X65371 AW392550	Hs.172550	polypyrimidine tract binding protein (he	
	432558	R97268	Hs.9280 Hs.177269	proteasome (prosome, macropain) subunit, ESTs	
5	408146	R45621	Hs.81057	hypothetical protein MGC2718	
	419865 439444	NM_007020 AI277652	Hs.93502	U1-snRNP binding protein homolog (70kD) ESTs, Wealdy similar to I38022 hypotheti	
	438407	A)457122	Hs.54578 Hs.129673	eukaryolic translation initiation factor	
:^	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447394, mRNA,	
0	409130 428844	BE076601 AW972635	Hs.75658	phosphorylase, glycogen; brain hypothetical protein FLJ12671	
	429489	AF008203	Hs.301904 Hs.204039		
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	
5	440658 408204	H29142 AA454501	Hs.143032 Hs.43666		
-	427498	NM_003926	Hs. 178728	protein tyrosine phosphatase type IVA, m methyl-CpG binding domain protein 3	
	408006	H57654	Hs.303345	ESTs, Wealdy similar to 138022 hypotheti	
	445703 431446	AV654845 AW294929	Hs.27 Hs.255369	glycine dehydrogenase (decarboxylating;	
0	456660	AA909249	Hs.112282		
	433099	NM_002504	Hs.3187	nuclear transcription factor, X-box bind	
	415857 415245	AA866115	Hs.127797		
	415245 44 <b>36</b> 57	N59650 R14973	Hs.27252	ESTs gb:yl42(10.s1 Soares fetal liver spleen	
5	402521	AW501216	Hs.108945	KIAA0515 protein	
	414819	BE177320	Hs.156148		
	446530 415797	AV658909 AI291896	Hs.282642 Hs.72800	PESTS ESTS	
00	414812	X72755	Hs.77367	monokine induced by gamma interferon	
30	453028	AB006532	Hs.31442	RecQ protein-like 4	
	412133 407881	U83460 AW072003	Hs.73614 Hs.40968	solute carrier family 31 (copper transpo heparen suffate (glucosamine) 3-O-suttot	
	437033		Hs.5409	RNA polymerase I subunit	

	422722	A A E 77 A E E	Hs.24937	hands a second	
	422732 416388	AA577455 AJ417358	Hs.73677	transformer-2 alpha (htra-2 alpha) ESTs	2.2
	452849	AF044924	Hs.30792	hook2 protein	22
	446615	BE513202	Hs.15589	PPAR binding protein	2.2 2.2
5	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.2
_	446279	AA490770	Hs.182382	ESTs	2.2
	422938	NM_001809	Hs.1594	centramere protein A (17kD)	2.2
	403969	-			2.2
• •	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
10	429738	AF125304	Hs.212680	tumor nacrosis factor receptor superfami	2.2
	447091	AW089648	Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.2
15	438726 453315	AB033103	Hs.6385	KIAA1277 protein	22
13	423244	BE\$44203 AL039379	Hs.24831	ESTs	2.2
	433610	AA806822	Hs.209602 Hs.112547	ESTs, Wealthy similar to ubiquitous TPR m	2.2
	429451	BE409861	Hs.202833	ESTs heme oxygenase (decycling) 1	2.2 2.2
	417980	R32235	10.2020	gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
20	406347			Borling to do and branging trasting to the	2.2
	414406	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	22
	401827				22
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr	2.2
25	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.2
25	404084				2.2
	456788	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI632091	Hs.116877	ESTs	2.2
	442609	AL020996	Hs.8518	selenoprotein N	21
30	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	21
30	421506	BE302796	Hs. 105097	thymidine kinase 1, soluble	21
	439253	AF086064	Hs.332252	ESTs	21
	409669 429574	AW177551	Hs.220255	hypothetical protein MGC13098	2.1
	437470	BE268321 AL390147	Hs.208912	hypothetical protein MGC861	2.1
35	408945	AW015089	Hs.134742 Hs.4964	hypothetical protein DKFZpS47D065	2.1
-	447687	AI627947	Hs.150186	DKFZP586J1624 protein hypothetical protein DKFZp566K1946	21
	459584	AI910884	Hs.207898	ESTs	2.1 2.1
	439130	AA306090	Hs.124707	ESTs	21
	428180	Al129767	Hs.182874	guanine nucleotide binding protein (G pr	21
40	442028	AI239437	Hs.48945	ESTs	2.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	21
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	21
	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.1
	444534	AW271626	Hs.42294	ESTs	2.1
45	438391	AI262248	Hs.25027	ESTs	21
	442003	AW297497	Hs.201891	ESTs	2.1
	456278	BE300369	Hs.289038	hypothetical protein MGC4126	2.1
	416976	BE243985	Hs.80680	major vault protein	21
60	417810	D28419	Hs.82609	hydroxymethylbilana synthase	2.1
50	445242	BE156478	Hs.21108	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.1
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0064 Homo	2.1
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	21
	421564	AB007864	Hs.105850	KIAA0404 protein	2.1
55	424927 432742	AW973666 AA564453	Hs.153850 Hs.162339	hypothetical protein C321D2.4	21
33	435958	H98180	Hs.117975	ESTS ESTS	21
	421531	AA713505	Hs.291769	ESTs	21
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.1 2.1
	420503	Al570943	Hs.337546	ESTs	2.1
60	448127	AJ478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	21
	452897	BE066058	Hs.269233	ESTs, Moderately similar to 178885 serin	2.1
	447112	H17800	Hs.7154	ESTs	2.1
	406577				2.1
65	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
65	451460	AJ797550	Hs.209652	ESTs	2.1
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	2.1
	435828	AA700705	Hs.13852	ESTs	2.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	21
70	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	21
70	452020	AA722012	Hs.255757	ESTs, Wealdy similar to AT2A_HUMAN POTEN	2.1
	415585	Z45481	Lin #46564	gb:HSC2QE041 normatized Infant brain cDN	2.1
	452620 457066	AA436504 BE244613	Hs.119286 Hs.158272		2.1
	435472	AW972330	Hs.283022		2.1
75	431741	ANS14783	Hs. 191701	triggering receptor expressed on myeloid ESTs	2.1
	446840	AW294828	Hs.209203		2.1
	440818	Al147060	Hs.146726		21 21
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.1
~~	400822				21
80	412760	AW379030	Hs.41324	EST8	2.1
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein bloding pr	21
	426925	NM_001196	Hs.315689		21
	424242	AA337476	Hs.293984		21
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	452560	BE077084	Hs.335432	ESTs	21
	456437	AI924228	Hs.115185	ESTs. Moderately similar to PC4259 femi	2.1
	458922	BE501831	Hs. 282053	ESTs	21
5	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.1
3	419488 411829	AA316241 AW865749	Hs.90691	nucleophosmin/nucleoplasmin 3	21
	457192	AL135682	Hs.22452	gb:QV3-SN0021-100500-185-c03 SN0021 Homo Homo sapiens mRNA for KIAA1737 protein,	21 21
	422128	AW881145		gb:QV0-QT0033-010400-182-a07 QT0033 Homo	2.1
• •	452571	W31518	Hs.34665	ESTs	21
10	423699	H41850	Hs.131846	PCAF associated factor 65 alpha	21
	405610 453638	AW814996		ALIMEN CT020C 170400 004 L00 CT020C U	21
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15	410908	AA121686	Hs.10592	ESTs	2.1
	420221	N25991	Hs.43725	ESTs	2.1
	424739 425398	AA346108 AL049689	Hs.221610 Hs.156369	ESTs hypothetical protein similar to tenascin	21 21
	424901	211933	Hs.182505	POU domain, class 3, transcription facto	21
20	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	21
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	21
	418181 407103	U37012 AA424881	Hs.83727 Hs.256301	cleavage and polyadenylation specific fa	21
	454389	AW752571	15.230301	hypothetical protein MGC13170 gb:R.3-CT0213-170100-055-F02 CT0213 Homo	2.1 2.1
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	439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	2.1
	456505 405258	AA504595	Hs.111418	ESTs .	2.1
	444645	A1184564	Hs.101654	ESTs	2.1 2.1
30	430245	AI269069	Hs.109268	hypothetical protein FLJ12552	21
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	21
	403857 400258				21
	422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	21 21
35	441054	AA913591	Hs. 126480	ESTs	21
	452700	A1859390	Hs.288940	five-span transmembrane protein M83	2.1
	454606 448954	AW809752 AB014564	Hs.22616	gb:MR4-ST0124-181299-020-b08 ST0124 Horno KIAA0664 protein	2.1
	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.1 2.1
40	453488	AL039201	Hs.173554	ubiquinol-cytochrome c reductase core pr	21
	437695	AA769202	Hs.192142	ESTs	21
	425449 447270	X52056 AC002551	Hs.157441 Hs.331	spleen focus forming virus (SFFV) provir general transcription factor IIIC, polyp	2.1 2.1
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	2.1
45	436382	AW977063	Hs.250181	ESTs	2.1
	435837 458287	Al689210 AA987556	Hs.187276 Hs.12867	Homo sapiens cONA FLJ11431 fs. clone HE ESTs	21
	423794	8E551781	Hs.231895	ESTs	21 21
	408049	AW076098	Hs.74316	desmoplakin (DPI, DPII)	2.1
50	402721	A141175404	11. 07404	DEADELYA D. M. A. AUM.	2.1
	451999 417541	AW176401 AI992191	Hs.27424 Hs.180040	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep hypothetical protein FLJ22439	2.1 2.1
	414857	AW402389	Hs.920	modulator recognition factor I	21
E E	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	21
55	428086	AL110193	Hs.224137	hypothetical protein	21
	447853 419034	AI434204 NM_002110	Hs.164285 Hs.89555	ESTs, Wealdy similar to AFG1_YEAST AFG1 hemopoletic cell kinase	2.1 2.1
	431019	NM_005249	Hs.2714	forkhead box G1B	21
60	421084	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.1
60	416435 437014	AI431301 AA808757	Hs.179703 Hs.222531	KIAA0129 gene product	21
	459369	T83080	NS.222331	ESTs, Weakly similar to S59501 interfero gb:yd40e03.r1 Soares fetat fiver spleen	21 21
	402239			Saila sagarus adouth same sale abunes	21
65	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	2.1
05	426012 438885	AA367507 AI886558	Hs.75874 Hs.184987	pregnancy-associated plasma protein A	21
	426076	AW962714	F15. 104307	ESTs gb:EST374787 MAGE resequences, MAGG Horno	2.1 2.1
	404561			Barran and an and an and an and a state of the state of t	21
70	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.1
, 0	408175 423867	W29089 AA331886	Hs.19066	hypothetical protein DKFZp667O2416	2.1
	458604	W37944	Hs.4007	gb:EST35757 Embryo, 8 week I Homo seplen Sercolemmal-essociated protein	21 21
	409650	T08490	Hs.288969	HSCARG protein	2.1
75	401729	414677000	14- 755.17	B	2.1
, ,	433675 456741	AW977653 W37608	Hs.75319 Hs.184492	ribonucleotide reductase M2 polypeptide ESTs	21
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80	439262 403108	AA832333	Hs.333045	ESTs	21
	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	2.1 2.1
	440696	AI762757	Hs.187660	putative RabS GDP/GTP exchange factor ho	2.1
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cONA	2.1

	453406	050007.4	11- 80000		_
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	457292	AI921270	Hs.334882	ESTS	2.1
	454434	AA083558		hypothetical protein FLJ14251	2.1
5	406085	~~003030	Hs.261286	ESTS	2.1
•	424441	X14850	Hs.147097	MOA blotone (the marrhage V	2.1
	422726	U11690	Hs.1572	H2A histone family, member X	2.1
	424576	BE154142	Hs.96833	faciogenital dysplasia (Aarskog-Scott sy ESTs	21
	423660	AL045228	Hs.130831	Homo sapiens mRNA; cDNA DKF2p434L137 (tr	2.1
10	403509	AF231919	Hs.18759	KIAA0539 gene product	21
- •	441940	AW298115	Hs.128152	ESTs	2.1
	439190	AW978693	Hs.293811	ESTs	21 21
	417791	AW965339	Hs.111471	ESTS	21
	423701	AA329856	Hs.143022	ESTs	21
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	459642	BE243103		gb:TCAAP2E0949 Pediatric acute myelogeno	21
	450385	AI631024	Hs.24948	synuclein, sipha interacting protein (sy	21
	425159	NM_004341	Hs.154868	carbamoyi-phosphate synthetase 2, aspart	21
	425591	AW294734	Hs_279727	Homo sapiens cDNA FLJ14035 fis, clone HE	21
20	445101	175202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	21
	412811	H06382	Hs.21400	ESTs	21
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	21
	435924	AW029203	Hs.191952	ESTs	21
26	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.1
25	452235	AL039743	Hs.28514	testes development-related NYD-SP21	2.1
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	2.1
	450704	H85157	Hs.40696	ESTs	2.1
	427539	AA405205	Hs.97960	ESTs, Wealthy similar to T51146 ring-box	2.1
30	402028				21
30	405362				2.1
	414718	H95348	Hs.107987	ESTs	2.1
	433424	R68252	Hs.163566	EST8	21
	444875	AI200759	Hs.44737	ESTs .	2.0
35	449523	NM_000579	Hs.54443	chemokina (C-C motif) receptor 5	2.0
,	456072	H54381	11. 400400	gb:yq89a03.s1 Soares fetal liver spleen	2.0
	436331 448418	AI239495	Hs.120169	ESTs	2.0
	447250	243704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
	448192	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
40	448966	R43915 AW372914	Hs.4958	ESTs	2.0
70	408605	AF025374	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.0
	410790	AW803357	Hs.46465	T-cell, immune regulator 1	2.0
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	432238	AL133057	Hs.274135	gb:Human H1 RNA	2.0
45	446307	T50083	Hs.9094	Homo sapiens mRNA; cONA DKFZp434K1815 (I ESTs	2.0
	436588	AA759233	Hs.126506	ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fs, clone OV	20
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	432036	AF224266	Hs.272373	interleukin 20	2.0
50	414460	L00727	Hs.898	dystrophia myotonica-protein kinase	2.0 2.0
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	427964	AA418082	Hs.98286	ESTs, Weakly similar to T20655 hypotheti	2.0
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55	454310	AW818390	Hs.175613	homolog of Xenopus Claspin	2.0
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	452682	AA456193	Hs.9071	progesterone membrane binding protein	2.0
60	412362	AW945484	Hs.184252	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
60	429341	X73874	Hs.2393	phosphorytase kinase, alpha 1 (muscle)	2.0
	435863	AF255346	Hs.62919	Jun dimerization protein p21SNFT	2.0
	400774	R58624	Hs.2186	eukaryotic translation elongation factor	2.0
	453944	AW975369	Hs.292570	Homo sapiens, clone IMAGE:3502107, mRNA,	2.0
65	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.0
05	448529	T26460	Hs.22550	ESTs .	2.0
	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	2.0
	439360	AA448488	Hs.336629	ribosomal protein L44	2.0
	436660	AI658870	Hs.184513	ESTs .	20
70	449030	AI365582	Hs.57100	Homo sapiens mRNA for FLJ00016 protein,	2.0
, 0	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	2.0
	406624 450666	AF052762 T99968	No 10700	gb:Homo sapiens clone csneg8-1 immunoglo	2.0
	446143		Hs.18799	ESTs, Wealdy similar to (38022 hypotheti	2.0
	437698	BE245342 R61837	Hs.305079	Sec61 homolog	2.0
75	426607	AA382330	Hs.7990 Hs.124223	ESTs, Moderately similar to 184505 celci	2.0
	449246	AW411209	Hs.23363	ESTs hypothetical evaluin St. 110092	2.0
	422564	A1148006	Hs.222120	hypothetical protein FLJ10983	2.0
	432682	AI376400	Hs.159588	ESTs ESTs	2.0
_	422140	8E295918	Hs.112193	mut\$ (E. coli) homolog 5	2.0
80	408215	BE614290	Hs.43812	syntaxin 10	2.0
	417129	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	2.0
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.0
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	2.0
					2.0

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	411380	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Hamo	20
	430603	AA148164	Hs.247280	HBV associated factor	20
	425905 401125	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	2.0 2.0
5	412939	AW411491	Hs.2186	eukaryotic translation elongation factor	20
_	448740	BE250632	Hs.8026	sestrin 2	2.0
	454390	AB020713	Hs.56966	KIAA0906 protein	20
	415012	NM_004383	Hs.77793	c-src tyrosine kinase	20
10	410407 403478	X56839	Hs.63287	carbonic anhydrase IX	2.0 2.0
• •	456485	AI393037	Hs.97871	Homo sepiens, clone IMAGE:3845253, mRNA,	20
	430294	A1538226	Hs.32976	guanine nucleotide binding protein 4	2.0
	411669	BE612676	Hs_303116	stromal cell-derived factor 2-like 1	20
15	451944 436395	AW445218	Hs.210876	ESTs gb:Homo sapiens partial mRNA; ID EE2-168	20
13	456457	AJ227900 AA252905	Hs.194477	E3 ubiquiún ligase SMURF2	20 20
	449123	D50920	Hs.23106	KIAA0130 gene product	2.0
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957135, mRNA,	2.0
20	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	2.0
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	447079	AA351898 AA280057	Hs. 105280	ESTs, Wealdy similar to dJ963K23.2 [H.se	2.0 2.0
	449501	AJ652924	Hs.231942	ESTs	2.0
25	422893	X98411	Hs.121555	myosin IF	20
25	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	20
	434845 410422	BE267057 AL042014	Hs.325321 Hs.334698	hypothetical protein R32184_1 Homo sapiens, clone MGC:15203, mRNA, com	20 20
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.0
	451656	BE327088	Hs.212752	ESTs .	2.0
30	442068	BE312873	Hs.314932	ESTs	2.0
	446846	AW197626	Hs.271901	ESTs, Moderately similar to S08586 finge	2.0
	442690 454277	AI014727 AW295069	Hs.160047 Hs.31743	ESTs, Weakly similar to 828096 line-1 pr ESTs, Weakly similar to Z157_HUMAN ZINC	2.0 2.0
_	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.0
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	TABLE 25	:O-			
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BE156306 BE156188 BE156298 BE156377 BE156374
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456094
                             1470256_1
1504780_1
                                              H54381 H54463 BE393262
H95091 C01228
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               457374
                                              AA493662 AW897396 BE154814
                             328758_1
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                             359618 .1
                                              AA578027
               457730
                             393905_1
                                              AW753613 AW753857 BE150374 BE150693 BE150394 AA808851 AA650159 AA654653 BE150419
  55
               TABLE 25C:
               Pkey:
Ref:
                                       Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                        sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                       Indicates DNA strand from which exons were predicted.
               Strand:
  60
               Nt_position:
                                       Indicates nucleotide positions of predicted exons.
               Pkey
400822
                             Ref
7465000
                                                               Nt_position
186223-186402,186878-187275
                                               Strand
                                              Plus
               400859
400917
                             9757499
                                               Minus
                                                               91888-92018,98131-98294,99474-99570
  65
                             7283186
                                               Minus
                                                               173259-173631
                400992
                                                               140390-140822
                             8096828
                                               Plus
               401012
401048
                             7230838
7232177
                                                               736-1137
132430-132761
                                               Minus
                                              Plus
               401125
                             8570296
                                               Minus
                                                               126863-126984
234057-234174
  70
               401324
                             9853791
                                              Plus
Minus
               401384
401558
                             6850939
7139678
                                                               58360-58545
103510-104090
                                               Plus
                401626
                             8575943
                                                               238100-238432
                                               Minus
               401676
                             9965536
                                               Plus
                                                               3891-4691
96484-96681
  75
                401714
                             6715702
                                               Plus
               401729
401827
                                                               90651-90878
94725-94860,98452-98660
                             8134856
                                               Minus
                             2262095
                                               Plus
               401876
402028
                             8099107
7139781
                                                               95913-96641
88749-89237
                                               Plus
                                               Plus
                                                               100159-100350,100445-100912
38175-38304,42133-42266
  80
               402064
402239
                             8117294
                                               Plus
                             7690131
                                               Plus
                402408
                                                               110326-110491
                             9796239
                                               Minus
               402424
                             9796344
                                               Minus
                                                               64925-65073
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	402516	9798099	Minus	195342-195511
	402604	9909420	Plus	20393-20767
	402627	9931216	Plus	12136-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-
5				26895, 29279-29469
3	402721	8969253	Minus	144428-144715
	402798 402856	3355547 9801288	Plus Minus	23596-23867 90119-90411
	4020 <del>30</del> 403048	4210991	Plus	4275-44592,49656-49955
	403108	8980955	Plus	93253-93667
10	403142	9444521	Ptus	89285-90131
	403166	9838127	Minus	67762-67940,68695-68856,70394-70507
	403478	9958258	Plus	116458-116564
	403680	7331517	Minus	157184-157415
16	403751	7229815	Minus	158794-160929
15	403790	8084957	Minus	87825-87947,89835-90002
	403797 403857	8099896	Minus	123065-125008 2524-3408
	403881	7708910 7710245	Minus Minus	107250-107685,108924-109213
	403961	7596976	Minus	110393-110603
20	403969	8569909	Phys	31237-31375,32405-32506
	404020	8655966	Minus	174449-174663
	404054	3548785	Plus	66713-69175
	404084	9944055	Plus	2795-2969
26	404108	8247074	Minus	63603-64942
25	404170	9930793	Plus	168836-169248
	404185 404240	4572584	Minus	129171-129327
	404295	5002624 9856663	Minus Minus	116132-116407,116653-116922 75747-75947
	404299	5738652	Minus	3826-4025
30	404366	9964977	Plus	95589-96801
	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69039-70100
	404584	9857511	Plus	138651-139153
35	404589	9931665	Minus	32824-32985
33	404642	9796810	Plus	102999-103145
	404652 404721	9796969 9856648	Minus	108172-108296
	404721	7706327	Minus Ptus	173763-174294 82849-83627
	404802	4581357	Minus	3003-3060
40	404984	6939882	Plus	87221-87505
	405159	9966252	Plus	79659-79804
	405258	7329310	Plus	129930-130076
	405288	6139075	Minus	126268-126436
45	405353	2811095	Plus	118525-118892
43	405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
	405558 405588	1621110 5002511	Plus Plus	4502-4644,5983-6083 46180-46366
	405605	5836195	Minus	117070-117270
	405701	4263751	Plus	93243-93364
50	405741	9966947	Minus	158747-158875,156936-157208
	405747	8469069	Minus	153933-154060
	405771	7018349	Plus	91191-91254,91510-91589
	405808	9929207	Plus	109758-111166
55	405884	6758747	Plus	62383-62583
55	405915 406028	7712162 8312303	Minus Minus	43717-43859 177469-177829
	406085	9123888	Plus	18665-18843
	406169	6684220	Minus	12620-14251
	406267	7528342	Minus	2570-2731
60	406326	9212385	Ptus	B4508-84655
	406347	9255981	Plus	90900-91091
	406474	9795567	Plus	52758-53211
	406577	7711730	Plus	11377-11509
65	406610	8312226	Plus	13096-13334
<b>~</b> -				

TABLE 26A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 26A fists about 592 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59580 probesets on the
Aflymetrix/Eco Hut3 GeneChip array such that the ratio of "average" normal CNS to "everage" glioblastoma was greater than or equal to 3. The "average" normal CNS to severage glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 85° percentile amongst various timor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play:

Unique Eos probeset identifier number
Exemptar Accession number, Genbank accession number
UnigenelD:
UnigenelD:
Unigene Title:
R1:

R2 ABOUT S82 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 26A fists about 592 genes sejected from 59580 probesets on the
Aflymetrix/Eco Hut03 GeneChip array such that the ratio of "average" glioblastoma was greater than or equal to 3. The "average" normal CNS tevel was set to the 85° percentile amongst various times sent to 10°. The "average" normal CNS tevel was set to the 85° percentile tumor 70

75

00	Pkey	ExAcon	UnigenelD	Unigene Title	R1
80	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	136.7
	417275	X63578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate potype	22.6

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	419954	D14720	Hs.93883	Myslin brotain year /Charnel Mysic Touth	21.2
	459247	N46243	Hs.110373	myelin protein zero (Charcot-Marlo-Tooth ESTs, Highly similar to T42626 secreted	21.2 18.5
	416133	NM_001683	Hs.89512	ATPase, Ca→ transporting, plasma membra	15,5
5	416018 417167	AW138239 AW206437	Hs.78977 Hs.4290	proprolein convertase subtilisin/kexin t ESTs	15.2
•	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	14.8 13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
	439830 408068	AA846666 AW148652	Hs.151489 Hs.167398	ESTs. Weakly similar to XE7_HUMAN PROTEI	12.6
10	412636	NM_004415	Hs.74316	ESTs desmoplakin (OPI, OPII)	12.6 12.5
	429096	A8011106	Hs.196012	KIAA0534 protein	12.2
	412638 423690	AA910199 AA329648	Hs.203838 Hs.23804	ESTs	12.2
	456844	Al264155	Hs.152981	ESTs, Weakly similar to PN0099 son3 prot CDP-diacylglycerol synthase (phosphatida	12.1 11.9
15	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39804	Hs.31961	ESTs	10.8
	446353 420290	Al290919 AW977318	Hs.153661 Hs.194480	ESTs ESTs	10.4 10.3
20	414220	BE298094		gb:601118231F1 NIH_MGC_17 Homo sapiens c	10.3
20	414290	AI568801	Hs.71721	ESTs	10.2
	426365 414937	AA376667 R38698	Hs.10283 Hs.12382	RNA binding motif protein 8B ESTs	10.0 10.0
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5
25	407173	164349 BEETAE	11- 407220	gb:yc10d08.s1 Stratagene lung (937210) H	9.5
23	412454 439366	R55745 AF100143	Hs.167330 Hs.6540	ESTs fibroblasi growth factor 13	9.5 9.4
	415315	F12240	Hs.250655	prothymosin, atpha (gene sequence 28)	9.3
	441790	AW294909	Hs.132208	ESTs .	9.2
30	448117 400661	H49129	Hs.172982	ESTs	9.1 9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453 408920	R20205	Hs.167330	ESTs	9.0
	409031	AL120071 AA376836	Hs.48998 Hs.76728	fibronectin leucine rich transmembrane p ESTs	8.9 8.7
35	428106	BE620016	Hs. 182470	PTD010 protein	8.3
	446544 423479	AI631932 NM_014326	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2
	439480	AL038511	Hs.129208 Hs.125316	death-associated protein kinase 2 ESTs, Weakly similar to S33990 finger pr	8,2 8.2
40	418036	Z37976	Hs.83337	latent transforming growth factor beta b	8.0
40	456490 410200	U83171 AA082557	Hs.97203 Hs.101915	small inducible cytokine subfamily A (Cy	8.0
	414602	AW630088	Hs.76550	Stargardt disease 3 (autosomal dominant) Homo sapiens mRNA; cDNA DKFZp564B1264 (f	8.0 8.0
	408428	NM_014787	Hs.44896	Dna.1 (Hsp40) homolog, subfamily B, membe	7.9
45	437073 408434	Al885608 AW195317	Hs.94122	ESTs	7.9
45	438150	AAD37534	Hs.107716 Hs.79059	hypothetical protein FLJ22344 transforming growth factor, beta recepto	7.9 7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
	408119 417421	W26213 AL138201	Hs.101672 Hs.82120	ESTs, Wealdy similar to T00331 hypotheti	7.8
50	410587	AA370706	Hs.88412	nuclear receptor subfamily 4, group A, m chromosome 9 open reading frame 5	7.8 7.8
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	405800 421750	AK000768	Hs.107872	honostholiani modeia EL 1997C4	7.7
	426356	BE536836	Hs.98682	hypothetical protein FLJ20761 hypothetical protein FKSG32	7.7 7.7
55	423440	R25234	Hs.143434	contactin 1	7.7
	445148 416294	AI214510 D86980	Hs.146304 Hs.79170	ESTs KIAA0227 protein	7.6
	424087	N89333	Hs.143434	contactin 1	7.6 7.6
60	437479	R61866	Hs.101277	ESTs	7.5
00	405071 421224	AW402154	Hs.125812	ESTs	7.5
	442025	AW887434	Hs.11810	CDA11 protein	7,4 7,4
	459476 430573	BE185844 AA744550	14- 420240	gb:ILS-HT0731-110500-087-c08 HT0731 Homo	7.2
65	401836	AA/44330	Hs.136345	ESTs	7.1 7.1
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152 419474	AB001325 AW968619	Hs.234542 Hs.155849	equaporin 3	7.1
	401780	A11300013	ns. /33643	ESTs	7.1 7.1
70	446052	AA358760		gb:EST67699 Fetal tung II Homo sapiens c	7.0
	423605 433098	AF047826 AW190593	Hs.129887 Hs.151143	cadherin 19, type 2 ESTs	7.0
	449511	AJ436187	Hs.296261	guanine nucleotide binding protein (G pr	7.0 6.9
75	451285	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11,23 L-	6.8
13	428414 419273	AL049980 BE271180	Hs.184216 Hs.293490	DKFZP564C152 protein ESTs, Weakly similar to 138022 hypotheti	6.8
	443155	R54485	Hs.23772	ESTs weakly similar to 138022 hypotheti	6.8 6.8
	450561	R49674	Hs.25909	ESTs	6.8
80	433068 440729	NM_006456 AA904739	Hs.288215 Hs.128204	sialytransferase ESTs	6.8
	448426	BE018315	Hs.280776		6.8 6.7
	423589	AA328082	Hs.209569	ESTs	6.6
	415681	A1379882	Hs.72630	ESTs	6.5
				352	
				•	

	413510	F13044		ALUCCONDICO COMPANIO DE LA COMPANIO DE	
	427992	Y15014	Hs.181353	gb:HSC3HH101 normalized infant brain cDN UDP-Gal:betaGlcNAc beta 1,3-gatactosyttr	6.4
	453344	BE349075	Hs.44571	ESTs	6.4 6.4
_	450642	R39773	Hs.7130	copine IV	6.4
5	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482 400332	AB033059 S66407	Hs.18705 Hs.248032	KIAA1233 protein FLT4	6.4
10	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3
	446129	AW244073	Hs.145946	ESTs	6.3 6.3
	454076	AW204712	Hs.61957	ESTs	6.3
	425526	AA359933		gb:EST69040 Fetal lung II Homo sapiens c	6.3
15	421913	AI934365	Hs.109439	Osteoglycin (osteoinductive factor, mime	6.3
13	434273 408480	AA913143 Al350337	Hs.26303	ESTs .	6.2
	451301	AI769514	Hs.164568 Hs.209890	fibroblast growth factor 7 (keratinocyte EST	6.2
	430754	AW862610	Hs.157068	ESTs	6.2 6.2
	438356	AA805530	Hs.48527	ESTs	6.2
20	422743	BE304678	Hs.119598	ribosomal protein L3	6.2
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	426388	AW081394	Hs.97103	ESTs	6.2
	452502 402546	AI904296		gb:PM-8T046-220199-286_1 8T046 Homo sapi	6.1
25	457534	AI761307	Hs.232226	ESTs	6.1 6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (I	6.1
	404958			,	6.1
	432501	BE546532	Hs.25682	Homo sepiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs	6.1
30	422262 408713	AL022315	Hs.113987	lactin, galactoside-binding, soluble, 2	6.0
	454065	NM_001248 BE394588	Hs.47042	ectonucleoside triphosphate diphosphohyd gb:601311808F1 NIH_MGC_44 Homo sapiens c	6.0
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	6.0 5.9
0.5	401521			ogosto or o proton ogracing t	5.9
35	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF 187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761 424806	R13727 AA382523	Hs.21435	ESTs	5.9
	441695	T12411	Hs.105689 Hs.183745	MSTP031 protein hypothetical protein FL113456	5.9
40	457483	AB034694	Hs.272558	endomucin-1	5.9 5.9
	417175	R44558	Hs.94002	ESTs	5.8
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
	436427	A1344378	Hs.143399	ESTs	5.8
45	411939	AI365585	Hs. 146246	ESTs	5.8
73	459053 411052	AI807052 AW814950	Hs.210361	ESTs	5.7
	431063	Z98949	Hs.326843	gb:MR1-ST0206-130400-023-d06 ST0206 Homo hypothetical protein bk125H2.1	5.7
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 ffs, clone PL	5.7 5.7
60	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7
50	442676	AI733585	Hs.130897	ESTs	5.7
	446443 400865	AV659082	Hs.134228	ESTs	5.7
	459080	AW192083	Hs.290855	ESTs	5.7
	407952	Al215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6 5.6
55	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256Q22	5.6
	425705	AF007833	Hs.159265	kruppel-related zinc finger protein hcKr	5.6
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	5.6
	422994 457148	AW891802 AF091035	Hs.296276	ESTs	5.6
60	428356	AL046991	Hs.184627 Hs.10338	KIAA0118 protein ESTs	5.6
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	5.6 5.5
	402092		1.0 000	And more fivesh broceroes (werenot brights	5.5 5.5
	440526	A1832243	Hs.211471	ESTs	5.5
65	444409	A1792140	Hs.49265	ESTs .	5.5
05	417877	AI025829	Hs.86320	ESTs	5.4
	458238 430702	AW071521 U56979	Hs.333541 Hs.250651	beta-amyloid binding protein precursor	5.4
	456189	H91010	Hs.44940	H factor 1 (complement) ESTs	5.4
	427424	AA402453	Hs.113011	ESTs	5.4 5.4
70	437354	AA749215	Hs.291886	ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-f02 BT0614 Homo	5.4
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3
	427861 408556	AA813185 U49516	Hs.98183	ESTs	5.3
75	444209	AJ753134	Hs.46362 Hs.146494	5-hydroxytryptamine (serotonin) receptor ESTs	5.3
	422831	R02504	Hs.332943	ESTS	5.3 5.3
	403180			<del></del>	5.3 5.3
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	5.3
80	430339	W28608	Hs.239625	integral membrane protein 28	5.2
OU	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.2
	431930 437403	AB035301 Al208149	Hs.272211	cadherin 7, type 2	5.2
	438285	AA782845	Hs.121196 Hs.22790	ESTs ESTs	5.2
			THE TANKS	•••	5.2

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	439901	N73885	Hs.124169	ESTs	5.2
	438507	AA809052	Hs.211275	ESTs	5.2
	449222	AW293984	Hs.197621	ESTs .	5.2
_	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	5.2
5	419042	T81429	Hs.221065	ESTs .	5.2
	438777	AA731199	Hs.293130	ESTs	5.2
	445071	AJ280246	Hs.149504	ESTs	5.1
	408016 412047	AW136827	Hs.256096	ESTs	5.1
10	436953	AA934589 AW959074	Hs.49696 Hs.23648	ESTs Homo sepiens cONA FLI13097 fts, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1 5.1
	453830	AA534296	Hs.20953	ESTs	5.1
	459580	AA022888	Hs.176065	ESTs	5.1
15	417616	R07728	Hs.268668	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate camer-li	5.1
	441535	AL135735	Hs.7885	phosphatidylinositol binding clatturin as	5.0
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
20	417284 447135	N62889 T58148	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
20	448605	AL109678	Hs.21597	gb:yb98g06.s1 Strategene lung (937210) H	5.0
	442240	A1791883	Hs.292719	Homo sapiens mRNA full length insert cDN ESTs	5.0 4.9
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
~-	427972	AA854870	Hs.181304	putative gene product	4.9
25	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093		gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	AI097452	Hs.135095	ESTs	4.9
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
30	444922 436670	AI921750 AI690021	Hs.144871 Hs.201536	Home sapiens cDNA FLJ 13752 fis, clone PL	4.8
50	448072	A1459306	Hs.24908	ESTs ESTs	4.8
	408936	AL138043	Hs.293549	ESTs	4.8 4.8
	412622	AW664708	Hs.171959	ESTs	4.8
~ -	414943	D80647	Hs.124193	ESTs	4.8
35	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
	453567	A1742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (I	4.8
	441028	A1333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
40	405130 455225	AW996689		-b-OVA DAMONE SERVICE SER -DO DAMONE U	4.7
70	446218	AV657159		gb:QV3-BN0046-150400-151-g09 BN0046 Homo gb:AV657159 GLC Homo sapiens cDNA clone	4.7
	443347	A1052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.7 4.7
	402176			The contract of the contract o	4.7
	416577	BE063207	Hs.79381	grancalcin	4.7
45	436221	AK001781	Hs.296543	Homo sapiens cDNA FLJ 10919 fis, ctone OV	4.7
	420480	AL137361	Hs.98173	hypothetical protein	4.7
	400800	Y10262	Hs.46925	eyes absent (Orosophila) homotog 3	4.6
	435161 404793	AF124150	Hs.272091	ESTs	4.6
50	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6
-	438571	AW020775	Hs.56022	ESTs	4.6 4.6
	445924	AJ264671	Hs.164166	ESTs	4.6
	444585	AW170015	Hs.6594	ESTs	4.6
e e	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
55	418274	AI458587	Hs.128677	Human DNA sequence from clone RP1-50O24	4.6
	425475	W56339	Hs.107057	ESTs	4.6
	434311 414272	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 ffs, clone MA	4.5
	445235	A1651603 A1564022	Hs.46988 Hs.138207	ESTs ESTs	4.5
60	414327	BE408145	Hs.185254	ESTs, Wealdy similar to T24435 hypotheti	4.5 4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Homo seplens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	4.5
	401024				4.5
65	414699	Al815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5
0.5	423449	AJ497900	Hs.33067	ESTs	4.5
	405138	05447006		Print (170007 001000 000 111 1770000 11	4.5
	413544 453880	BE147225 AI803166	Un 20462	gb:PM2-HT0225-031299-003-111 HT0225 Homo	4.5
	433521	T66087	Hs.28462 Hs.112482	ESTs, Wealdy similar to I38022 hypotheti Homo sapiens unknown mRNA sequence	4.5
70	441184	AA922009	Hs.150269	ESTs	4.4 4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4
	445481	AW661846	Hs.148836	ESTs	4.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	4.4
75	404769				4.4
75	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW628326	Hs.27151	ESTs	4.4
	449093 451959	AB035356 AA056203	Hs.22998	neuraxin 1	4.4
	415716	N59294	Hs.27337 Hs.179662	hypothetical protein FLJ20623 nucleosome assembly protein 1-like 1	4.4
80	417888	R23053		gbyh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4 4.4
	425864	U56420	Hs.159903	olfactory receptor, lamily 5, subfamily	4.4
	435078	AW518888	Hs.40937	ESTs	4.4

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	413493	BE144444	11- 500004	gb:MR0-HT0168-141199-002-09 HT0168 Homo	4.3
	432712 459650	AB015247 R25754	Hs.288031 Hs.301185	sterol-C5-des aturase (fungal ERG3, detta ESTs	4.3
_	404828	100,00	10.301103		4.3 4.3
5	423782	Al472209	Hs.323117	ESTs	4.3
	426867	AA450967	Hs.22668	ESTs	4.3
	426802 457353	AA385182 X65633	Hs.46699 Hs.248144	ESTs	4.3
	412112	BE180342	143.240144	melanocortin 2 receptor (adrenocorticotr gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3 4.3
10	401522	N47812	Hs.306198	CGI-35 protein	4.3
	419055	Al365384	Hs.11571	Homo seplens cDNA FLJ11570 fis, clone HE	4.3
	410171	H07892	Hs. 12431	ESTs	4.3
	419564 458789	U08989 AL157468	Hs.91139 Hs.325825	solute carrier family 1 (neuronal/epithe Homo sapiens cDNA FLJ20848 fis, clone AD	4.3 4.3
15	455040	AW852286	. 4.325425	gb:QV0-CT0225-100400-187-d08 CT0225 Homo	4.3
	438533	A1440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	4.3
	459005	AA447679	Hs.144558	ESTs. Weakly similar to ALU1_HUMAN ALU S	4.2
	418489 433389	U76421 AF038171	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2
20	454356	AW390363	Hs.11522	gb:Homo saplens clone 2367f mRNA sequenc hypothetical protein from Xq28	4.2 4.2
- •	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3	4.2
	443998 452197	AI620661	Hs.296276	ESTs	4.2
25	451117	AW023595 AA015752	Hs.232048 Hs.205173	ESTs ESTs	4.2 4.2
	404501	AW247252	Hs.75514	nucleoside phosphorylase	4.2
	410378	R23324	Hs.41693	OnaJ (Hsp40) homolog, subfamily 8, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2
30	440323 425767	AA970614 AF054176	Hs.127992 Hs.159483	ESTS	4.1
	434460	AA478486	Hs.3852	chromosome 1 open reading frame 7 KIAA0368 protein	4.1 4.1
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1
	413121	T96090	Hs.142678	ESTs	4.1
35	409403	AA668224	Hs.6634 Hs.17538	Homo sapiens cDNA: FLJ22547 fls, clone H	4.1
33	450235 449754	AA007512 H00820	Hs.30977	ESTs ESTs, Wealdy similar to 834087 hypotheti	4.1
	421813	BE048255	. 43.50377	gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1 4.1
	408496	AI683802	Hs.136182	ESTs	4.1
40	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
40	434101 451837	AA625205 T92157	Hs.259599 Hs.16970	KIAA1622 protein ESTs	4.1
	411772	BE170301	ns.103/0	gb:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1 4.1
	437630	AI252782	Hs.153026	SWAP-70 protein	4.1
45	430212	AA469153		gb:nc67f04.s1 NCl_CGAP_Pr1 Homo sapiens	4.0
45	400216 429830	AI537278	U- 225044	DVFTD404D400	4.0
	453165	874727	Hs.225841 Hs.32042	DKFZP434D193 protein aspartoacytase (aminoacytase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0 4.0
50	405354				4.0
50	427931	AW206512		ESTs	4.0
	428775 449422	AA434579 AA001373	Hs.143691 Hs.59821	ESTs ESTs	4.0
	453864	AW021407	Hs.21068	hypothetical protein	4.0 4.0
<i></i>	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0
55	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0
	420784 425195	T65158 AA352026	Hs.102399 Hs.94319	ESTs, Moderately similar to \$65657 glpha	4.0
	429628	H09604	Hs.13268	VPS10 domain receptor protein ESTs	4.0 4.0
<b>60</b>	410087	F12079	Hs.332579	ESTs	4.0
60	409840	AW502122		gb:UI-HF-BROp-air-c-08-0-UI.r1 NIH_MGC_5	4.0
	452854 419910	AA437061 AA662913	Hs.14060 Hs.190173	prokineticin 1 precursor	4.0
	427443	AA402713	Hs.97872	ESTs, Wealdy similar to A46010 X-finked ESTs	4.0 4.0
	414990	C17758	Hs.221652	Homo sapiens cDNA FLJ14323 fis, clone PL	3.9
65	412678	AA115575	Hs.114914		3.9
	405629	A10EC074	11- 15336	PAT.	3.9
	420299 453098	AI056871 ZZ5935	Hs.15276 Hs.86379	ESTs ESTs	3.9
	435752	AF230801	14.00373	gb:Horno sapiens growth hormone receptor	3.9 3.9
70	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9
	414516	AI307802	Hs.135560	ESTs, Wealdy similar to T43458 hypotheti	3.9
	442257 4225 <b>63</b>	AW503831 BE299342	Hs.323370 Hs.19348	Human EST clone 25267 mariner transposon hypothetical protein FLJ13119	3.9
	406697	M21388	Hs.123017		3.9 3.9
75	443850	AW014723	Hs.334612		3.9
	412677	AW029608	Hs.17384	E\$T\$	3.9
	422788 405377	AL117352	Hs.120828	Human DNA sequence from clone RP5-876910	3.9
	414376	BE393856	Hs.66915	ESTs, Wealthy similar to 16.7Kd protein [	3.9
80	453341	AI758912	Hs.296341		3.9 3.9
	431960	AW241821	Hs.301927	c6.1A	3.9
	416854 427264	H40164 AA400117	Hs.80298	Purkinje celi protein 4	3.9
	721209	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Hs.125747	ESTs	3.9

	422746	NM_004484	Hs.119651	glypican 3	3.9
	452345 414666	BE243534 NM_004466	Hs.76828	gb:TC8AP1D0885 Pediatric pre-B cell acut glypican 5	3.9 3.8
_	418217	AI910647	Hs.13442	ESTs	3.8
5	419118	AA234223	Hs.139204	ESTs	3.8
	445017	AI205493	Hs.176860	EST ₆	3.8
	405867 422760	BE409561		gb:60129986SF1 NIH_MGC_21 Homo sapiens c	3.8
	453863	X02544	Hs.572	orosomucoid 1	3.8 3.8
10	457821	H47166	Hs.124322	ESTs, Wealtly similar to A47582 B-cell gr	3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600 456083	AL047034 U46922	Hs.119747	ESTs	3.8
	413341	H78472	Hs.77252 Hs.191325	fragile histidine triad gene ESTs, Wealdy similar to T18967 hypotheti	3.8 3.8
15	449057	AB037784	Hs.22941	KIAA1363 protein	3.6
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
	414764	AW013887	Hs.72047	EST6	3.8
	404391 433629	R13140	Hs.13359	ESTs	3.7
20	424738	AI963740	Hs.46826	ESTs	3.7 3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to \$23650 retro	3.7
	440530 433930	AA888646 AA620338	Hs.174187	ESTs	3.7
25	409662	AW452320	Hs.273781 Hs.279726	ESTs ESTs	3.7 3.7
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	A1248205	Hs.153244	ESTs	3.7
	408593	R19566	Hs.197617	ESTs	3.7
30	417091 448556	AA193283 AW885606	Hs.291990 Hs.5064	ESTS	3.7
20	423135	N67655	Hs.26411	ESTs ESTs	3.7 3.7
	400135				3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	3.7
35	457221 451560	AW383197	Hs.218260	ESTs	3.7
55	401600	AJ807927 BE247275	Hs.249601 Hs.151787	ESTs U5 snRNP-specific protein, 116 kD	3.7
	446818	AI342668	Hs.279765	ESTs	3.7 3.7
	447795	AW295151	Hs.163612	ESTs	3.7
40	427562	R56424	Hs.26534	ESTs	3.6
70	412258 454339	AA376768 AW381980	Hs.324841	hypothetical protein FLJ22622	3.6
	439274	AF086092	Hs.48372	gb:QV4-HT0316-091199-028-d05 HT0316 Homo ESTs	3.6 3.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
45	422897	AA679784	Hs.4290	ESTS	3.6
45	429656 421908	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6
	407978	AW935200 AW385129	Hs.285814 Hs.41717	sprouty (Drosophila) homolog 4 phosphodiesterase 1A, calmodulin-depende	3.6 3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	3.6 3.6
60	400685				3.6
50	417154	AI674701	Hs.21388	ESTs	3.6
	447176 423893	Z42549 AL031709	Hs.160893 Hs.134846	ESTs Human DNA sequence from clone 316G12 on	3.6
	449231	BE410360	Hs.298573	KIAA1720 protein	3.6 3.6
66	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
55	405977 441470 .	DE 602074	H- nataon	CAT-	3.6
	423568	BE503874 NM_005256	Hs.301986 Hs.129818	ESTs growth arrest-specific 2	3.6
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6 3.6
60	450236	AW162998	Hs.24684	KIAA1376 protein	3.6
60	425364	AF052150	Hs.155959	Homo sapiens clone 24533 mRNA sequence	3.6
	426775 414831	AA384564 M31158	Hs.108829 Hs.77439	ESTs protein kinasa, cAMP-dependent, regulato	3.6
	416876	AW501916	Hs.117897	ESTs	3.6 3.6
<i>.</i> .	400878				3.6
65	425153	AW023193	Hs.27046	ESTs	3.6
	432222 415047	A1204995 F13142		gb:sn03c03.x1 Stratagene schizo brain S1	3.5
	401532	F13142		gb:HSC3JD031 normalized Infant brain cDN	3.5 3.5
	446495	D60923	Hs.153460	ESTs	3.5 3.5
70	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901 416421	BE155527 AA134006	Hs.79306	gb:PM1-HT0350-190400-013-b08 HT0350 Homo eukaryotic translation initiation factor	3.5
~~	455697	BE067952	3000	gb:CMO-BT0365-061299-122-g09-BT0365 Homo	3.5 3.5
75	405678			2	3.5
	418207	C14685	Hs.34772	ESTs	3.5
	425383 417027	D83407 AA192306	Hs.156007 Hs.23926	Down syndrome critical region gene 1-lik triadin	3.5
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5 3.5
80	417702	R09935	Hs.191148		3.5
	445687	W80382	Hs.149297		3.5
	408776 413164	AA057365 8E068494	Hs.63356	ESTs. Weakly similar to 138022 hypotheti	3.5
	713104	0000434		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5

	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo sapiens c	3.5
•	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein.	3.5
	415621	AI648602	Hs.55488 Hs.191460	ESTS	3.5
5	454437 446066	AI248173 AI343931	Hs.149383	hypothetical protein MGC12936	3.5
-	423374	AB037770	Hs.127656	ESTs KIAA1349 protein	3.5
	419347	C15944	Hs.90005	superiorozavical ganglia, neural specifi	3.5
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	3.5 3.5
	451776	W45679	Hs.169854	hypothetical protein SP192	3.5 3.5
10	432305	M62402	Hs.274313	insutin-like growth factor binding prote	3.5
	456995	T89832	Hs.170278	ESTs	3.5
	403323				3.5
	425022	M95724	Hs.154207	centromere protein C 1	3.5
1.5	439394	AA149250	Hs.56105	EST8	3.4
15	433803	AI823593	Hs.27688	ESTs	3.4
	450715	AI256484	Hs.31570	ESTs, Wealtly similar to KIAA1324 protein	3.4
	411474	AW848427		gb:IL3-CT0214-150200-075-H10 CT0214 Horno	3.4
•	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4
20	423826 459495	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4
20	427173	BE544158 BE255017	Hs.97540	gb:601076707F1 NtH_MGC_12 Homo sapiens c	3.4
	408112	AW451982	Hs.248613	ESTs ESTs	3.4
	446092	N33522	Hs.145894	ESTS	3.4
	416868	AI656856	Hs.292597	ESTs	3.4 3.4
25	458234	BE551408	Hs.127196	ESTs	3.4
	419555	AA244416		gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	414314	BE312991		gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	400425	AY004252	Hs.287385	PR domain containing 12	3.4
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	3.4
30	434053	AW445136	Hs.134946	ESTs	3.4
	449997	A1683052	Hs.201577	KIAA 1829 protein	3.4
	433461	AI636047	Hs.197623	ESTs	3.4
	428006	AA418743	Hs.98306	KIAA1862 protein	3.4
35	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-asso	3.4
"	443294 428212	A1733625	Hs.133053	ESTs	3.4
	457673	AW444451 AA551569	Hs.134812 Hs.272034	ESTs	3.4
	446390	AA233393	Hs.14992	hypothetical protein PRO2822 hypothetical protein FLJ11151	3.4
	428536	AI143139	Hs.2288	visinin-like 1	3.3
40	426597	AA382250	Hs.145601	ESTs	3.3 3.3
. –	410366	Al267589	Hs.302689	hypothetical protein	3.3 3.3
	458258	AW406546	Hs.127971	ESTs	3.3
	401738			****	3.3
	409038	T97490	Hs.50002	small inducible cytokine sublamily A (Cy	3.3
45	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3
	433328	AW298159	Hs.23844	ESTs, Wealdy similar to S65824 reverse t	3.3
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3
	434998	AW975157	Hs.26037	ESTs	3.3
50	456359	AI967991	Hs.93574	homeo box D3	3.3
50	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type I, b	3.3
	454267 400302	AA437199 N48056	Hs.656 Hs.1915	cell division cycle 25C	3.3
	434077	AF116659	Hs.321151	folate hydrolase (prostate-specific memb Homo sapiens PRO1412 mRNA, complete cds	3.3
	436602	AJ793222	Hs.166817	ESTs	3.3 3.3
55	449204	AB000099	Hs.23251	Down syndrome critical region gene 4	3.3
	417935	R53697	Hs.170044	ESTs	3.3
	423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	3.3
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	3.3
40	453406	AI192987	Hs.61784	hypothetical protein FLJ14451	3.3
60	420164	AW339037	Hs.24908	ESTs	3.3
	447826	AW779317	Hs.258556	ESTs	3.3
	419875	AA853410	Hs.93557	proenkephalin	3.3
	444612 418504	AW138111 BE159718	Hs.22902	ESTS	3.3
65	415242	R45988	Hs.85335 Hs.295014	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	3.2
~~	418188	AW139413	Ha.151880	ESTs ESTs	3.2
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	3.2
	421640	AW966652	14.255010	gb:EST378726 MAGE resequences, MAGI Homo	3.2
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.2 3.2
70	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2 3.2
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	3.2
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2
75	403092			-	3.2
75	452971	AI873878	Hs.91789	ESTs .	3.2
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
	401485				3.2
	401949	A1407727		-A.F.C.T.2047CF 144.CF	3.2
80	457452	AW972675 AI693231	U- 4000-0	gb:EST384766 MAGE resequences, MAGL Homo	3.2
	454100 448440	AA173467	Hs.126043 Hs.62402	chromosome 21 open reading frame 51	3.2
	421200	AA284811	Hs.264433	p21/Cdc42/Rac1-activated kinase 1 (yeast ESTs	3.2
	430142	NM_000437		platelet-activating factor acetylhydrota	3.2
				parameter and the parameter of the param	3.2
				^ -	

	430403	4004000		44	
	433197 443509	AB040889 AV645470	Hs.281022	KIAA1456 protein gb:AV645470 GLC Homo sapiens cDNA clone	3.2 3.2
	440827	AI733110	Hs.128128	ESTs	3.2
5	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyttransferas	3.2
3	409257	AW370362	LL 9744C0	gb:RC1-BT0255-181099-012-d07 BT0255 Homo	3.2
	459235 416789	BE246010 AA223439	Hs.271468 Hs.79933	Homo sapiens mRNA for FLJ00038 protein, cyclin I	3.2 3.2
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761009121 (	3.2
10	420156	AW449258	Hs.6187	ESTs	3.2
10	455577 400617	BE006341 AF151064	Hs.36069	gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
	437129	AL049327	Hs.302057	hypothetical protein Homo sapiens mRNA; cDNA DKFZp564E016 (fr	3.2 3.2
	451820	AW058357	Hs.337353	ESTs	3.2
15	457535	AA609685	Hs.278572	membrane component, chromosome 11, surfa	3.2
13	419956 456235	AL137939 AA203637	Hs.40096	ESTS	3.1
	423930	AA332697	Hs.42721	gb:zx58b12.r1 Soares_fetal_fiver_spleen_ ESTs	3.1 3.1
	403796				3.1
20	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
20	445886 414401	AI793176 AI760159	Hs.145596 Hs.124833	ESTs ESTs	3.1
	441573	BE563966	Hs.6529	ESTs, Weakly similar to (78885 serine/th	3.1 3.1
	450725	R71389	Hs.175951	ESTa	3.1
25	458805 417868	AI282933	Hs.23294	hypothetical protein FLJ14393	3.1
23	458391	A1078534 A1792628	Hs.122592 Hs.133273	ESTs ESTs	3.1 3.1
	423346	AI267677	Hs.127416	synaptojanin 1	3.1
	454486	AW857077		gb:RC1-CT0302-140300-016-f04 CT0302 Homo	3.1
30	408341	AW182952 AW805749	Hs.249957	ESTs	3.1
50	410669 404907	WANDOLOR	Hs.318885	superoxide dismutase 2, milochondrial	3.1 3.1
	434910	A1333863	Hs.215474	ESTs, Moderately similar to alternativel	3.1
	436990	Al149729	Hs.120557	ESTs	3.1
35	441921 454673	A1733376 AW812807	Hs.164478	hypothetical protein FLJ21939 similar to	31
22	429470	A1878901	Hs.203862	gb:RC3-ST0186-070100-016-c04 ST0186 Homo guanine nucleotide binding protein (G pr	3.1 3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1
	408217	AJ433201	Hs.279860	tumor protein, translationally-controlle	3.1
40	417313 427322	AA195602 AK002017	Hs.176227	gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi	3.1
-10	411003	AA181018	Hs.13056	hypothetical protein FLJ11155 hypothetical protein FLJ13920	3.1 3.1
	425339	AA935330	Hs.198113	ESTs	3.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.1
45	449078 429608	AK001258 U49250	Hs.22975	KIAA1576 protein	3.1
75	442308	AA989402	Hs.210862 Hs.111	T-box, brain, 1 fibroblast growth factor 9 (glia-activat	3.1 3.1
	428465	AW970976	Hs.293653	ESTs	3.1
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1
50	447965 413918	AW292577 AW015898	Hs.94445 Hs.71245	ESTs ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription (a	3.1 3.1
	425810	AI923627	Hs.31903	ESTs	3.1
	427865	AA416931	Hs.126065	ESTs	3.1
55	429060 430708	AW139155 U78308	Hs.194995 Hs.278485	hypothetical protein DKFZp43400320 olfactory receptor, family 1, subfamily	3.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	3.1 3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.0
60	422963 417696	M79141 BE241524	Hs.13234 Hs.82401	ESTs CD69 antigen (p60, early T-cell activati	3.0
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	3.0 3.0
	414686	BE409757	Hs.23189	ESTs, Moderately similar to TBB2_HUMAN T	3.0 .
	458360	AI027207	Hs.132253	ESTs	3.0
65	451829 445179	AW964081 AI949743	Hs.247377 Hs.224768	ESTs ESTs	3.0 3.0
	433090	AJ720050	Hs.145362	immortafization-upregulated protein	3.0
	432018	AA524447	Hs.152377	ESTs	3.0
	407988 405911	N47760	Hs.285107	hypothetical protein FLJ13397	3.0
70	418808	AI821836	Hs.10359	ESTs	30
	431900	AW972048	Hs. 192534		3.0 3.0
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
	423952	AW877787	Hs.136102		3.0
75	412000 405793	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0 3.0
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3.0
	423957	AW978309	Hs.135235	Homo sepiens cDNA FLJ13542 fis, clone PL	3.0
80	427071 434961	AA397958 AW974956	Hs.192719	ESTs gb:EST387061 MAGE resequences, MAGN Homo	3.0
				Barras son on under rendinance WARNA MOUN	3.0
	TABLE 2				
	Pkey:	Uni	dna Foz buope	set identifier number	

358



	CAT numb	er. Ges	ne duster number	
	Accession		bank accession r	numbers
5	Pkey		r Accession	
3	409257 409840	1112994_1 1156071_1	AW370362 AV	7809101 YS02125 AW501663 AW501720
	411052	1230374_1		88513 H69459 BE176242 H54583
	411279	1237516_1	AW884776 AV	N935737 AWB35261 AWB35247 AWB35246 AWB35263 AWB35240 AWB35258
10	411474 411607	1247047_2		N848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162
10	411772	1251251_1 1257386_1		N853442 AW853590 AW853433 AW853592 V881539 AW904851 BE154338 BE154090 BE154275
	412112	1277883_1		180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898
			BE180223 BE	180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345
15	413164	1351422_1		W893615 H85799 H83501 BE180220 068414 BE068332 BE068347 BE068766 BE068623 BE068450 BE068480 BE068350 BE068295 BE068498 BE068765 BE068328
1.5	413104	1551422_1	BE068778 BE	068871 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068509 BE06845 BE06857 BE068521 BE068549 BE068549 BE068579 BE068574 BE068576 BE068585 BE068578 BE068578 BE068578 BE068578 BE068578 BE068578 BE068578 BE068578
				068529 BE068689 BE068383 BE068422 BE066470 BE066522 BE068518 BE06354 BE066748 BE068683 BE068303 BE068602
20			BE068739 BE	968374 BE068302 BE068625 BE068596 BE068663 BE068429 BE068605 BE068693 BE068672 BE068401 BE068579 BE068329
20			BE068390 BE	058419 BE068393 BE068447 BE068675 BE068311 BE068540 BE068301 BE068543 BE068719 BE068369 BE068324 BE068588
			8E068293 BE	(068317 BE068384 BE068547 BE068674 BE068436 BE068321 BE068361 BE068676 BE068499 BE068299 BE068352 BE0683410 (068418 BE068552 BE068598 BE068327 BE068550 BE068712 BE068661 BE068733 BE068525 BE068752 BE068357 BE068330
				068538 BE068340 BE068537 BE068761 BE068632 BE068758
25	413493	1373555_1	BE144444 BE	
23	413510 413544	1374377_1 1375671_1		09 BE145525 BE145493 E147205 BE147234
	414220	1426940_1		
	414314	1435028_1		
30	414366 414456	1438636_1 1447655_1		E390513 BE277344
50	414593	1464909_1		
	414630	1468083_1	8E410857 BI	
	415047	1517450_1		26 F06135 F06147 H08517 D51360 T75341
35	417313 417888	166644_1 1706092_1		01148 N40632 984 076271
••	419555	185884_1	AA244416 A	
	421249	200649_1		N752386 AW847156 AA285373 AW879575 AW879558
	421640 421813	204833_1 207654_1		W966653 AA294989 AA385977 A313083 AA298419
40	422760	221034_1		E162756 AW732798
	425526	252776_1		A358889 AW955306 AW962995 AW837746 AW837755 AW837697
	430212 432222	314437_1		718503 AAA69225
	433389	343347_1 36497_1		Y827539 AW969908 AW440776 AA528756 13209 F07347
45	434961	396357_1		A781075 AA654944
	435752	41050_1		F230800 AA401795 AA398260
	437483 440198	43756_1 488242	AL390174 A ¹ BE560093	N898817
	443509	57199_1		84636 T82805
50	446052	65988_1		A158850 AW062737 AW062738 AV656291
	446218 447135	66688_1 70963_1		E145509 BE145512 BE145505 BE145507 316579 AW059603
	452346	912206_1		E243752 AI880228 L44326
55	452502	919733_1		007223 R30687
23	454065 454186	998401_1 1049791_		W024754 BE183166 BE183167 E141474 BE141487 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
	701100			E141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
	45.4000	4400000	BE141749 A	
60	454339 454486	1122972_ 1215703_		3E152244 BE152235 BE152238 BE152232 NW861268 AW847383 AW795787
	454506	1219857_		AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787
	454673	1228669_	1 AW812807	AW812815 AW812802
	455040 455225	1250028_ 1262318_		AW851934 AW852096 AW852274 AW996380 AW996453 Be085650 AW868687 Be085595
65	455577	1333898		IE006307 BE006311
	455617	1348117_		E061030 BE077927
	455697 455901	1351148_ 1381569_	1 BE067952 E	12067945 BE067942 BE067943 BE067949 92067954 BE067944 BE067953 BE067956 BE067945 12155503 BE155188 BE155126
	456235	168686_1	AA203637	A832266 H67452
70	456407	184986_1	AW968614	AA243209 AA281411
	457452	339381_1		AA541366 AA523039
	459150	919196_1	DE 133336 I	3E153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE156492
75	TABLE 2	16C:		
75	Pkey:	,	Inique number co	responding to an Eos probesel
	Ref:	5	equence of huma	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	l.	ndicates DNA stra	nd from which exons were predicted.
80	Nt_positi	ion: t	ndicates nucleotid	e positions of predicted exons.
50	Pkey	Ref	Strand	Nt position
	400661	8118474	Ptus	84912-85187
	400685	8118768	Minus	72969-73050,73713-73800

WO 03/025138 PCT/US02/29560

	400865	1945037	Minus	44482-45526
	400878	9864757	Ptus	31493-32842
	401024	8117489	Plus	60551-60802
_	401315	9212516	Minus	198960-199619
5	401485	7341723	Plus	58009-68209,58841-69077
	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
	401738	2982169	Minus	41547-41757
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
10	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
	402178	7543687	Minus	10-750
	402546	7637348	Plus	24873-25170
15	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
	403796	8099896	Minus	75073-77664
	404391	3135305	Minus	26030-26173,27852-27997
20	404769	8099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
	404907	7331453	Minus	102880-103828
0.5	404958	7407941	Minus	2731-4531
25	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
20	405377	5649375	Plus	216656-216848
30	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
25	405867	6758731	Minus	74553-75173
35	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 27A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 27A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on
the Aflymatrity/Eos Hu03 GeneChip erray such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS issues set to the 85° percentile amongst various normal CNS issues. The "average" glioblastoma level was set to the 85° percentile amongst various tumor samples. To enrich for CNS
specific genes, the ratio of "average" CNS to "average" normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85°
percentile amongst various CNS tissues. The "average" normal adult tissue level was set to the 85° percentile amongst various non-CNS normal tissues. In order to
remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and
the denominator before the ratios were evaluated.

Place: 40 45

Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigenetD: Unigene Title: 50

R1:

Charges Accessor names, General accessor mance.
Unigene gene title
Ratio of 75° percentile normal central nervous system tissue to 85° percentile tumor
Ratio of 85° percentile central nervous system tissue to 85° percentile normal body tissue R2:

	PKey	EXACCI	UnigenelD	Unigene Title	Ri	R2
55	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs .	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
<b>~</b> ^	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
60	416018	AW138239	Hs.78977	proprotein convertase subfilisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
	439830	AA846666	Hs. 151489	ESTs, Wealty similar to XE7_HUMAN PROTEI	12.6	16.5
65	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
~~	446353	Al290919	Hs.153661	ESTs	10.4	13.2
70	428365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	RS5745	Hs.167330	ESTs	9.5	14.1
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
75	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Wealdy similar to T24435 hypotheti	9.0	14.7
	412453	R20205	Hs.187330	ESTs	9.0	13.7
00	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
80	409031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.saple	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Wealtly similar to S33990 finger pr	8.2	8.3
	410200	AA082557	Hs.101915	Starpardt disease 3 (autosomal dominant)	8.0	8.9
				- · · · · · · · · · · · · · · · · · · ·		

	408428	NM_014787	Hs.44896	OnaJ (Hsp40) homolog, subfamily B, membe	7.9	0.6
	437073	AI885608	Hs.94122	ESTs	7.9 7.9	9.6 11.3
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9	16.4
-	440209	H05049	Hs.22269	neutexin 3	7.8	34.3
5	408119	W26213	Hs. 101672	ESTs, Wealdy similar to T00331 hypotheti	7.8	9.0
	429611 423440	A1889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7	5.0
	445148	R25234 AI214510	Hs.143434 Hs.146304	contactin 1 ESTs	7.7	9.9
	415294	D86980	Hs.79170	KIAA0227 protein	7.6 7.6	9.1
10	424087	N69333	Hs.143434	contactin 1	7.6	7.6 10.3
	437479	R61866	Hs.101277	ESTs	7.5	9.3
	430573	AA744550	Hs.138345	ESTs .	7.1	2.8
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1	10.4
15	419474 423605	AW968619 AF047826	Hs.155849	ESTs	7.1	3.0
	433098	AW190593	Hs.129887 Hs.151143	cadherin 19, type 2 ESTs	7.0	6.9
	449511	AJ436187	Hs.296261	guanine nucleotide binding protein (G pr	7.0 6.9	9.2
	428414	AL049980	Hs.184216	OKFZP564C152 protein	6.8	3.1 5.0
20	443155	R54485	Hs.23772	ESTs	6.8	3.5
20	450561	R49674	Hs.25909	ESTs	6.8	8.1
	433068 423589	NM_006456	Hs.288215	sialytransferase	6.8	2.0
	415681	AA328082 AI379882	Hs.209569 Hs.72630	ESTs ESTs	6.6	10.5
_	413510	F13044	13.72030	gb:HSC3HH101 normalized infant brein cDN	6.5 6.4	9.0
25	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	7.1 9.5
	450642	R39773	Hs.7130	copine IV	6.4	5.7
	429322	D86984	Hs.199243	KIAA0231 protein	6.4	8.2
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4	2.3
30	446129 421913	AW244073 AI934365	Hs.145946 Hs.109439	ESTs	6.3	8.3
20	434273	AA913143	Hs.26303	osteoglycin (osteoinductive factor, mime ESTs	6.3	2.1
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2 6.2	10.3 3.5
	451301	AJ769514	Hs.209890	EST	6.2	12.4
25	438356	AA805530	Hs.48527	EST _{\$}	6.2	8.1
35	426388	AW081394	Hs.97103	EST _S	6.2	8.6
	452502 408165	AI904296 AL137573	Un 42442	gb:PM-8T046-220199-286_1 BT046 Homo sapi	6.1	2.8
	442979	AW440782	Hs.43143 Hs.174743	Homo sapiens mRNA; cDNA DKFZp564A2463 (f ESTs	6.1	6.3
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.1 6.0	6.3 3.8
40	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9	21.4
	425087	R62424	Hs.126059	ESTs	5.9	8.1
	441695	T12411	Hs.183745	hypothetical protein FLJ 13456	5.9	3.1
	417175	R44558	Hs.94002	ESTs	5.8	12.5
45	437483 436427	AL390174 Al344378	Hs.143399	gb:Homo sapiens mRNA; cDNA OKFZp547J184 ESTs	5.8	2.2
10	450382	AA39765B	Hs.60257	Homo sepiens cDNA FLJ13598 fis, clone PL	5.8 5.7	13.8
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7 5.7	4,4 12.5
	442676	A1733585	Hs.130897	ESTs	5.7	6.8
50	446443	AV659082	Hs.13422B	EST\$	5.7	6.4
50	459080	AW192083	Hs.290855	ESTs	5.6	15.6
	431984 428356	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	5.6	8.2
	417877	AL046991 Al025829	Hs.10338 Hs.86320	ESTs ESTs	5.6	6.2
	429290	AF203032	Hs.198760	neurofitament, heavy polypeptide (200kD)	5.4 5.3	4.9
55	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3	13.1 6.6
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.2	6.0
	438285	AA782845	Hs.22790	EST _{\$}	5.2	7.3
	439901 449222	N73885 AW293984	Hs.124169	EST _S	5.2	2.7
60	408016	AW136827	Hs.197621 Hs.256096	ESTs ESTs	5.2	8.1
••	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1 5.1	25
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1 5.1	3.0 7.3
	409263	AA069573	Hs.50319	ESTs	5.1	12.9
65	453830	AA534296	Hs.20953	ESTs	5.1	3.4
Ų.	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0	4.8
	416490 417284	AF090116 N62889	Hs.79348	regulator of G-protein signalling 7	5.0	20.1
	448505	AL109678	Hs.107242 Hs.21597	Homo sapiens cDNA FLJ 12965 fis, clone NT Homo sapiens mRNA full length insert cDN	5.0	3.9
	442240	AI791883	Hs.292719	ESTs	5.0 4.9	6.1
70	427972	AA864870	Hs.181304	putative gene product	4.9	6.7 5.2
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9	2.8
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8	3.7
	408936	AL138043	Hs.293549	ESTs	4.8	6.6
75	414943 429254	D80647 H10133	Hs.124193 Hs.91846	ESTs	4.8	3.1
. •	407906	AA369665	Hs.41185	hypothetical protein DKFZp761C121 Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8	23
	416577	BE063207	Hs.79381	grancation	4.8 4.7	9.1 2.7
	420480	AL137361	Hs.98173	hypothetical protein	4.7 4.7	2.8
80	404793				4.6	2.2
80	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6	7.4
	438571 444585	AW020775	Hs.56022	ESTs	4.6	5.4
	414272	AW170015 AI651603	Hs.6594 Hs.46988	ESTs	4.6 .	6.0
			110.70300	EGID	4.5	2.2



	414699	AI815523	Hs.76930	menulais, alaba foon A.f	4.5	30.9
	423449	Al497900	Hs.33067	synuclein, alpha (non A4 component of am ESTs	4.5	20.8
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0.
•	429876	AB028977	Hs.225974	KIAA1054 protein	4.4	19.2
5	429726	AW628326	Hs.27151	ESTs	4.4	10.2
	449093 415716	AB035356 N59294	Hs.22998 Hs.179662	neurexin 1 nucleosome assembly protein 1-like 1	4.4 4.4	9.4 15.1
	419656	AB002314	Hs.92025	KIAA0315 gene product	4.4	8.2
10	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4	24
10	435078	AW518888	Hs.40937	ESTs	4.4	5.7
	432712 426887	AB016247 AA460967	Hs.288031 Hs.22668	sterol-C5-desaturase (fungal ERG3, della ESTs	4.3 4.3	5.9 6.0
	412112	BE180342	114.62.000	gb:RC3-HT0622-130400-012-807 HT0622 Homo	4.3	3.2
1.5	410171	H07892	Hs.12431	ESTs	4.3	5.3
15	442339	BE299668	Hs.227591	ESTs, Wealdy similar to 1901303A Lau zip	4.2	5.0
	421249 422528	AA285362 AB011182	Hs.118087	gb:HTH277 HTCDL1 Homo saplens cDNA 5/3* KIAA0610 protein	4.2 4.2	3.5 3.9
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
0.0	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1	7.0
20	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	4.1	3.9
	408496	AI683802	Hs.136182	ESTs	4.1	4.7
	434101 430212	AA625205 AA469153	Hs.259599	KIAA1622 protein gb:nc67f04.s1 NOI_CGAP_Pr1 Homo sapiens	4.1 4.0	6.3 2.5
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0	7.4
25	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0	5.1
	441869	NM_003947	Hs.6004	huntingtin-associated protein interactin	4.0	32.3
	429628 410087	H09604 F12079	Hs.13268 Hs.332579	ESTs ESTs	4.0 4.0	4.5
	419910	AA662913	Hs.190173	ESTs, Wealtly similar to A46010 X-linked	4.0	6.9 2.6
30	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9	21.7
	412677	AW029608	Hs.17384	ESTs	3.9	2.2
	453341	AI758912	Hs.296341	adenytyl cyclase-associated protein 2	3.9	7.2
	416854 414666	H40164 NM_004466	Hs.80296 Hs.76828	Purkinje cell protein 4 alvoican 5	3.9 3.8	2.2 6.2
35	418217	AI910647	Hs.13442	ESTs	3.8	3.2
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	ESTs	3.8	10.7
	433629 424738	R13140 Al963740	Hs.13359	ESTs	3.7	2.7
40	424736	AA191085	Hs.46826 Hs.26612	ESTs ESTs, Moderately similar to S23650 retro	3.7 3.7	2.1 5.3
. •	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.7	53.7
	423135	N87655	Hs.26411	ESTs	3.7	21.7
	446818	AI342668	Hs.279765	ESTs	3.7	2.6
45	427562 439274	R56424 AF086092	Hs.26534 Hs.48372	ESTs ESTs	3.6 3.6	3.6 34.5
	452381	H23329	Hs.290880	ESTs, Wesley similar to ALU1_HUMAN ALU S	3.6	6.0
	422897	AA679784	Hs.4290	ESTs	3.6	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6	24.6
50	417154 447176	A1674701 <b>Z</b> 42549	Hs.21388 Hs.160893	ESTs ESTs	3.6	5.8
50	405977	242343	ns. 100033	5318	3.6 3.6	6.4 3.9
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6	5.4
55	426775 414831	AA384564 M31158	Hs.108829 Hs.77439	ESTs	3.6	3.4
<b>J</b>	425153	AW023193	Hs.27046	protein kinase, cAMP-dependent, regulato ESTs	3.6 3.6	2.8 4.9
	446495	D60923	Hs.153460		3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
60	418421 418207	AA134006 C14685	Hs.79306 Hs.34772	eukaryotic translation initiation factor	3.5	5.0
00	425383	D83407	Hs.156007	ESTs  Down syndrome critical region gene 1-lik	3.5 3.5	16.0 6.2
	417027	AA192306	Hs.23926	triadin	3.5	2.5
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
65	408776 453220	AA057365	Hs.63356	ESTs, Wealdy similar to 138022 hypotheti	3.5	5.5
05	419347	AB033089 C15944	Hs.32452 Hs.90005	Homo sapiens mRNA for KIAA1263 protein, superiorcervical ganglia, neural specifi	3.5 3.5	23.6 42.3
	433803	AI823593	Hs.27688	ESTs	3.4	3.6
	450715	AJ266484	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	3.4	4,1
70	415076	NM_000857		guanylate cyclase 1, soluble, bela 3	3.4	9.8
70	423826 427173	U20325 BE255017	Hs.1707 Hs.97540	cocaine- and amphetamine-regulated trans ESTs	3.4	4.7
	446092	N33522	Hs.145894		3.4 3.4	2.4 3.5
	416868	A)656856	Hs.292597	ESTs	3.4	4.5
75	458234	BE551408	Hs.127196		3.4	4.5
13	434053 428536	AW445136	Hs.134946		3.4	3.9
	410366	Al143139 Al267589	Hs.2288 Hs.302689	visinin-like 1 hypothetical protein	3.3 3.3	42.3 14.4
	425785	T27017	Hs.159528		3.3 3.3	4.6
οΛ	434998	AW975157	Hs.26037	ESTs	3.3	4.7
80	456359 4265 <i>2</i> 7	AI967991	Hs.93574	homeo box D3	3.3	4.4
	400302	NM_001037 N48056	Hs.170238 Hs.1915	sodium channel, voltage-gated, type I, b folate hydrolase (prostate-specific memb	3.3	5.2 9.0
	419875	AA853410	Hs.93557	proenkephalin	3.3 3.3	3.6



	444612 415242	AW138111	Hs.22902	ESTs	3.3 3.2	3.0
	421640	R45986 AW966652	Hs.295014	ESTs gb:EST378726 MAGE resequences, MAGI Homo	3.2	2.2 3.8
_	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2	24
5	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2	3.2
	425495 403092	AA358454	Hs.78026	ESTs, Wealty similar to similar to ankyr	3.2 3.2	2.2 2.9
	452971	AJ873878	Hs.91789	ESTs	3.2	4.5
10	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2	2.7
10	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2	2.6
	421200 440827	AA284811 AI733110	Hs.264433 Hs.128128	ESTs ESTs	3.2 3.2	2.7 2.1
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (	3.2	4.3
1.0	420156	AW449258	Hs.6187	ESTs	3.2	19.0
15	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2	2.0
	419956 423930	AL137939 AA332697	Hs.40096 Hs.42721	ESTs ESTs	31 31	8.7 2.7
	417868	AI078534	Hs.122592	ESTs	3.1	12.6
••	423346	AI267677	Hs.127416	synaptojanin 1	3.1	12.0
20	441921	AI733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1	4.3
	429470 408217	AI878901 AI433201	Hs.203862 Hs.279860	guanine nucleotide binding protein (G pr	3.1 3.1	5.3 7.1
	427322	AK002017	Hs.176227	tumor protein, translationally-controlle hypothetical protein FLJ11155	3.1	6.3
	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	30.1
25	429608	U49250	Hs.210862	T-box, brain, 1	3.1	2.2
	442308 411666	AA989402 AF106564	Hs.111 Hs.71346	fibroblast growth factor 9 (glia-activat	3.1 3.1	3.0 10.9
	427865	AA416931	Hs.126065	neurofilament 3 (150kD medium) ESTs	3.1	7.5
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1	3.4
30	451829	AW964081	Hs.247377	ESTs	3.0	6.2
	405911 418808	AI821836	Hs.10359	ESTs	3.0 3.0	2.4 6.2
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0	5.1
	423952	AW877787	Hs.136102	KIAA0853 protein	3.0	21
35	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC)	3.0	2.1
	405793 410711	AB002316	Hs.65746	KIAA0318 protein	3.0 3.0	2.7 14.3
	427071	AA397958	Hs.192719	ESTS	3.0	2.1
40	453534	NM_014796	Hs.33187	KIAA0748 gene product	3.0	14.5
40	413903	AA496493	Hs.23136	ESTs	3.0	2.2
	426866 434945	U02330 AB033065	Hs.172816 Hs.4280	neuregulin 1 KIAA1239 protein	3.0 3.0	11.3 3.5
	412639	AW961284	Hs.296235	ESTs	2.9	4.9
4.5	453590	AF150278	Hs.33578	KIAA0820 protein	2.9	33.1
45	414502	AL133721	Hs.224680	ESTs	2.9	2.3
	434367 425121	AB020700 AJ797511	Hs.3830 Hs.154679	KIAA0893 protein synaptotagmin I	2.9 2.9	23.1 8.1
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	29	20.8
60	401213				2.9	3.2
50	401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9	3.4
	415191 449275	AA190381 AW450848	Hs.120810 Hs.205457	ESTs perlaxin	2.9 2.9	3.0 5.6
	419863	AW952691	Hs.93485	Homo saplens mRNA; cDNA DKFZp761D191 (fr	2.9	35.0
<i>E E</i>	411421	BE272110	Hs.21177	ESTs	2.9	2.0
55	430865 437486	A1073424	Hs.5232	HSPC125 protein	29	11.4
	442357	AW952089 AI458586	Hs.5636 Hs.135706	RAB6A, member RAS oncogene family ESTs	2.9 2.9	2.2 6.0
	408274	R17315		gb:yg12g11.r1 Soares Infant brain 1NIB H	2.9	2.2
60	444185	AW298350	Hs.66020	ESTS	2.8	5.0
60	420173 428358	AA256151 AA993222	Hs.22999	ESTs	2.8	5.1
	447252	R90916	Hs.101915 Hs.12449	Stargardt disease 3 (autosomal dominant) Homo sapiens transmembrane protein HTMP1	2.8 2.8	7.0 4.4
	440260	AI972867	Hs.7130	copine IV	2.8	10.6
65	417084	H08370	Hs.33067	ESTs	2.8	8.4
05	438257	AW474419	Hs.224794	FAT.	28	2.8
	447885	T23939 F11528	Hs.7344 Hs.303172	ES13 Horno sapiens mRNA; cDNA DKFZp547G133 (fr	2.8 2.8	6.2 3.5
	423552	AF107028	Hs.129783		2.8	3.4
70	450940	AI744943	Hs.143209	ESTs, Weakly similar to 138022 hypotheti	2.8	14.4
70	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.8	21.7
	445887 425494	A1263105 N55540	Hs.145597 Hs.78026	' ESTs ESTs, Wealtly similar to similar to anklyr	2.8 2.8	5.1 2.4
	438202	AW169287	Hs.22588	ESTs	2.8	11.9
75	435199	R38946	Hs.127951	hypothetical protein FLJ14503	2.8	6.0
75	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.8	2.4
	415462 418070	R52692 NM_000844	Hs.12698 Hs.83407	ESTs glutamate receptor, metabotropic 7	2.8 2.8	3.4 4.5
	432149	AW614326	Hs.157027		2.8	9.5
00	430371	D87466	Hs.240112	KIAA0276 protein	2.8	7.0
80	437357	AL359559	Hs.331666		2.7	2.5
	415838 438675	R44336 AA813725	Hs.7093 Hs.213566	ESTS B ESTs	2.7	3.6
	419558	AW953679	110.213300	gb:EST365749 MAGE resequences, MAGC Homo	2.7 2.7	2.5 3.1

	446318	A1949389	Hs.18067	ESTs	2.7	4.1
	445183	AB007877	Hs.12385	KIAA0417 gene product	2.7	5.3
	457012 431988	R41480 AC002302	Hs.127630 Hs.77202	ESTs	2.7	19.0
5	430223	NM_002514	Hs.235935	protein kinase C, beta 1 nephroblastoma overexpressed gene	2.7 2.7	7.2 2.8
_	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.7	20 38
•	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.7	6.9
	434731	AA648049	Hs.121518	ESTs	2.7	5.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fts, clone NT	2.7	5.2
10	407709 422420	AA456135 U03398	Hs.23023	ESTs	2.7	2.5
	443305	AI050693	Hs.1524 Hs.133318	tumor necrosis factor (figand) superfami ESTs	2.7	3.3
	435648	H24347	Hs.27524	ESTs	27 27	5.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	27	15.0 2.7
15	436771	AW975687	Hs.292979	ESTs	27	6.0
	428689	NM_014351	Hs_189810	sulfortranferase family 4A, member 1	27	4.8
	440503 441006	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	2.7	4,4
	410330	AW605267 AW023630	Hs.7627 Hs.48786	CGI-60 protein ESTs	2.7	3.1
20	434398	AA121098	Hs.3838	serum-inducible kinase	26 26	29.5
	438831	BE263273	Hs.6439	synapsin (I	26	2.5 7.8
	419066	298492	Hs.6975	PRO1073 protein	2.6	3.4
	412643	AW971239	Hs.293982	ESTs	2.6	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	26	17.9
23	416498 401421	U33632	Hs.79351	potassium channel, subfamily K, member 1	26	29
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	26	2.0
	441817	AW969706	Hs.293332	ESTs	2.6 2.6	4.2 3.8
	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
30	426054	U12431	Hs.168109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583	AW994403	Hs.100861	hypothetical protein FLJ14600	2.6	3.7
	417919	A1928203	Hs.86379	ESTS	2.6	3.0
	434293 431716	NM_004445 D89053	Hs.3796 Hs.268012	EphB6	2.6	3.2
35	443037	AW\$00305	Hs.299166	fatty-acid-Coenzyme A figase, long-chain syntaxin 7	2.6 2.6	6.4
	440736	D56919	Hs.265848	myomegalin	2.6	2.2 7.1
	404648			,	2.6	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
40	436508 441190	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.6	3.9
70	432278	H09073 AL137506	Hs.25046 Hs.274256	ESTS	2.6	3.1
	442731	AI868167	Hs.131044	hypothetical protein FLJ23563 ESTs	2.6 2.6	2.9
	416836	D54745	Hs.80247	cholecystokinin	2.6	4.1 14.9
40	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
45	436321	AA709133	Hs.180144	ESTs	2.5	2.8
	439693	A1741816	Hs.125897	ESTs	2.5	3.6
	443212 423981	AW269515 AL122104	Hs.102500 Hs.136664	hypothetical protein FLJ20481	25	2.8
	407868	NM 000950	Hs.40637	Homo sapiens mRNA; cDNA DKFZp434A1627 (f proline-rich Gla (G-carboxyglutamic acid	2.5 2.5	3.8
50	443992	AW022228	Hs.322922	ESTs	2.5	3.1 27.9
	444124	R43097	Hs.6818	ESTs	2.5	5.3
	411379	AI816344	Hs.12554	ESTs, Wealty similar to NPL4_HUMAN NUCLE	2.5	38.0
	440474 446277	A1207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	25	3.8
55	410111	AI284218 AI620206	Hs.159204 Hs.189647	ESTS ESTS	2.5	2.2
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	2.5 2.5	3.5
	410718	AI920783	Hs.191435	ESTs	25	4.8 4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
60	420274	AW968000	Hs.143389	ESTs, Weakly similar to T14318 ubiquitin	2.5	2.8
00	433496 437331	AF064254 AL353933	Hs.49765 Hs.21710	VLCS-H1 protein	2.5	4.7
	437368	Al471969	Hs.182606	hypothetical protein DKFZp761G0313	2.5	3.3
	441985	BE047625	Hs.169815	ESTs ESTs	2.5 2.5	3.0
	410025	BE220489	Hs.113592	ESTs, Moderately similar to 154374 gene	2.5	3.6 9.2
65	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.5	3.6
	429956	Al374651	Hs.22542	ESTs	2.5	23.9
	429028	AA443439	Hs.48797	ESTs	2.5	2.8
	438109 439780	AI076621 AL109688	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	440888	N45600	Hs.326880	gb:Homo sapiens mRNA full length insert ESTs	2.5	2.3
	445246	AI217713	Hs.147586	ESTS	2.5 2.5	3.9 2.6
	440152	AB002376	Hs.7006	KIAA0378 protein	2.4	23.6
	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	2.4	21
75	415122	D60708	Hs.22245	ESTs	2.4	3.9
75	432298	AL118812	Hs.274293	Homo sapiens mRNA; cONA DKFZp761G1111 (f	2.4	9.8
	437948 421360	AA772920 AA297012	Hs.303527	ESTs	2.4	9.8
	427115	AW972853	Hs.103839 Hs.112237	erythrocyte membrane protein band 4.1-li ESTs	2.4	2.8
00	452074	BE299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4 2.4	2.2 10.0
80	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-activat	24	3.5
	434520	AA205273	Hs.177011	hypothetical protein	2.4	3.1
	411529	AA430348	Hs.317596	Homo sepiens cDNA FUJ12927 fis, clone NT	2.4	3.0
	442272	AA988302	Hs.129172	ESTs	2.4	2.1

	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.4	2.7
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	24	2.7 2.8
	415827	H17462	Hs.23079	ESTs	2.4	15.0
_	451397	AA017432	Hs.84529	ESTs, Weakly similar to 2202_HUMAN ZINC	2.4	3.9
5	445200	AA084460	Hs.12409	somatostatin	24	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	2.4	24
	420328	Y19062	Hs.96870	stauten (Drosophila, RNA-binding protein	2.4	4.3
	432122 444125	AA526514 AI124882	Un 440424	gb:ni60f02.s1 NCI_CGAP_Ov2 Homo sapiens	2.4	4.3
10	430538	AB032435	Hs.118121 Hs.242821	ESTs differentiation-associated Na-dependent	24 24	3.5
	457519	X69438	Hs.3052	early growth response 4	2.4	10.8 2.4
	409371	R51736	Hs.12381	ESTs	24	21
	456303	AA224872	Hs.115088	ESTs	2.4	3.2
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.4	23.4
15	400979			• • •	2.4	4.1
	435296	R49685	Hs.24980	ESTs	24	6.5
	408950	AA707814	Hs.14945	long latty acyl-CoA synthetase 2 gene	2.4	18.5
	452032 432098	BE244005	Hs.27610	retinoic acid- and interferon-inducible	24	2.2
20	408974	AF252297 AW015458	Hs.91546 Hs.297017	cytochrome P450 retinoid metabolizing pr ESTs	24 24	2.7
	412177	ZZ3091	Hs.73734	glycoprotein V (platelet)	24	2.5 2.8
	413153	N94205	140.70.00	gb:za27a08.r1 Soares fetal liver spicen	24	2.5
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	24	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
25	424940	AA985308	Hs.194327	ESTs	2.3	6.3
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	2.3	4.1
	419125 423641	AA642452 AL137256	Hs.130881	8-cell CLL/lymphoma 11A (zinc finger pro	23	2.9
	436407	T88803	Hs.130489 Hs.271507	ATPase, aminophospholipid transporter-li ESTs, Wealdy similar to TIM_HUMAN PROBAB	23 23	8.7
30	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	23	3.2 5.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	23	54.7
	410765	Al694972	Hs.66180	nucleosome assembly protein 1-tike 2	2.3	9.1
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
25	414828	AA156651		gb:zI05h05.r1 Soares_pregnant_utenus_NbH	23	2.4
35	445556	AI910241	Hs.12887	actin-related protein 3-beta	23	8.5
	426968 444562	U07616 AA186715	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	23	26.3
	423420	AI571364	Hs.336429 Hs.128382	RIKEN cDNA 9130422N19 gene Homo saplens mRNA; cDNA DKFZp761I1224 (f	23	2.5
	439450	R51613	Hs.125304	EST8	2.3 2.3	7.6 26.3
40	427127	AW802282	Hs.22265	pyruvale dehydrogenase phosphatase	23	2.2
	447179	AW015633	Hs.157299	EST ₈	2.3	3.8
	414711	AJ310440	Hs.288735	Homo sapiens cONA FLJ13522 fis, clone PL	2.3	2.3
	433449	AW772282		gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.3	3.8
45	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	23	2.5
43	416778 425130	M16505	Hs.79876	steroid sutfatase (microsomal), arytsutf	2.3	7.8
	456664	AA448208 AW963354	Hs.99163 Hs.334409	ESTs metallothionein 1G	2.3	4.1
	438283	AJ458931	Hs.37282	ESTs	2.3 2.3	2.5 4.2
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.3	3.0
50	412100	AW892731		gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.7
	448981	AI968719	Hs.195387	ESTs	2.3	3.2
	416101	R24854	Hs.268806	EST ₈	2.3	6.5
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734 424598	NM_014747 AB020639	Hs.78748	KIAA0237 gene product	2.3	40.1
55	420230	AL034344	Hs.151017 Hs.284188	estrogen-related receptor gamma forthead box C1	2.3 2.3	2.9
	451559	AL119980	Hs.20935	hypothetical protein DKFZp761D221	2.3	2.4 5.7
	404835			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	2.3	21
<b>60</b>	456765	AI497900	Hs.33067	ESTs	2.3	4.1
60	455517	AW984068		gb:RC0-HN0006-160300-011-e08 HN0006 Homo	2.3	2.4
	408206	AF041853	Hs.43670	kinesin family member 3A	2.2	18.5
	411770 430105	NM_014278 X70297	Hs.71992	heat shock protein (hsp110 family)	2.2	3.9
	458694	F12832	Hs.2540 Hs.13298	cholinergic receptor, nicotinic, alpha p ESTs	2.2	2.6
65	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2 2.2	4.9 4.4
	439642	W81441	Hs.153967	ESTs	2.2	2.4
	450138	AW152104	Hs.200879	ESTs	2.2	4.9
	454222	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	2.2	3.7
70	405328				2.2	2.7
70	431342	AW971018	Hs.21659	ESTs	2.2	5.2
	453101 408897	AW952776 N50204	Hs.94943 Hs.283709	ESTs	2.2	3.3
	451398	AI793124	Hs.144479		2.2	2.8
	438208	AL041224	Hs.65379	ESTS	2.2 2.2	4.6 10.4
75	408449	NM_004408			2.2	6.1
	414130	AJ570831	Hs.71592	Homo sapiens cDNA: FLJ21893 fis, clone H	2.2	3.1
	445016	U79716	Hs.12246	reelin	2.2	3.9
	424375	AF070547	Hs.146312		2.2	2.3
80	424645	NM_014682			2.2	11.7
<b>50</b>	409729 432809	D51315	Hs.106289		2.2	4.9
	422890	AA565509 Z43784	Hs.131703 Hs.75893	ESTs ankyrin 3, node of Ranvier (ankyrin G)	2.2	19.9
	428532	AF157326	Hs.184786		2.2 2.2	10.4 6.5
	_	-			<b>-</b>	0.0



	413074	A1871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442 452768	AA156238 AW069459	Hs.32501 Hs.61539	ESTs ESTs	2.2 2.2	3.2 2.0
_	450440	AB024334	Hs.25001	tyrosine 3-monophygenase/typtophan 5-mo	2.2	3.2
5	426281	AK000987	Hs.169111	oxidation resistance 1	2.2	2.3
	428411	AW291464	Hs.10338	ESTs	2.2	2.3
	413787 451734	AJ352558 NM_006176	Hs.75544 Hs.26944	tyrosine 3-monooxygenase/tryptophan 5-mo neurogranin (protein kinase C substrate,	2.2 2.2	3.1 8.5
	439108	AW163034	Hs.6467	synaplogyrin 3	2.2	7.9
10	405385				2.2	2.4
	447285	AI371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	452667 422234	T87219 AF119818	Hs.13219 Hs.113287	ESTs discs, large (Drosophila) homolog-associ	2.2 2.1	3.1 8.3
	410339	Al916499	Hs.298258	ESTs	21	3.2
15	413231	D87461	Hs.75244	BCL2-like 2	2.1	4.5
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fls, clone NT	21	2.2
	451952 415841	AL120173 Z45837	Hs.301663 Hs.7093	ESTs ESTs	2.1 2.1	36.5
	441086	A1928489	Hs.213490	ESTs, Wealdy similar to N33_HUMAN N33 PR	2.1	2.4 2.2
<b>20</b> .	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	21	5.3
	449712 409660	R56545 AW452065	Hs.6100 Hs.258905	ESTs ESTs	21 21	4.5 2.1
	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	21	5.4
25	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.1	3.0
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	21	4.8
	418948 414876	A1217097 AW950925	Hs.924	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W crystallin, mu	21 21	2.9
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.4 3.7
30	451249	AA016227	Hs.27280	ESTs	2.1	4.1
	451475	T19093	Hs.26450	KIAA0725 protein	2.1	2.1
	448743 430814	AB032962 U89336	Hs.21896 Hs.247993	KIAA1136 protein NG5 protein	2.1 2.1	29.7
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	21	2.7 2.3
35	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrotase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	Gantigen 7B	2.1	2.2
	459089 435832	F13036 AA425688	Hs.27373 Hs.41641	Homo sapiens mRNA; cDNA DKFZp56401763 (f Bruno (Drosophila) -fike 4, RNA binding	2.1 2.1	. 2.3 5.9
4.0	446383	T05816	Hs.92511	ESTs	21	2.9
40	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	21	2.1
	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111 452238	R39039 F01811	Hs.328455 Hs.187931	EST ESTs	2.1 2.1	3.3
	445279	R41900	Hs.22245	ESTs	2.1	4.9 9.8
45	448799	AI937094	Hs.179080	ESTs	2.1	3.1
	418338	NM_002522	Hs.84154	neuronal pentraxin i	2.1	8.3
	445725 443537	AK000956 D13305	Hs.13209 Hs.203	hypothetical protein FLJ10094 cholecystokinin B receptor	2.1 2.1	5.4
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	4.1 6.4
50	429954	AI918130	Hs.21374	ESTs	2.1	7.2
	415292	H29016	Hs.200576	ESTs	21	3.9
	423563 424906	R34734 AI566086	Hs.7 <b>5209</b> Hs.153715	protein kinase (cAMP-dependent, catalyti Homo sapiens mRNA for Hmob33 protein, 3'	21 21	3.1 4.7
	459309	AA040620	Hs.5672	hypothetical protein AF 140225	21	2.2
55	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
	402598 435406	8E314624 F26698	Hs.3128 Hs.4884	polymerase (RNA) II (DNA directed) polyp	2.1	5.4
	448792	R42550	Hs.12826	calclum/calmodulin-dependent protein kin ESTs	21 21	6.6 4.1
<b>~</b> 0	449500	AW956345	Hs.12926	ESTs	21	2.4
60	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	21	5.0
	433361 452946	AW469373 X95425	Hs.300141 Hs.31092	ribosomal protein L39 EphA5	2.1	2.7
	426167	AF039023	Hs.167496	RAN binding protein 6	2.1 2.0	5.0 2.2
	453666	AW015681	Hs.135229	ESTs, Wealdy similar to A2BP_HUMAN ATAXI	2.0	3.1
65	424632	AB014523	Hs.151406	KIAA0623 gene product	2.0	3.5
	448589 430416	AF017090 AC005531	Hs.21554 Hs.57806	KIAA1107 protein	2.0	4.1
	445627	AW818475	Hs.7363	Homo sapiens PAC clone RP4-701016 from 7 ESTs	2.0 2.0	2.3 2.1
70	417092	H97508	Hs.181165	eukaryotic translation elongation factor	2.0	2.5
70	453653	AW505554	Hs.144559	ESTs	2.0	4.7
	435850 435086	AF250847 AW975243	Hs.283514 Hs.122596	mitochondrial ceramidase ESTs	2.0	3.7
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0 2.0	2,1 2.1
26	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.0	2.8
75	431645	AF078849	Hs.266483	dynein light chain-A	2.0	2.5
	429834 439607	A1929645 BE540565	Hs.225938		20	3.6
	408033	AW138045	Hs.159460 Hs.242256	ESTs ESTs	2.0 2.0	17.5 4.0
00	430317	AB020645	Hs.239189	glutaminase	2.0	2.7
80	419631	AW188117	Hs.303154	popeye protein 3	2.0	2.6
	432660 454048	AI288430 H05626	Hs.64004	ESTs ESTs	2.0	2.3
	426917	AA913814	Hs.6921 Hs.172854	UKFZP586B0923 protein	2.0 2.0	15.9 3.1
					2.0	



	423246	AL119114	Hs.77196	constring pinks and another size 5 total	2.0	2.9		
	415989	AI267700		spectrin, alpha, non-erythrocytic 1 (alp ESTs	2.0	4.8		
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORTI	2.0	5.1		
-	424983	AJ742434	Hs.169911	ESTs	2.0	15.9		
5	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.0	2.7		
	450006	Al241555	Hs.60171	ESTS	2.0	3.5		
	TABLE 276	3:						
10	Pkey:	Uniqu	ie Eos probese	t identifier number				
10	CAT numb		chuster numbe					
	Accession:	Genti	ank accession	numbers				
	Pkey	CAT Number	Accession					
	408274	104999_1	R17315 Z439	964 AA053547				
15	412100	1277224_1		108502 Z45826				
	412112	1277883_1		E180347 AW901900 BE180222 BE180218 BE181 E180219 BE180346 BE180343 BE180418 BE180				
				W893615 H85799 H83501 BE180220	2230110021	DE 10001 ATTSOTOS DE 1002	7 DE 100221 ANSOTOST DE 1000AS	
	413153	1350849_1		67565 BE067556				
20	413510	1374377_1		009 BE145525 BE145493				
	414828 418948	149563_1 180808_1		A156622 R14472 N886090 W38035 W38792 AA232835 AW936043				
	419558	185904_1		W953680 AA244436 H82527 AA361046 AA2444				
26	421249	200649_1	AA285362 A	W752386 AW847156 AA285373 AW879575 AW8				
25	421640	204833_1		W966653 AA294989 AA385977				
	429995 430212	311738_1 314437_1		J277645 AL118763 J718503 AA469225				
	432122	341756_1		W973343 AA554293				
20	433449	366532_1	AW772282	NA592974				
30	434138 437483	380572_1		W418787 AW074833 Al675642 Al393368				
	439780	43756_1 47673_1	AL390174 A AL109688 R	17 123665 R26578				
	452502	919733_1		E007223 R30687		•		
35	455517	1321782_1		AW984072 AW984077				
23	456407	184986_1	AVV908014	AA243209 AA281411				
	TABLE 27	rc:						
	Pkey: Unique number corresponding to an Eos probeset							
40	Ref:			The 7 digit numbers in this column are Genbank I n chromosome 22" Dunham, et al. (1999) Nature 4		umbers. "Dunnam, et al." refers (	to the publication entitled "The UNA	
•••	Strand:			nd from which exons were predicted.	102.105.450.			
	Nt_positio			e positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position				
45	400979	8072554	Plus	160842-161028				
	401213	9858408	Plus	98243-98380,98489-98619				
	401421	7452889	Minus	142291-142461				
	403092 404648	8954241 9796894	Ptus Minus	174720-175016,175104-175406,175508-17581 115334-116020	13			
50	404793	7232206	Minus	61087-61590				
	404835	6970743	Plus	85462-85684,88139-88287,90338-91018,9482				
	405326 405385	4375975 6552772	Plus Plus	10633-10709,30805-30893,38078-38253,5511 48332-48454	2-55327,57718	-57818,66696-66841		
	405793	1405887	Minus	89197-89453				
55	405911	6758795	Plus	101008-101643				
	405977	8247789	Minus	135548-136177				
				lated in glioma compared to normal adult tissues				
60				ulated in glioma compared to normal adult tissues				
				ied were removed from the starting collection of 5! og 53005 probesets such that the ratio of "average"				
				to 50 units (this selects for the most abundant of t				
				ma, and oligodendroglioma specimens; the "avera				
65				r non-malignant brain tissues. In order to remove				
	amongsi Pkey:			was subtracted from both the numerator and the set identifier number	denominator be	store the 1800 was evaluated. Pr	edicted protein domains are noted.	
	ExAcon:			ion number, Genbank accession number				
~^	Unigene	IO: Uni	lgene number					
70	Unigene		igene gene title					
	Prot. Do R1:		edicted Protein oma vs normal					
		914	THEFTINGS					
75	Pkey	ExAcon		O Unigene Title	Prot	ein Domains	R1	
75	443902	W28470	Hs.12600	N-ethylmatelmide-sensitive factor a			4.0	
	441476 446048	R44566 Al272364	Hs.173134 Hs.18208				4.0 3.8	
	407061	X97748		gb:H.sapiens PTX3 gene promotor reg		•	3.7	
PΛ	414323	NM_014759			m3;		3.6	
80	439769 429319		Hs.30596 Hs.19906			amase_8,Rhombold,TPR	3.6 3.6	
	443412		Hs.9305	angiotensin receptor-like 1	pkin	ese;TM;SS	3.6 3.5	
	425533		Hs.9305	angiotensin receptor-like 1			3.5	
					267			



	408610	AW026692	Hs.285050	ESTs	ion_trans,K_tetra,Kv2chan	3.4
	450678 419171	AL109703 NM_002846	Hs.25314 Hs.89655	Homo sapiens mRNA full length inser protein tyrosine phosphatase, recep	Y_phosphatase,ART;TM;SS	3.4 3.4
_	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA seque	1_pitospiiaese;iff,iff,55	3.4
5	412581	AA224244	Hs.182704	ESTs, Moderately similar to alterna		3.3
	424911	AA984354	Hs.7913	ESTs		3.3
	452753 436648	AA028049 R18656	Hs.277728 Hs.352385	SEC14 (S. cerevisiae)-like 2 ESTs	CRAL_TRIO pkinase,pkinase_C,PMP22_C	3.3 3.2
	452130	AW248349	Hs.28088	SGC32445 protein	TB2_OP1_HVA22;TM;SS	3.2
10	448848	AF131851	Hs.22241	hypothetical protein	12425. 12 — (11425	3.2
	426470	AA528794	Hs.128644	ESTs		3.2
	419344 439783	U94905 Al125760	Hs.277445 Hs.24835	diacylglycerol kinase, zeta (104kD)	ank,DAGKa,DAGKc,DAG_PE-bi	3.2
	411358	R47479	Hs.94761	hypothetical protein FLJ14594 KIAA1691 protein	ig.LRR.LRRNT,LRRCT;TM;S TM;SS	3.2 3.2
15	409433	AA074382	Hs.135255	ADAMTS14	***************************************	3.2
	456940	H46986	Hs.31861	ESTs	_	3.1
	423744	D26158	Hs.1701	ELAV (embryonic lethal, abnormal vi	mm,Gene66;	3.1
	432227 449181	U28389 X96783	Hs.274122 Hs.23179	erythrocyte membrane protein band 4 synaptotagmin V	VHP;TM; C2:TM;SS	3.1 3.1
20	422274	NM_015564	Hs.114169	KIAA0416 protein	LRR,LRRNT,LRRCT;TM;SS	31
	424607	NM_016848	Hs.151123	neuronal Shc	PID,SH2;	3.1
	416898	BE219510	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02	EGF,Rhabd_glycop;TM;SS=	3.1
	438162 439892	NM_014618 AL043463	Hs.6090 Hs.6755	deleted in bladder cancer chromosom RaP2 interacting protein 8	TM;SS Run;SS	3.1 3.1
25	445330	R52656	Hs.21691	ESTs	7tm_1	3.0
	451768	NM_001406	Hs.26988	ephrin-83	Ephrin;TM;SS	3.0
	444457	- AI204146	Hs.92556	ESTS	Fork_head	3.0
	458247 424616	R14439 U72671	Hs.209194 Hs.151250	ESTs intercellular adhesion molecule 5.	ig,ICAM_N;TM;SS	3.0 3.0
30	408971	R38990	Hs.13485	ESTs	W.10-01-11,1 M.0-0	3.0
	423940	NM_012429	Hs.277728	SEC14 (S. cerevisiae)-like 2	CRAL_TRIO;TM;	3.0
	458124	AW005548	Hs.124590	ESTs		3.0
	410491 444808	AA465131 H20019	Hs.64001 Hs.286084	Homo sapiens clone 25218 mRNA seque ESTs	ank,ras,PH,ArfGap,HCO3_co	3.0 3.0
35	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase;TM;	2.9
	424016	AW163729	Hs.6140	hypothetical protein MGC15730	ig:SS	2.9
	421680	AL031186 R18516	Hs.289106	Human DNA sequence from clone CTA-9	Collagen;TM;SS	2.9
	418055 444819	A1697836	Hs.351299 Hs.148433	ESTs, Wealty similar to I38022 hypo ESTs	22,72	2.9 2.9
40	420524	AB010575	Hs.98547	amiloride-sensitive cation channel	ASC;TM;	2.9
	416237	H30684	Hs.159863	ESTs	•	2.9
	432270	AK001008	Hs.274233	Homo sapiens cDNA FLJ10146 ffs, clo		2.9
	405569 428950	BE311879	Hs.194673	NM_031481*:Homo sapiens solute carr phosphoprotein enriched in astrocyt	mito_carr,TM;SS DED:TM:	2.9 2.9
45	426128	NM_001471	Hs.167017	gamma-aminobutyric acid (GABA) B re	7tm_3,sushi,ANF_receptor;	2.9
	447758	H17302	Hs.93967	ESTs, Wealthy similar to NBHUC8 deco	LRR, LRRNT, LRRCT; TM; SS	2.9
	445331 431010	H04489 BE251246	Hs.12520 Hs.248214	Homo saplens clone 23568, 23621, 23 complexin 1	PC_rep TM;	2.9 2.9
	433065	N62902	Hs.343660	Homo sapiens PAC clone RP4-651K2 fr	:SS	2.9
50	426845	AB025186	Hs.172740	microtubule-associated protein, RP/	EB1,CH;TM;	2.9
	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_tran_ABC_membrane,PRK	2.9
	438859 410515	AI559626 F12086	Hs.93522 Hs.4257	Homo sapiens mRNA for KIAA1647 prot ESTs	bZIP,K-box,7tm_2,EGF,cadh PID,SH2,PID,SH2	2.9 2.8
	434022	R18374	Hs.117956	ESTs	hormone_rec,zf-C4	2.8
55	428960	AF052224	Hs.194684	bassoon (presynaptic cytomatrix pro	Carta_C4,RPH3A_effector,T	2.8
	426290	AB007918	Hs.169182		WD40;TM;	2.8
	417287 422575	AJ831678 AK000546	Hs.285714 Hs.118552		C2:TM; PTR2;TM;SS	2.8 2.8
	417941	A1056049	Hs.96297	ESTs	Band_41,ERM	2.8
60	452707	AI093823	Hs.45070	ESTs	_	2.8
	424873	AB018294	Hs.153610		C2.PDZ:TM;	28
	408209 415935	NM_004454 H09663	Hs.43597 Hs.106490	ets variant gene 5 (ets-related mol ESTs	Ets;TM; PID	2.8 2.8
	437999	AW905038	Hs.90242	ESTE	ion_trans	2.8
65	428248	AJ126772	Hs.40479	ESTS		2.8
	414001	AI610347	Hs.103812		Gelsolin,VHP,p450	2.8
	406634 453439	AA386235 AI572438	Hs.74576 Hs.32976	GDP dissociation inhibitor 1 guanine nucleotide binding protein	GDI;TM; G-gamma;TM;	2.8 2.8
	433320	D60647	Hs.250879		um Garingt w	2.8
70	420888	AB006713	Hs.100058	dihydropyrimidinase-like 4	Dihydroorotase;TM;	27
	440001	AJ740721	Hs.128292			2.7
	417622 438626	AW298163 AI198059	Hs.82318 Hs.26370	WAS protein family, member 3 ESTs	WH2;TM;	2.7 2.7
	404439	M100044	115.20370	ENSP00000067222*:Mitochondrial 28S	OLF;SS	2.7
75	448375	NM_004644		adaptor-related protein complex 3,	Adaptin_N;TM;	2.7
	420989	AB002372	Hs.323833		TM;	2.7
	419651 414562	NM_007023 AW955734	Hs.91971 Hs.112199	cAMP-regulated guanine nucleotide e S ESTs, Weakly similar to 2108402A ca	cNMP_binding,DEP,RasGEF,R	2.7 2.7
	410865		Hs.66727		IRK	2.7
80	421146	AI082215	Hs.97993	ESTs, Moderately similar to SERP1 [		27
	419087		Hs.24835	trypothetical protein FLJ14594 I homeodomain-interacting protein kin	ig,LRR,LRRNT,LRRCT;TM;S	2.7
	421499 425014		Hs.236131 Hs.171939		pkinase,Peptidase_M1;TM P(D,PDZ	2.7 2.7
				<del>-</del>	. 10% 000	2.,

	448655	AL035289	Hs.21708	hypothetical protein from clone 248	TM;SS	2.7
	424410	W79027	Hs.271762 Hs.40183	ESTS		2.7 2.7
	447117 447478	AI352798 BE618843	Hs.28144	ESTs fibronectin type 3 and SPRY domain-	fn3,SPRY;TM;	2.7
5	437645	R20728	Hs.21164	ESTs	110,00 111,110,	27
-	433698	H24201	Hs.247423	adducin 2 (beta)	Aldolase_II;TM;	2.7
	419701	AA248999	Hs.7913	ESTs		2.7
	410510	AW294625	Hs.64064	potassium voltage-gated channel, su	cNMP_binding.ion_trans,PA	27
10	452869 428045	AB014534 T15465	Hs.30898 Hs.182231	KIAA0634 protein thyrotropin-releasing hormone	fn3;SS ;SS	27 27
10	425218	NM_014909		KIAA1038 protein	TM:	27
	425558	AF040723	Hs.158300	huntingtin-associated protein 1 (ne	TM:	26
	440789	AB007857	Hs.7416	KIAA0397 gene product	TBC,RUN;TM;	2.6
1.5	418423	NM_014732		KIAA0513 gene product	TM;	2.6
15	450400	AI694722	Hs.279744	ESTS	lectin_c	2.6
	413566 443759	AW604451 BE390832	Hs.285814 Hs.134729	sprouty (Drosophila) homolog 4 FXYD domain-containing ion transpor	SH2,SH3;TM;SS ATP1G1_PLM_MAT8;TM;SS	26 26
	425069	AA687465	Hs.298184	potassium voltage-gated channel, sh	ado_ket_red	26
••	429291	AI933057	Hs.349189	mannosyl (alpha-1,3-)-glycoprotein	2.2.2.3.0.3.	2.6
20	424798	AW016523	Hs.182850	ESTs		2.6
	447455	H38335	Hs.6750	Homo sepiens mRNA for FLJ00058 prot	TM;\$S	26
	417212 432265	AW952823 BE382679	Hs.351547 Hs.285753	NS1-binding protein SCG10-like-protein	E2_N,E2_C,DNA_mis_repair.	2.6 2.6
	432205	C21115	Hs.26612	ESTs, Moderately similar to \$23650	Stathmin;TM;SS	2.6
25	421091	W22821	Hs.351612	ribosomal protein L26	TM;	26
	445472	AB005631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene	homeobox,CUT;TM;	2.6
	431967	AJ243653	Hs.373498	organic cation transporter	sugar_tr;TM;SS	26
	439151	AW135066	Hs.283110	carbonic anhydrase X	carb_anhydrase;TM;SS	26
30	424134 430213	AF070637 AW993446	Hs.140950 Hs.235445	hypothetical protein hypothetical protein FLJ21313	DUF 176;SS GRAM:TM:	2.6 2.6
50	445954	AA148926	Hs.27836	hypothetical protein FLJ22362	fn3;TM;	2.6
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM;SS	2.6
	446236	NM_006293		TYRO3 protein tyrosine kinase	fn3,ig,pkinase;TM;	2.6
25	433706	AW947250	Hs.283645	ESTs	PH,RhoGAP	2.6
35	423606 438915	AB011094 AA280174	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7;TM;	25
	448923	AL034562	Hs.285681 Hs.22584	Williams-Beuren syndrome chromosome prodynorphin	Opiods_neuropep;SS	2.5 2.5
	408115	AB033107	Hs.42796	KIAA1281 protein	opous_newopap,so	2.5
40	446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clo		2.5
40	427989	H85525	Hs.40479	gb:yv88h06.r1 Soares melanocyte 2Nb	TM;SS	2.5
	435833	8E259178	Hs.41641	Bruno (Orosophila) -like 4, RNA bin	rm;TM;	2.5
	423797 448277	8E259364 BE622827	Hs.132898 Hs.99486	fatty acid desaturase 1 hypothetical protein FLJ13044	heme_1.FA_desaturase;TM	2.5 2.5
	417298	AW665639		ESTs	mito_carr;TM;SS	2.5
45	415577	AF257770	Hs.20930	poly(rC)-binding protein 4	KH-domain;TM;	2.5
	420742	U79251	Hs.99902	opicid-binding protein/cell adhesio	ig;TM;SS	2.5
	419109	BE169157	Hs.172717	ESTs	pkinase,LRRCT,ig,LRR,LRRN	2.5
	TABLE 2	ec.				
50	Pkey:		iaue number co	rresponding to an Eos probeset		
	Ref:				cidentifier (GI) numbers. "Dunham, et al." refers t	o the publication entitled "The ONA
		58	quence of huma	in chromosome 22° Dunham, et al. (1999) Nature	402:489-495.	•
	Strand:			and from which exons were predicted.		
55	Nt_positi	ion: Inc	ocates nucleon	de positions of predicted exons.		
55	Pkey	Ref	Strand	Nt_position		
	405569	6006906	Plus	99719-99873		
	404439	7139680	Plus	55316-55585		
۲۸	=======================================					
60	TABLE :	29A: ABOUT 30	52 GENES UP-F	REGULATED IN GLIOMA COMPARED TO NON	MALIGNANT ADULT BRAIN TISSUE	
					It brain tissue. These were selected as for Table : as set to the 99th percentile value amongst variou	
					luli brain specimens, the "average" glioma value w	
		d protein doma			and the speciment of the second secon	and ground trial or depth to do divide
65	Pkey:			set identifier number		,
	ExAccn:			ion number, Genbank accession number		
	Unigene Unigene		nigene number nigene gene titi			
			redicted Protein			
70	R1:			dignant adult brain tissue		
_		-				
	Pkey	ExAcon	Unigene II		Protein Domains	RI
	414477		Hs.76228		pkinase,LRR,TM;SS	11.2
75	407241 408972		Hs.49378	gb:Human ornega light chain protein OKFZP586D0919 protein	TM;	10.9 7.0
, ,	417512		Hs.82226		TM; PKD:TM:SS	7.0 6.9
	414001	AI610347	Hs.10381		Getsolin, VHP,p450	6.3
	428847	A1954833	Hs.98881	ESTs	annanna n Maraa	6.2
80	407061			gb:H.sapiens PTX3 gene promotor reg		5.4
οU	440020 408832					5.4
	406837		0 Hs.63428 Hs.15611			5.3 5.2
	407607				crystalt,TMt	5.1
		_			• • • •	

	435013	H91923		NM_020142:Homo sapiens NADH:ubiquin		5.1
	424916	AW867440	Hs.23096	ESTs	rm -co	5.1
	409659	AW970843	Hs.55682 Hs.165954	eukaryotic translation initiation f	;SS	5.1
5	432576 406621	AW157424 X57809	Hs.181125	ESTs, Wealtly similar to I38022 hypo immunoglobulin tambda locus	mm ig,HSP70,Ppx-GppA;TM;SS	5.1 5.1
-	430418	R98852	Hs.36029	heart and neural crest derivatives	HLH	5.1
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific	TM:SS	5.0
	429707	W76631	Hs.211819	matrix metalloproteinase 238	ig.Peptidase_M10;TM;SS=	5.0
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome		5.0
10	441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	5.0
	406848	A1264844	Hs.275865	ribosomal protein S18	Ribosomal_S13;	4.9
	423505	AF064090	Hs.129708	tumor necrosis factor (ligand) supe	TNF;TMLSS	4.8
	433848	AF095719	Hs.93764	carboxypeptidase A4	Zn_carbOpept.Propep_M14:T	4.8
15	431882	NM_001426	Hs.271977	engrailed homolog 1	homeobox;TM;	4.8
13	446295	A1355029	Hs.101660	ESTs, Wealdy similar to T14171 etax	UM	4.8
	409170 421155	W91994 H87879	Hs.16145 Hs.102267	ESTs hand authors	ffm	4.8 4.7
	409202	AA236881	Hs.51043	lysyl oxidase hexosaminidase B (beta polypeptide)	Lysyl_oxidase,Aldose_epim Glyco_hydro_20,Glyco_hydr	4.7
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	:SS	4.7
20	450463	AW952018	Hs.201398	G protein coupled receptor interact	C1g_Collagen;TM;SS	4.7
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN	zl-C2H2,bZIP	4.7
	406807	AA057605	Hs.180920	ribosomal protein \$9	<ul> <li>Ribosomal_\$4,\$4,tRNA_int_</li> </ul>	4.6
	409190	AU076536	Hs.50984	sarcoma amplified sequence	transmembrane4;TM;SS	4.6
26	401599			Target Exon	TM;	4.6
25	408901	AK001330	Hs.48855	hypothetical protein FLJ 10468	TM;	4.6
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 ffs, clo		4.6
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma	ig:TM;	4.6
	406699	L06505	Hs.182979	ribosomal protein L12	Ribosomal_L11;TM;	4.6
30	406663 427714	U24683 AF119850	Hs.2186	immunoglobutin heavy constant mu eukaryotic translation etongation f	SS COM CHAIR ME COT CECAC	4.6 4.6
50	407260	L09095	ns.2100	gb:Homo sapiens mRNA fragment	COX8,SHMT,MIF,GST_C,EF1G_	4.5
	406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18ae;TM;	4.5
	430397	AI924533	Hs.105607	bicarbonate transporter related pro	HCO3_cotransp:TM:	4.5
	414044	BE614194	Hs.75721	profilin 1	profilin;TM;	4.5
35	424238	AA337401	Hs.137635	ESTs	TM;SS	4.5
	421532	AW138207	Hs.146170	hypothetical protein FLJ22989	Armadillo_seg,HEAT;TM;S	4.4
	421241	X91817	Hs.102866	transketolase-like 1	transketolase,transket_py	4.4
	436398	H87136	Hs.5174	ribosomal protein S17	Ribosomal_S17e,PotyA_pol;	4.4
40	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and	pkinase,ICE_p10.ICE_p20;T	4.4
40	446921	AB012113	Hs.16530	small inducible cytokine subfamily	IL8;SS	4.3
	433271	BE621697	Hs.14317	nucleolar protein family A, member	<b>:</b>	4.3
	406964	M21305	U- 073400	FGENES predicted novel secreted pro	4004.704	4.3
	432191 420890	AA043193 AA434058	Hs.273186 Hs.100071	hypothetical protein, clone Teletho	ABC1;TM; Glucosamine_iso;TM;	4.3 4.3
45	413053	AW963263	Hs.65377	6-phosphogluconolactonase ESTs, Moderately similar to KIAA139	TM:	4.3
10	406687	M31126	Hs.352054	matrix metalloproteinase 11 (strome	hemopexin,Peptidase_M10;T	4.2
	425157	NM_006227	Hs.283007	phospholipid transfer protein	LBP_BPI_CETP.LBP_BPI_CETP	4.2
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei	an In Italy 100 In Italy	4.2
	446490	AK000706	Hs.15125	hypothetical protein FLJ20699	TM;	4.2
50	431750	AA514986	Hs.283705	ESTs	cpn60_TCP1	4.2
	428327	AW205236	Hs.28773	ESTs	cystatin,Coprogen_oxidas,	4.2
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	TM;	4.1
	433688	AA628467	Hs.112572		<b></b> .	4,1
55	433170	A8037816	Hs.8982	KIAA1395	TM;	4.1
25	423084 407926	AU076474	Hs.123178	translocase of inner mitochondrial	mn TVA-CC	4.1
	445636	AW956382 AW105401	Hs.59771 Hs.350068	ESTs ribosomal protein L29	TYA;SS	4.1
	418689	AI360883	Hs.375584		filament,GTP_EFTU,EFG_C,G	4.1 4.1
	450690	AA296696	Hs.333418		ATP1G1_PLM_MATB;TM;SS	4.1
60	419092	J05581	Hs.89603	mucin 1, transmembrane	SEA:TM:SS	4.0
	447813	AI394345	Hs.238513		ubiquitin;TM;SS	4.0
	436419	AI948626	Hs.171356		AT_hook,ATHILA	4.0
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214	PMM	4.0
	443402	U77846	Hs.356316	elastin (supravalvular aortic steno	PDZ,UM,pkinase	4.0
65	433435	BE545277	Hs.340959	Ts translation elongation factor, m	EF_TS,UBA;	4.0
	413595	AW235215	Hs.16145	ESTs	rm.	4.0
	412607	Z33642	Hs.74115	Immunoglobulin superfamily, member	ig:TM;SS	4.0
	419913	AW270040	Hs.34455	ESTs	EPH_fbd,fn3,pkinase,	4.0
70	415209	F00183	Hs.172004			4.0
70	439310	AF086120	Hs.102793		casein_kappa,pkinase,ig,n	3.9
	421777	BE562088	Hs.108196		TM;	3.9
	409485 402241	S80990	Hs.252136	ficolin (collager/fibrinogen domain Target Exon	Collagen_fibrinogen_C;TM=	3.9
	432716	AI762964	Hs.205180		p450;TM;SS	3.9
75	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	LRR.UPAR_LY6;TM;	3.9
	434214	AF119871	Hs.155860		TM;SS ;SS	3.9 3.9
	406855	AA902829	113.13.000	gb:ok72e06.s1 NCI_CGAP_GC4 Homo sap	,33	3.9 3.9
	421567	AJ272137	Hs.198265		hemopexin,Peptidase_M10;T	3.9
	403364			Target Exon	SH2,Y_phosphatase	3.9
80	412339	8E151267	Hs.314466		tubulin	3.8
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot	TIMP	3.8
	427600		Hs.179774		PA28_alpha,PA28_beta;	3.8
	405201			Target Exon	mito_carr,SH2,SH3,Alpha_a	3.8

	436906	H95990	Hs.181244	major histocompatibility complex, c	ig MHC_I;TM;SS	3.8
	407319	AI743332	Hs.257729	ESTs, Moderately similar to ALU7_HU	rm.Upoprotein_2	3.8
	400290	H18836	Hs.31608	hypothetical protein FLI 20041	Cys_knot	3.8
5	430240	BE303038	Hs.236547	Homo sapiens, clone IMAGE:2905978,	HEAT_PBS;TM;	3.8
5	442487	AF191019	Hs.8361	hypothetical protein, estradiol-ind	URRURRNT;TM;SS	3.8
	408135 419942	AA317248	Hs.42957 Hs.93841	methyltransferase-like 1	Methyltransf_4;TM;	3.8
	410584	U25138 AB011112	Hs.64742	potassium large conductance calcium	CaKB;TM;SS	3.6
	440676	NM_004987	Hs.112378	KIAA0540 protein UM and senescent cell antigen-like	18400	3.8
10	406874	AW161706	Hs.180842	ribosomal protein L13	LIM;SS	3.8
10	429249	X81479	Hs.2375	egl-like module containing, mucin-l	Ribosomal_L13e;SS	3.7
	430799	C19035	Hs.164259	ESTs	7tm_2,EGF,GPS,S_locus_gly	3.7
	453099	H62087	Hs.31659	thyroid hormone receptor-essociated	FKBP,TPR	3.7
	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1	WD40;TM; E2F_TDP,KQW,Ribosomal_L14	3.7
15	444795	AI193356	Hs.160316	ESTs	Tropomyosin,ACOX	3.7
	443834	AI741510	Hs.173548	ESTs	CUB,MAM,F5_F8_type_C	3.7 3.7
	429731	AKD01592	Hs.212172	beta-carotene 15,15'-dioxygenase	RPE65;SS	3.7
	426433	L38969	Hs.169875	thrombospondin 3	TSPN.tsp_3.EGF,toxin;TM	3.7
	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	pkinase	3.7
20	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardia	myosin_head,IQ,Myosin_tai	3.7
	447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	Ammonium_transp.FecCD;TM=	3.7
	430281	AI878842	Hs.237924	CGI-69 protein	mito_carr,homeobox;TM;S	3.7
	448360	AL117560	Hs.306352	Homo sapiens mRNA; cDNA DKFZp566P23		3.7
~-	446057	A1420227	Hs.366053	Trp-p8 transient receptor potential		3.7
25	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM;SS	3.7
	406854	AA613705	Hs.252259	ribosomal protein S3	KH-domain,Ribosomal_S3_C;	3.7
	422532	AL008726	Hs.118126	protective protein for beta-galacto	serine_carbpept.GalP_UDP_	3.7
	428171	AA489323	Hs.182825	ribosomal protein L35	Ribosomal_L29;	3.6
20	442285	W28729	Hs.356072	uncharacterized hypothalamus protei		3.6
30	411281	BE392792	Hs.4786	Homo sepiens cDNA: FtJ22849 fis, cl	cadherin	3.6
	457657	AW411509	Hs.352567	hypothetical protein PRO2121	UQ_con;TM;	3.6
	414524	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid		3.6
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation;TM□	3.6
35	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	hormone_rec,zf-CCCH;TM;	3.6
22	400785	0000000	11- 224240	C11000861:gi[9938016 ref NP_064687.	TM;SS	3.6
	413343 427380	BE392026	Hs.334346	hypothetical protein MGC13045	TM;	3.6
	427818	NM_005534 AW511222	Hs.177559	Interferon gamma receptor 2 (interf	fn3;TM;SS	3.6
	449957	D31385	Hs.193765	ESTS	*	3.6
40	451529	AI917901	Hs.24220 Hs.208641	hypothetical protein ESTs	TM;	3.6
-10	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	actin	3.6
	431659	AA031875	Hs.266940	1-complex-associated-testis-express	NoI1_Nop2_Sun;TM;	3.6
	433350	BE583152	Hs.10362	Homo sapiens cDNA: FLJ20944 fs, cl	Tctex-1;TM; zI-C3HC4,SPRY	3.6
	412896	AW804157	Hs.375570	major histocompatibility complex, c	ig,MHC_II_beta;TM;\$S	3.6 3.6
45	441748	R14439	Hs.209194	ESTs	WWW.CTITOERT INCOO	3.6
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	KH-domain,Ribosomal_S3_C;	3.5
	457464	AW972234	Hs.126680	ESTs	14 P4411,14044118_05_01	3.5
	429619	AL120751	Hs.211568	eukaryotic translation initiation f		3.5
	423309	8E006775	Hs.126782	sushi-repeat protein	sushi,HYR;SS	3.5
50	438682	AA354489	Hs.375594	EBP50-PDZ interactor of 64 kD	***************************************	3.5
	453022	AA031499	Hs.118489	ESTs	Amino_oxidase	. 3.5
	434042	AI589941	Hs.8254	Homo sepiens, Similar to tumor diff	_	3.5
	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protei	TM;S\$	3.5
E E	417298	AW665839	Hs.37958	ESTs		3.5
55	403943			C5000355:gi 4503225 ref[NP_000765.1		3.5
	429497	AB028953	Hs.204121	KIAA1030 protein	fn3;TM;	• 3.5
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenas	adh_short;TM;\$S	3.5
	428343	AL043021	Hs.12705	ESTs	WD40;SS	3.5
60	456376 400348	AA683904	Hs.89862	TNFRSF1A-associated via death domai	death;TM;	3.5
00	404854	AJ251708	Hs.352588	Target	.00	3.5
	427930	AA417696	Hs.372121	Target Exon	;SS	3.5
	453143	AA382234	Hs.356289	ESTs		3.5
	406806	AW088535	Hs.350108	protein tyrosine phosphatase, recep	serpin;SS	3.5
65	406793	AW264291	Hs.5662	ribosomal protein, large, P0 guanine nucleotide binding protein	TM;	3.5
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ 12284 fis, clo	WD40;TM;	3.5
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	Chara haden AZITIACC	3.5
	404243	74.00.010	1.0.00071	NM_006778:Homo sapiens ring finger	Glyco_hydro_47;TM;SS	3.5
	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain trans	zf-C3HC4,zf-B_box;TM;SS Ets;SS	3.4 3.4
70	432831	AJ821702	Hs.115959	ESTs, Weakly similar to I38022 hypo	26,33	3.4
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clo	TM;	3.4
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death	death, DED: SS	3.4
	408930	AA146721	Hs.334686		CUE;TM;	3.4
	403246	·-·-•		Target Exon	HMG_box;SS	3.4
75	416330	AU077101	Hs.79222	galactosidase, beta 1	Glyco_hydro_35;TM;SS	3.4
	404864			NM_025204":Homo saplens hypothetica		3.4
	441384	AA447849	Hs.288660		7tm_3	3.4
	430284	AI693534	Hs.293196		· • · • · •	3.4
00	433669	AL047879	Hs.194251	ESTs. Wealtly similar to ALU2_HUMAN	RNA_pol_L,RNA_pol_L,RasGA	3.4
80	456050	R79445	Hs.76230	ribosomal protein \$10	S10_plectin;TM;	3.4
	422311	AF073515	Hs.114948		tn3;TM;	3.4
	408909	AW502034	Hs.287379			3.4
	428028	U52112	Hs.182018	interleukin-1 receptor-associated k	death,pkinase;TM;	3.4

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	424242	000000	11- 440405			
	424213 416432	BE390125 BE391767	Hs.143187 Hs.79322	hypothetical protein glutaminyl-IRNA synthetase	DEAD,helicase_C;TM;	3.4
	400233	00001101	15.13522	Eos Control	Discount CO.	3.4
_	403252			Target Exon	Ribosomat_S9; TM;SS	3.4
5	409433	AA074382	Hs.135255	ADAMTS14	11100	3.4
	426053	U68105	Hs.172182	poty(A)-binding protein, cytoptasmi	mm,PABP;TM;	3.4 3.4
	448222	A1648587	Hs.20725	Mov 10 (Moloney leukemia virus 10, m	TM:	3.4
	432982	AA531058	Hs.182248	truncated calcium binding protein	OPR.ZZ:TM:	3.4
10	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	FBPase;TM;	3.4
10	444626	AA320893	Hs.117062	hypothetical protein FLJ14497	Pyt_redox;TM;SS	3.4
	427751 416971	AF000152	Hs.355816	conserved gene amplified in osteosa	NIF;TM;	3.4
	428046	R34657 AW812795	Hs.80658	uncoupling protein 2 (mitochondrial	mito_cam,TM;	3.4
	456575	AW063659	Hs.337534 Hs.191649	ESTs, Moderately similar to 138022 ESTs	ank	3.4
15	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	Myosin_tail	3.4
	414738	L24038	Hs.77183	v-raf murine sarcoma 3611 viral onc	IBR	3.4
	456356	M74715	Hs.89560	iduronidase, alpha-L-	pkinase,DAG_PE-bind,RBD;T Glyco_hydro_39;SS	3.4
	429668	AA626142	Hs.179991	ESTs, Weakly similar to S28942 prot	@Joo_11/0/0_33,33	3.3
20	404913			NM_024408*:Homo sapiens Notch (Dros	EGF, ank notch, metalthio, E	3.3 3.3
20	426059	BE292842	Hs.166120	interferon regulatory factor 7	IRF:SS	3.3
	451619	AA018854	Hs.353196	glutathione peroxidase 3 (plasma)	PH:SS	3.3
	410225	AW508964	Hs.12030	EST ₆		33
	402534	W16440	11 04000	Target Exon	į	3.3
25	433750 421712	H15448 AK000140	Hs.31330	Homo sepiens clone HQ0319	GLFV_dehydrog,GLFV_dehydr	3.3
27	433333	AX000140 AX016521	Hs.107139	hypothetical protein	TM;SS	3.3
	424915	R42755	Hs.71816 Hs.23096	v-akt murine thymoma viral oncogene ESTs	pkinase,PH,pkinase_C	3.3
	408494	AA554714	Hs.187578	Homo sapiens cDNA FL/11639 fts, clo	<del>(m</del>	3.3
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM:SS	3.3
30	446478	AJ950021	Hs.370306	ESTs	TM;	3.3
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM;TM;	3.3 3.3
	<b>456</b> 655	Al376736	Hs.111779	secreted protein, acidic, cysteine-	kazel;SS	3.3
	438912	AF085843		gb:Homo saplens full length insert		3.3
35	428396	U70539	Hs.184161	exostoses (multiple) 1	Exostosin;TM;SS	3.3
33	437546	AW074836	Hs.173984	T-box 1	T-box,WD40;TM;	3.3
	410693 414961	BE044206	41-000	gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H	C1q,Collagen,cystati	3.3
	422766	U27266 AA334108	Hs.927	myosin-binding protein H	fn3,ig;TM;	3.3
	426120	AA325243	Hs.159572 Hs.166887	heparan suffate (glucosamine) 3-O-s copine (		3.3
40	452383	T70900	Hs.27189	ESTs	C2,rm;TM;	3.3
	456799	AC004923	Hs. 135187	unc93 (C.elegans) homolog 8	zf-C2H2,PRK	3.3
	409227	AA806165	Hs.130323	Homo sepiens, clone IMAGE:3950432,	TM; NA;NA	33
	432659	AA281633	Hs.278586	KIAA1108 protein	TBC:TM;	3.3
4.5	448997	AA130390	Hs.25549	hypothetical protein FLJ20898	TM;SS	3.3 3.3
45	446990	AI354717	Hs.223908	ESTs	transmembrane4	3.3
	437259	AI377755	Hs.120695	ESTs	MHC_II_alpha.ig	3.3
	423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_tr;TM;	33
	421563	NM_006433	Hs.105806	granulysin	;SS	3.3
50	453804 428810	AA300204 AF068236	Hs.35276	KIAA0852 protein	TM;	3.3
50	453933	AI452933	Hs.193788	nitric oxide synthase 2A (inducible	NAD_binding,flavodoxin,FA	3.3
	449267	A1638640	Hs.65377 Hs.220624	ESTs ESTs	EF_TS,UBA,transmembr	3.3
	418165	R45959	Hs.6637	ESTs		3.3
	446673	NM_016361	Hs.15871	LPAP for hysophosphatidic acid phos	mito_can	3.3
55	402475			ubiquitin specific protesse 18	acid_phosphat;TM;SS	3.3
	404233			Target Exon	нт	3.2 3.2
	406655	M21533	Hs.277477	major histocompatibility complex, c	ig,MHC_I;TM;SS	3.2
	414556	AW975063	Hs.343443	ribosomal protein L36	Ribosomal_t.36e;	3.2
60	450191	AW137243	Hs.248074	ESTs	homeobox;TM;	3.2
OU	435906	AI686379	Hs.110796	SAR1 protein	art,ras:TM;	3.2
	412540 422562	C18341	Hs.73999	thyroid hormone receptor interactor	SH3,FCH;SS	3.2
	431051	AJ962060 AA491143	Hs.118397	AE-binding protein 1	Zn_carbOpept,F5_F8_type_C	3.2
	407984	AW134708	Hs.283374 Hs.243569	ESTs, Weakly similar to CA15_HUMAN	TM;	3.2
65	441494	AW452344	Hs.129977	ESTs ESTs		3.2
	423114	AU076497	Hs.1614	cholinergic receptor, nicotinic, al	11 1 <b>76</b> -11	3.2
	419833	AA251131	Hs.220697	ESTs	Neur_chan_LBD.Neur_chan_m	3.2
	419036	T80967	Hs.372603	gb:yd23f12.s1 Soares fetal liver sp	WHEP-TRS,IRNA-synt_1b,non	3.2
70	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_pellucida;TM;SS	3.2
70	453094	AA740928	Hs.27356	ESTs	cons_policosa, i m, oo	3.2 3.2
	426989	AI815206	Hs.367644	ESTs	BAG,ubiquitin	3.2
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2	ank;	3.2
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn sub	SH3,HS1_rep;TM;	3.2
75	438930	AW843633	Hs.343261	hypothetical protein AL110115	HLH	3.2
, ,	438183 421310	8E263252	Hs.6101	hypothetical protein MGC3178	thiored;TM;	3.2
	409293	AW630087 R02673	Hs.103315	trinucleotide repeat containing 1	PHD	3.2
	407115	AA084921	Hs.110156 Hs.76230	ESTs	*** ***	3.2
	401174	77707741	13.70230	ribosomal protein \$10 Target Exon	S10_plectin;TM;	3.2
80	400217			Eos Control	transmembrane4,EF_TS,UBA	3.2
	408676	AI815189	Hs.\$7475	sex comb on midleg homotog 1	ras;SS	3.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen in	TM;SS	3.2
	403694			Target Exon	UDPGT	3.2
				•		3.2
				2-	77	

	414265	BE410411	Hs.75864	and advantage to the state of t		
	451118	AI852096	Hs.60640	endoplasmic reticulum glycoprotein ESTs	ECE THUCO	3.2
	422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic	EGF,vwc,TiL;SS	3.2
_	437388	AL359586	Hs.14478	Homo sapiens mRNA; cDNA DKFZp762H18	ER_lumen_recept	3.2
5	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G_	3.2
	430379	AF134149	Hs.240395	polassium channel, subfamily K, mem	ion_trans;TMtSS	3.2 3.2
	434956	BE266566	Hs.4288	hypothetical protein DKFZp434KD46	Cullin; TM:	3.2
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (ca	ethand, S_100, TM;	3.2
10	452493	Al904031	Hs.106826	KIAA1696 protein	PHD, Myc-LZ, DC1, AT_hook; TM	3.2
10	413100 420764	BE065208	U- 10000	gb:RC1-BT0314-310300-015-b09 BT0314		3.2
	421680	BE250676 AL031186	Hs.19928 Hs.289106	hypothetical protein SP329	F-box;TM;	3.2
	406738	AA587983	113.203100	Human DNA sequence from clone CTA-9	Collagen;TM;SS	3.2
	434288	AW189075	Hs.116265	gb:nj30b09.s1 NCI_CGAP_AA1 Homo sap fibrilin3	TIM,Ribosomal_S5;TM;SS=	3.1
15	438264	T88773	Hs.6133	calpain 5	EGF.granulin,TB,EB,TIL;TM	3.1
	436819	AA731746	Hs.120232	ESTs	Carpain_III,Peptidase_C2,	3.1
	459298	R85701		gb:ym86d09.r1 Soares adult brain N2	TM;	3.1 3.1
	452127	BE562126	Hs.28081	eukaryotic translation initiation f	mm.7tm_1,SNF:TM:	3.1
20	422305	AJ928242	Hs.293438	ESTs, Highly similar to AF198488 1		3.1
20	414393	AA146855		gb:zo41h10.r1 Stratagene endothelia		3.1
	423369 429457	BE219099	Hs.279513	ESTs		3.1
	409124	BE243065 AW292809	Hs.202955 Hs.50727	hypothetical protein FLJ20507	Cys-protease-3C;TM;	3.1
	429615	AF258627	Hs.211562	N-acetylglucosaminidase, alpha- (Sa ATP-binding cassette, sub-family A	TMISS	3.1
25	445519	AI635202	Hs.170132	hypothetical protein FLJ22494	ABC_tran;TM;SS	3.1
	410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TM; TFIIS;TM;	31
	407228	M25079	Hs.155376	hemoglobin, beta	globin;TM;	3.1
	411573	AB029000	Hs.70823	KIAA1077 protein	Sulfatase;TM;	3.1 3.1
20	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, c	ig,MHC_I;TM;SS	3.1
30	435072	AW592176	Hs.116932	ESTs	zf-RanBP,MDM2	3.1
	456642 445457	AW451623	Hs.109752	putative c-Myc-responsive	:\$\$	3.1
	448389	AF168793 AW188950	Hs.12743	camitine O-octanoyitransferase	Carn_acythansf;TM;	3.1
	458248	BE407379	Hs.345838 Hs.108082	ESTS	20G-Fell_Oxy,rm,SH3,ras	3.1
35	451310	AW250651	Hs.26213	ESTs, Wealdy similar to T31636 hypo Human DNA sequence from clone RP3-4	C1q,Collagen;TM;SS	3.1
	414688	A1750246	Hs.76901	for protein disutide isomerase-rel	TM;	3.1
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I03	thiored;\$S LIM,Ran_BP1,GRIP,TPR,pro_	3.1
	425067	BE223071	Hs.169142	ESTs	contrast_or tode, rescho_	3.1 3.1
40	410639	BE269047	Hs.65234	hypothetical protein FLJ20596	DEAD.helicase_C,PRK,AIP3;	3.1
40	413011	AW068115	Hs.821	biglycan	LRR LRRNT;SS	3.1
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	Ribosomal_L20,Na_Pi_cotra	3.1
	447164 414907	AF026941 X90725	Hs.17518	vipinin; similar to inflammatory r	MoaA_NifB_PogE:TM:	3.1
	418613	AA744529	Hs.77697	polo (Drosophia)-like kinase	Ribosomal_L37ae,pkinase,P	3.1
45	406734	AI565616	Hs.86575	mitogen-activated protein kinase ki	pkinase,CNH;TM;	3.1
	410188	AL096739	Hs.107260	gb:to16h12.x1 NCI_CGAP_Ut2 Homo sap hypothetical protein DKFZp586H0623	511 B. 4 B	3.1
	437959	AI472068	Hs.375604	KIAA1856 protein	Ricin_6_lectin,Glycos_tra	3.1
	406764	AA429825	Hs.343443	ribosomal protein L36	elF5_elF2B,W2;TM; Ribosomal_L36e;	3.1
50	406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p;	3.1 3.1
50	451080	H41082	Hs.271783	ESTs .	24.46	3.1
	414875	H42679	Hs.77522	major histocompatibility complex, c	ig.MHC_II_alpha;TM;SS	3.1
	416365 400261	U15131	Hs.79265	suppression of tumorigenicity 5	DENN, dDENN, uDENN; TM; SS=	3.1
	412270	AQ005262	Hs.73797	Eos Control	ig.MHC_II_beta:TM:SS	3.1
55	456843	BE301883	Hs.152707	guanine nucleotide binding protein glioblastorna amplified sequence	G-alpha,art;TM;	3.1
	443071	AL080021	Hs.8986	complement component 1, q subcompon	; C4- C-!!	3.1
	426196	BE272095	Hs.167791	reficulocathin 1, EF-hand calcium b	C1q,Cotlagen;SS efhand;SS	3.1
	424010	AL080188	Hs.137558	Homo sapiens mRNA; cDNA DKFZp434A13	cadherin;TM;SS	3.1
60	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside	Hamip_like;TM;	3.1 3.1
60	450761	R75930	Hs.174838	Homo sapiens cDNA FLJ14192 fis, clo		3.1
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3	Y_phosphatase,DSPc;TM;S	3.1
	432396 407904	AW295956	Hs.11900	hypothetical protein FLJ14972	Xink,zf-CCCH,G-patch,non	3.1
	452500	W44735 AW373011	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl		3.1
65	432171	AJ202503	Hs.54558 Hs.343661	hypothetical protein FLJ22222 ESTs. Weakly similar to ALUB_HUMAN		3.1
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha	W040	3.1
	442492	AA528489	Hs.234518	nibosomai prolein L23	lectin_c;TM;SS	3.1
	421210	U80016	Hs. 102598	mucosal vascular addressin cell adh	Ribosomal_L14; TM:SS	3.0
70	439429	AF150288		gb:AF150286 Human mRNA from cd34 st	RA,Band_7,MBQAT	3.0
70	447463	AW378685	Hs.18625	Mitochondrial Acyl-CoA Thioesterase	Acyl-Coa_hydro;TM;	3.0 3.0
	448352	AA337951	Hs.20991	SET domain, bifurcated 1	AhpC-TSA,SET,MBD,TM;SS=	3.0
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)		3.0
	445669 452862	AI570830 AW378065	Hs.174870	EST8	_	3.0
75	430069	AV1370005 AI219293	Hs.8687 Hs.293660	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep.tsp_1,Rep	3.0
	451028	AA021258	Hs.123073	Homo sapiens, clone IMAGE:3535476, ESTs	SPRY,zl-B_box,zl-C3HC4;TM	3.0
	446021	BE389213	Hs.286	ribosomal protein L4	Dhannat 1 4714	3.0
	434652	AF148713	Hs.125830	bladder cancer overexpressed protei	Ribosomal_14;TM;	3.0
00	425829	AL133079	Hs.134126	crystallin, gamma S	WD40,DUF6; crystal;TM;	3.0
80	424909	\$78187	Hs. 153752		Rhodanese;SS	3.0 3.0
	423579	NM_004121	Hs.1675	gamma-glutamyltransferaso-like acti	G_glu_transpept;TM;SS	3.0 3.0
	444652 441283	8E513613	Hs.11538	actin related protein 2/3 complex.	WD40;TM;	3.0
	,~~ 120 <b>3</b>	AA927670	Hs.131704	ESTs	CUB,MAM,F5_F8_type_C	3.0
						-

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	437415	AL137400	Hs.306456	pre-mRNA processing factor 18	Band_41,hormone2,Prp18;TM	3.0
	444542	Al161293	Hs.280380	aminopeptidase	NAD_binding.flavodoxin.FA	3.0
	442426	AJ373062	Hs.332938	hypothetical protein MGC5370	zf-RanBP,MDM2	3.0
_	447910	AL137679	Hs.20000	Homo sepiens mRNA; cDNA DKFZp434D24	Exonuclease; SS	3.0
5	426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	DUF232;SS	3.0
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprote	tsp_1.Reprolysin.Pep_M12B	3.0
	430482	AF131810	Hs.241545	hypothetical protein	TM;SS	3.0
	427661	AA410292	Hs.104761	ESTs	wni	3.0
	451876	T63141		gb:yb99a12.s1 Stratagene lung (9372	SH3	3.0
10	453862	AL137493	Hs.35945	Homo sapiens mRNA; cDNA DKFZp434B12	ig:TM;	3.0
	452965	Al904779	Hs.247525	Human DNA sequence from clone RP11-	C2,PHD,RPH3A_effector,zf-	3.0
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-lik	Zip;TM;SS	3.0
	452600	AI910842	Hs.103381	ESTs	Exo_endo_phos	3.0
10	450775	AA902384	Hs.73853	bone morphogenetic protein 2	TGFb_propeptide,TGF-beta,	3.0
15	417634	W27202	Hs.82327	giutathione synthetase	GSH_synthase;TM;	3.0
	415152	W22644	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clo		3.0
	410093	AW589558	Hs.299883	ESTs, Wealtly similar to KIAA0970 pr		3.0
	412404	AW075995	Hs.86228	TRIAD3 protein		30
20	443466	BE243123	Hs.321045	IKK-related kinase epsilon; inducib	pkinase,RIO1;TM;	3.0
20		_				
	TABLE 29					
	Pkey:			et identifier number		
	CAT numb		e cluster numb			
25	Accession	: Geni	bank accession	n numbers		
23	_					
	Pkey	CAT Number		ALIEN AD AND AND ADDRESS AND A		
	458147	1030220_1		AW848490 AW849062 AW752597 AW752699		
	406855	0_0	AA902829	1114 004000 D0007077 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	**************************************	
30	400233	11259_1			9809 BE385504 BG744451 BI826914 BE440007 B	
50					08 BE392513 AV722219 AW328077 BM424171 BI 995 BE791985 BF967484 BI193635 BG761859 BM	
					880 BG831707 BG324692 BM470427 Bi083889 B	
					5675 BE899041 BE271558 Bi193807 Bi159866 Bi	
35					31082 BG829943 BG829501 BF306557 BE562511 337 BE388168 BM009051 BH192794 BG831002 BG	
55					11684 BG829852 BG765030 BG760419 BG760268	
					0033 BG829626 BM050064 BI193014 BI161360 B	
					178 BG481969 BG474870 BF974048 BF971122 B	
					29471 BG686284 BG337575 BG336551 BF20667	
40					545 BI160968 BG755930 BG706018 BE743865 BI	
••					091 BG546643 BF984863 BI160206 BI226402 BI2	
					360 BF568228 BI818282 8I457127 BG831491 BG	
					9404 AI929068 BE906354 BE408564 BM045000 B	
					2228 BE301975 AW516055 BG480919 BG480626	
45					1536 BE394727 BE257695 BE905344 AI433577 B	
					5767 AI871751 BE744523 BI192663 BG831669 A	
					95410 BE744572 BE392297 BE391448 BE390780	
					0753 BE390131 AA650542 BE744156 BE394125	
					0999 BE515162 BE378753 BE272370 BE907458	
50					3576 BE908826 BE620180 BF037570 BE908312	
					5746 BE561195 BE908825 BE906472 BE906509	
					119 BE395707 BE378298 AW327827 BE394422 6	
					5096 AI681675 BE395674 AA138372 BE279892 A	
					300009 F34063 F29455 AU099691 AI905085 AI90	
55				F29022 BF089981 F31013 F24305		
	438912	4071_1	AF085843	R70623 R70523		
	410693	1054267_1	BE044206	AW797320 BE161676 AW797356 AW797352		
	413100	1490226_1		BE065168 BE065313 BE065208		
60	406738	0_0	AA587983			
60	459298	90831_2		BF802216 R86701 BF802224 R84600 BF3S6151		
	414393	15833_3			38 AW519008 A4432598 AW295856 A1650941 A14	70541 AL550388 AA146856 A1074762
				AA393867 BI052082		
	406734	0_0	A1565516			
65	400261	23110_1			127 Al299772 AW518149 Al144456 AW628070 Al	1629032 AI358810 AI880433 AI440472
03				AI865365 AW014799 AI767973 AW518041 AA90	9398 AW768606	
	439429	452694_1		AV739062 AA835857		
	451876	2328579_1	163141 A	1821021 BF370092 BF370127 BF370060 T62998		
	T400 5 6	MA.				
70	TABLE 2					•
70	Pkey:			orresponding to an Eos probeset		as a second of the Phila
	Ref:				dentifier (GI) numbers. "Dunham, et al." refers to	the publication entitled The UNA
	Channel			nan chromosome 22° Dunham, et al. (1999) Nature	402:489-495.	
	Strand:			rand from which exons were predicted.		
75	Nt_posit	ant inc	arsuez uncieo;	ide positions of predicted exons.		
, ,	D1-~	Pot	C+d	Att accilion		
	Pkey 401599	Ref 3176654	Strand Minus	Nt_position 33285-34084		
	402241	7690131	Minus	125073-125206,130996-131125		
	403364	8571785	Plus	120351-120465		
80	405201	7230116	Plus	36934-37314		
	400785	8131682	Plus	43113-43967		
	403943		Plus	100742-100904,101322-101503		
	404854		Plus	14260-14537		

	404243	5672609	Plus	74695-75123
	403246	7637831	Minus	143547-143654,143741-143900
_	404884	5263010	Phus	94495-94681,95055-95195,97396-97506,9760
	403252	7677983	Plus	102214-102692
5	404913	7341740	Plus	97717-97976
	402534	9801061	Plus	58989-59457
	402475	7547191	Plus	65363-65725
	404233	8218045	Minus	84791-85123
	401174	9438414	Minus	132847-133917
10	403694	7107765	Plus	142925-143080,165505-166186,167486-16763

	Pkev	Accession	HaiCasa IO	Uniqene Title	Protein Domains	Rí
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma	ig:TM;	37.6
	407241	M34516	113.000031	gb:Human ornega light chain protein	TM:	22.7
30	414477	U41635	Hs.76228	amplified in osleosarcoma	pkinase,LRR:TM;SS	22.7
••	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	PKD:TM:SS	15.4
	406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18ae;TM;	14.2
	429707	W76631	Hs.211819	matrix metalloproteinase 238	ig.Peptidase_M10,TM:SS=	12.8
	419092	J05581	Hs.89603	mucin 1, transmembrane	SEA:TM:SS	12.8
35	414738	L24038	Hs.77183	v-raf murine sarcoma 3511 viral onc	pkinase,DAG_PE-bind,RBD;T	12.4
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, d	7tm_3,none	11.6
	406621	X57809	Hs.181125	immunoglobulin tambda locus	ig,HSP70,Ppx-GppA;TM;SS	11.0
	410584	AB011112	Hs.64742	KIAA0540 protein	none	11.0
	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	pkinase.none	10.7
40	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b an	ig;TM;SS	10.7
	430379	AF134149	Hs.240395	potassium channel, subfamily K, mem	ion_trans;TM;SS	10.3
	408972	AL050100	Hs.49378	DKFZP586D0919 protein	TM:	9.9
	446921	AB012113	Hs.16530	small inducible cytokine subfamily	1L8:SS	9.9
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep,tsp_1,Rep	9.7
45	418101	AL047476	Hs.296310	gap junction protein, alpha 4, 37kD	connexin:TM:SS	8.5
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	Cys_knot	8.4
	401699			Target Exon	TM:	8.1
	423309	BE006775	Hs.126782	sushi-repeat protein	sushi,HYR:SS	8.1
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) act	PA28_alpha,PA28_beta;	7.9
50	436906	H95990	Hs.181244	major histocompatibility complex, c	ig,MHC_I;TMtSS	7.8
•	425335	BE394327	Hs.296267	follistatin-like 1	efhand,kazal,arf,ras,7tm_	7.7
	413011	AW068115	Hs.821	biglycan	LRR.LRRNT:SS	7.7
	446295	Al355029	Hs.101660	ESTs, Wealdy similar to 714171 atax	UM	7.7
	436398	H87136	Hs.5174	ribosomal protein S17	Ribosomal_S17e,PolyA_pol;	7.6
55	435013	H91923	Hs.110024	NM_020142:Homo sepiens NAOH:ublquin	none	7.4
	431809	A1623488	Hs.333488	Homo sapiens, clone IMAGE:3603998,	TM;SS	7.4
	424608	X80695	Hs.151134	oxidase (cytochrome c) assembly 1-1	60KD_IMP;TM;	7.3
	438560	AA481690	Hs.300697	immunoglobulin heavy constant gamma	ig	7.3
	429297	X82494	Hs.198862	fibutin 2	EGF,ANATO,TIL,spidertoxin	7.3
60	450463	AW952018	Hs.201398	G protein coupled receptor interact	C1q,Collagen;TM;SS	7.2
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	TM;	7.2
	414688	A)750246	Hs.76901	for protein disulfide isomerase-rel	thiored;SS	7.2
	414044	BE614194	Hs.75721	profilin 1	profilin;TM;	7.1
~ ~	404864			NM_025204*:Homo sapiens hypothetica	;	7.1
65	452127	BE562126	Hs.28081	eukaryotic translation initiation f	rm,7tm_1,SNF;TM;	7.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	;SS	7.0
	409826	AW\$01112	Hs.353013		none	6.9
	434343	AW956705	Hs.3804	DKFZP564C1940 protein	ktl_recept_a;TM;	6.9
70	427714	AF119850	Hs.2186	eukaryotic translation elongation f	COX8,SHMT,MIF,GST_C,EF1G_	6.9
70	437259	A1377755	Hs.120695		MHC_II_alpha.ig,none	6.9
	429212	NM_001504	Hs.198252		7tm_1;TM;	6.8
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A re	Neur_chan_LBO,Neur_chan_m	6.8
	423505	AF064090	Hs.129708		TNF;TM;SS	6.8
75	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA139	TM;	6.7
75	430542	AI557486	Hs.119122		Ribosomal_L13,LACT,arf,ra	6.7
•	435906	A1686379	Hs.110796		arl,ras;TM;	6.6
	429307	AU076592	Hs.198951		bZIP;TM;	6.4
	437388	AL359586	Hs.14478	Homo sapiens mRNA; cDNA DKFZp762H18	none	6.4
80	415714	NM_002290		laminin, alpha 4	laminin_EGF,taminin_G,Tro	6.3
ou	406733	AA976565	Hs.297753		filament bZIP Apolipoprot	6.3
	411295	BE207307	Hs.10114	growth suppressor 1	20G-Fell_Oxy;TM:SS	6.3
	441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	6.3
	444637	T19101	Hs.11494	fibulin 5	EGF,TIL;\$\$	6.3

	44.0704	DC242046				
	413731 422901	BE243845 R81936	Hs.75511	connective tissue growth factor	Cys_knot.tsp_1.vwc,tGF8P;	6.2
	430397	AI924533	Hs.374568 Hs.105607	ribosomal protein L44 bicarbonale transporter related pro	sushi,none	6.2
	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (per	HCO3_cotransp;TM; EGF.ig.taminin_B.taminin	6.1
5	434867	AF159442	Hs.103382	phospholipid scramblase 3	SAPA,Scramblase;TM;SS	6.1 6.1
	431449	M55994	Hs.256278	tumor necrosis factor receptor supe	TNFR_c6;TM;SS	6.1
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like	LIM:SS	6.0
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein	GNT-I,Glycos_transf_2;TM=	5.9
10	439310	AF086120	Hs.102793	ESTs	casein_kappa,pkinase,iq,n	5.9
10	410169	AI373741	Hs.59384	hypothetical protein MGC3047	ig;TM;	5.8
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot	TIMP,none	5.8
	414265 427715	BE410411 BE245274	Hs.75864 Hs.180428	endoplasmic reticulum glycoprotein	none	5.8
	409220	BE243323	Hs.51233	KIAA11B1 protein	TM;	5.8
15	450690	AA296696	Hs.333418	tumor necrosis factor receptor supe FXYO domain-containing Ion transpor	TNFR_c6,death,tipoprotein	5.8
	433848	AF095719	Hs.93764	carboxypepidase A4	ATP1G1_PLM_MAT8;TM;SS Zn_carbOpept,Propep_M14;T	5.8
	446404	AAD19961	Hs.26216	LOC50627	none	5.7 5.7
	441641	AI650417	Hs.247068	ESTs. Moderately similar to ALU8_HU	Pterin_4a,fibrinogen_C,Co	5.7
20	418875	W19971	Hs.233459	ESTs	XIInk,none	5.7
20	424748	AA346257	Hs.134933	ESTs	none	5.7
	439737	AJ751438	Hs.41271	Homo sapiens collagen, type VIII, a	C1q,Coffagen,none	5.7
	448950	AF288687	Hs.9275	CGI-152 protein	E1-E2_ATPase, Hydrolase; TM	5.6
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, c	Ig.MHC_I;TM;SS	5.6
25	423084 402241	AU076474	Hs.123178	translocase of inner mitochondrial	m	5.6
	425157	NM_006227	Hs.283007	Target Exon phospholipid transfer protein	p450;TM;SS	5.6
	428343	AL043021	Hs.12705	ESTs	LBP_BPI_CETP,LBP_BPI_CETP	5.6
	447990	BE048821	Hs.20144	small inducible cytokine subfamily	WD40;SS IL8;SS	5.6
	412607	Z33642	Hs.74115	immunoglobulin superfamily, member	ig:TM;SS	5.6 5.5
30	447625	AW505364	Hs.19074	LATS (targe turnor suppressor, Droso	pkinase,pkinase_C,UBA,Pol	5.5
	408056	AA312329	Hs.42331	ephrin-A4	Ephrin:TM;SS	5.5
	445960	AI268399	Hs.140489	ESTs, Weakly similar to UN1_HUMAN	zf-C2H2,bZIP,none	5.5
	406874	AW161706	Hs.180842	ribosomal protein L13	Ribosomal_L13e;SS	5.4
35	418558	AW082266	Hs.86131	Fas (TNFRSF6) associated via death	death,DED;SS	5.4
33	414638	W03516	Hs.76698	stress-associated endoplasmic retic	TM;SS	5.4
	409190 429150	AU076536 AF120103	Hs.50984	sarcoma amplified sequence	transmembrane4;TM;SS	5.4
	453099	H62087	Hs.197366 Hs.31659	smoothened (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G_	5.3
	414443	AU077268	Hs.76144	thyroid hormone receptor-associated platelet-derived growth factor rece	WD40;TM;	5.3
40	441283	AA927670	Hs.131704	EST ₈	ig.pkinase;TM; CUB,MAM,F5_F8_type_C,none	5.3 5.3
-	414249	AI797994	Hs.279929	gp25L2 protein	Sulfotrensfer, EMP24_GP25L	5.3
	451154	AA015879	Hs.33536	ESTs	TIMP,none	5.2
	406655	M21533	Hs.277477	major histocompatibility complex, c	ig.MHC_I;TM;SS	5.2
45	406656	M16714	Hs.89643	major histocompatibility complex, c	transketolase.transket_py	5.2
45	449224	AW995911	Hs.299883	hypothetical protein FLJ23399	m3;TM;	5.2
	422562	AI962060	Hs.118397	AE-binding protein 1	Zn_carbOpept_F5_F8_type_C	5.2
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	TM;SS	5.2
	428327 427080	AW206236	Hs.28773	ESTs	cystatin,Coprogen_oxidas,	5.2
50	414624	AW068287 BE389320	Hs.301175 Hs.23628	ras-related C3 botulinum toxin subs	ras;TM;	5.2
50	430281	AI878842	Hs.237924	3 beta-hydroxy-delta 5-C27-staroid CGI-69 protein	none	5.2
	426433	L38969	Hs.169875	thrombospondin 3	mito_carr,homeobox;TM;\$	5.2
	432716	A1762954	Hs.205180	ESTs	TSPN,tsp_3,EGF,toxin;TM LRR.UPAR_LY6;TM;	5.1
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation;TM=	5.1 5.1
55	409340	BE174629	Hs.321130	hypothetical protein MGC2771	aa_permeases,pyridoxal_de	5.1
	432680	T47384	Hs.278613	interleron, alpha-inducible protein	TM:SS	5.1
	404913			NM_024408*:Homo sapiens Notch (Dros	EGF, ank, notch, metalthio, E	5.1
	409485	680990	Hs.252136	ficolin (collagen/fibrinogen domain	Collagen,fibrinogen_C;TM=	5.1
60	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM:SS	5.1
00	406687 423712	M31126 W46802	Hs.352054	matrix metalloproteinase 11 (strome	hemopexin,Peptidase_M10;T	5.1
	441595	AW206035	Hs.81988 Hs.356457	disabled (Orosophila) homolog 2 (mi	PID,MACPF,ld1_recept_a,ts	5.0
	450435	AI695975	Hs.201805	ESTs ESTs	sugar_tr,none	5.0
	443177	BE268461	Hs.202	benzodiazapine receptor (peripheral	EGF laminin_B laminin_EGF	5.0
65	433435	BE545277	Hs.340959	Ts translation elongation factor, m	TspO_MBR;TM;SS	5.0
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei	EF_TS,UBA;	5.0 5.0
	419913	AW270040	Hs.34455	ESTs	EPH_lbd,fn3,pkinase,	5.0
	446696	AF279265	Hs.298476	solute carrier family 26, member 6	Sulfate_transp,STAS,xan_u	5.0
70	448997	AA130390	Hs.25549	hypothetical protein FLJ20898	TM:SS	5.0
70	413891	8E271020	Hs.355753	tumor suppressor deleted in oral ca	none	5.0
	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep	serpin;SS	5.0
	448249	AW855331	Hs.337124	ESTs	carb_anhydrase,UCH-1,UCH-	5.0
	412819	T25829	Hs.24048	FK506 binding protein precursor	FKBP;TM;SS	5.0
75	426059 432295	BE292842	Hs.166120	interferon regulatory factor 7	IRF;SS	5.0
	432295	BE091049 C18341	Hs.343665	ribosomal protein S15a	Ribosomaf_S8,RNase_PHLKH-	5.0
	414465	AW270645	Hs.73999 Hs.76194	thyroid hormone receptor interactor ribosomal protein S5	SH3,FCH:SS	5.0
	456655	AL376736	Hs.111779	secreted protein, ecidic, cysteine-	Ribosomal_S7;	5.0
	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1	kazal;SS E2E_TDP_KOW_Pibetom2l_L14	50
80	444824	AA843575	Hs.12056	asialoglycoprotein receptor 1	E2F_TDP,KOW,Ribosomal_L14 tectin_c,Tropomyosin;TM	4.9 4.9
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 simil	TFIIS,RNA_POL_M_15KD,UPF0	4.9
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	THESS	4.9
	429457	BE243065	Hs.202955	hypothetical protein FLJ20507	Cys-protease-3C;TM;	4.9



	449475	A1348027	Hs.108557	hypothetical protein PP1057	transmembrane4;TM;SS	4.9
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM;TM;	4.9
	442110 415209	AF113008 F00183	Hs.8102	ribosomal protein S20	Ribosomal_S10;TM;	4.9
5	451849	Al199261	Hs.172004 Hs.27191	itin	none	4.9
-	421567	AJ272137	Hs.198265	hypothetical protein from clone 247 matrix metalloproteinase 25	TM;	4.9
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interf	hemopexin,Peptidase_M10,T fn3;TM;SS	4.9 4.9
	431303	AW241605	Hs.253928	ESTs	none	4.9
• •	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	Xlink,zf-CCCH,G-patch,non	4.9
10	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994,	none	4.8
	430498	X02910	Hs.241570	tumor necrosis factor (TNF superfam	TNF;TM;SS	4.8
	449957	D31365	Hs.24220	hypothetical protein	TM:	4.8
	419603	BE262579	Hs.91566	PL6 protein	OMPdecase;TM;SS	4.8
15	427588	L25081	Hs.179735	ras homolog gene family, member C	ras,none	4.8
13	421502 404854	AF111856	Hs.105039	solute carrier family 34 (sodium ph	Ribosomal_L20,Na_Pi_cotra	4.8
	411281	BE392792	Hs.4786	Target Exon Homo sapiens cDNA: FLJ22849 fis, cl	;\$\$ 	4.7
	414045	NM_002951	Hs.75722	ribophorin II	catherin	4.7 4.7
	431830	Y16645	Hs.271387	small inducible cytokine subfamily	gpdh.gpdh_C.plii_assembly IL8;SS	4.7
20	412896	AW804157	Hs.375570	major histocompatibility complex, c	ig,MHC_II_beta;TM;SS	4.7
	429305	AF095727	Hs.287832	myelin protein zero-like 1	ig.transmembrane4;TM;SS	4.7
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	4.7
	422687	AW068823	Hs.119206	insufin-like growth factor binding	zf-C2H2,ig,none	4.7
25	444542	AI161293	Hs.280380	aminopeptidase	NAD_binding.flavodoxin,FA	4.7
LJ	429833 456376	NM_012079 AA663904	Hs.288627	diacylglycerol O-acyltransferase (m	ACAT;TM;	4.7
	438568	R98865	Hs.89862 Hs.11135	TNFRSF1A-associated via death domai	death;TM;	4.7
	456356	M74715	Hs.89560	major histocompatibility complex, c iduronidase, alpha-L-	MHC_II_alpha,ig,none	4.7
	420486	AF036365	Hs.98303	caveolin 3	Glyco_hydro_39;SS Caveofin;TM;	4.7
30	425123	AW205274	Hs.154695	phosphomannomutase 2	PMM:SS	· 4.6 4.6
	439512	AA418287	Hs.58093	Homo sapiens, clone IMAGE:3163559.	laminin_EGF;TM;	4.6
	418424	Y13622	Hs.85087	latent transforming growth factor b	EGF,TB,spidertoxin,granut	4.6
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, cl	zf-C3HC4,SPRY,none	4.6
35	432659	AA281633	Hs.278586	KIAA1108 protein	TBC:TM:	4.6
33	445417	AK001058	Hs.12680	a disintegrin-like and metalloprote	tsp_1,Reprolysin,Pep_M12B	4.6
	437408 427349	AL359598 AA360154	Hs.36606	Homo sapiens mRNA; cDNA DKFZp547B08	none	4.6
	418918	X07871	Hs.177415 Hs.89476	Finkel-Biskis-Reitly murine sarcoma	ubiquitin;TM;	4.6
	421310	AW630087	Hs.103315	CD2 antigen (p50), sheep red blood trinucleotide repeat containing 1	ig;TM;SS	4.6
40	427969	NM_001963	Hs.2230	epidermal growth factor (beta-uroga	PHD EGF.ldl_recept_b,EB;TM;	4.6
	447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	Ammonium_transp_FecCD;TM=	4.6 4.6
	418916	BE392781	Hs.89474	ADP-ribosylation factor 6	arl,ras;TM;	4.6
	425720	AA362394	Hs.293984	hypothetical protein MGC13102	TM;SS	4.6
46	419942	U25138	Hs.93841	potassium large conductance calcium	CaKB:TM:SS	4.6
45	403105			Target Exon	ISK_Channel;TM;SS	4.6
	418067	AI127958	Hs.83393	cystatin E/M	cystatin;SS	4.6
	427863	AF189712	Hs.181002		GTP_CDC;TM;	4.5
	458147 456799	AW752597 AC004923	Hs.135187	gb:IL3-CT0214-161299-045-B06 CT0214	PMM,none	4.5
50	427136	AL117415	Hs.173716	unc93 (C.elegans) homolog B a disintegrin and metalloproteinase	TM;	4.5
-	458766	AW183618	Hs.55610	solute carrier family 30 (zinc tran	ig Cotton offenstrace	4.5
	445033	AV652402	Hs.72901	cyclin-dependent kinese inhibitor 2	Cation_efflux;TM;SS ank:	4.5
	441281	BE501247	Hs. 144084	ESTs	Collagen, C4, none	4.5 4.5
	439720	AJ935202	Hs.31181	Homo saplens cDNA: FLJ23230 fis, cl	SDF,sugar_tr	4.5
55	410184	AW503667	Hs.59545	ring finger protein 15	SPRY,zf-B_box,zf-C3HC4;TM	4.5
	431760	NM_005317	Hs.268531	granzyme M (lymphocyte met-ase 1)	trypsin;TM;SS	4.5
	446990	AI354717	Hs.223908	ESTs	transmembrane4	4.5
	407366 426158	AF026942 BE244537	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	IBR	4.5
60	442941	AU076728	Hs.167382 Hs.8867	natriuretic peptide receptor A/guan	ANF_receptor.guanylate_cy	4.5
~ ~	451118	AI862096	Hs.60640	cysteine-rich, angiogenic inducer, ESTs	Cys_knot,tsp_1,vwc,tGFBP;	4.5
	457657	AW411509	Hs.352567	hypothetical protein PRO2121	EGF,vwc,Til;SS UQ_con;TM;	4.5
	437016	AU076916	Hs.5398	guanine monphosphate synthetase	PHD.SET.zf-CXXC,EGF,anton	4.4 4.4
	429497	AB028953	Hs.204121	KIAA1030 protein	fn3:TM:	4.4
65	444090	S69115	Hs.10306	natural killer cell group 7 sequenc	PMP22_Claudin;TM;SS	4.4
	454005	AF039237	Hs.288600	hypothetical protein MGC3123	TM;SS	4.4
	412270	AC005262	Hs.73797	guanine nucleatide binding protein	G-elpha,arf;TM;	4.4
	406729	AA069711		gb:zm52b11.a1 Stratagene fibroblast	filament,bZIP,Apolipoprot	4.4
70	404610	AF077516	44 4848	Homo sapiens cDNA FLJ11027 fis, clo	EGF,laminin_B,laminin_EGF	4.4
, 0	422311 406973	AF073515 M34996	Hs.114948	cytokina receptor-like factor 1	m3;TM;	4.4
	407196	D11747	Hs.198253 Hs.177415	major histocompatibility comptex, c Finkel-Biskis-Reilly murine sercoma	ig.MHC_II_alpha;TM;SS	4.4
	404243		110.777410	NM_006778:Homo sapiens ring finger	ERG4_ERG24,none	4.4
	443834	AI741510	Hs.173548	ESTs	zf-C3HC4,zf-B_box;TM;SS CLIR MAM ES ER Nove C cook	4.4
75	446057	AI420227	Hs.366053	Trp-p8 transient receptor potential	CUB,MAM,F5_F8_type_C,none none	4.4 4.4
	413661	AA071146	Hs.343354	ribosomal protein L18	Ribosomal_L18e,L15;TM;S	4.4
	414875	H42679	Hs.77522	major histocompatibility complex, c	ig.MHC_II_alpha;TM;SS	4.4
	439730	AF035292	Hs.6654	KIAA0657 protein	fn3.ig:	4.3
80	406257			Target Exon	7tm_1,none	4.3
ov	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mR	ig:TM;	4.3
	414961 430265	U27265	Hs.927 Hs.237358	myosin-binding protein H	fn3,ig:TM;	4.3
	429249	L36033 X81479	Hs.237330	stromal cell-derived factor 1 egf-like modute containing, mucin-l	ILB;SS	4.3
		W1413	, 4.2313	on the second containing, macini	7tm_2,EGF,GPS,S_locus_gly	4.3
				25	-	

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	433541	AW081538	Hs.220324	hypothetical protein FLJ13052	NAD_kinase;TM;	4.3			
	400575			NM_022146:Homo sapiens neuropeptide	7tm_1;TM;SS	4.3			
	427661	AA410292	Hs.104761	ESTs .	wntnone	4.3			
_	452056	AW955065	Hs.101150	Horno sapiens, clone IMAGE:4054156,	TM:	4.3			
5	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN	RNA_pol_L,RNA_pol_L,RasGA	4.3			
	422624	BE615578	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoptasmic	ER_turnen_recept.none	4.3			
	421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen; TM; SS	4.3			
	422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-O-s	none	4.3			
• •	437596	AA761490	Hs.351250	ESTs, Moderately similar to \$65657	pkinase.WD40	4.3			
10	419285	D31887	Hs.89868	KIAA0062 protein	Zip;TM;SS	4.3			
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans;TM;SS	4.2			
	410693	BE044206		gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H	C1g Collagen cystati	4.2			
	413100	BE065208		gb:RC1-BT0314-310300-015-609 BT0314	none	4.2			
	432497	AA551104		ESTs, Moderately similar to ALUC_HU	none	4.2			
15	423041	BE170842	Hs.123059	chloride channel Kb	CBS,voltage_CLC;TM;SS	4.2			
	449799	AI143466	Hs.125060	ESTs	none	4.2			
	438472	AW974907	Hs.85228	TRIAD3 protein	none	4.2			
	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3.pkinase,SAM;T	4.2			
	424488	AK000413	Hs.149227	hypothetical protein FLJ20406	XIInk_xi-CCCH,G-patch;TM=	4.2			
20	406809	AF000574	Hs.22405	leukocyte immunogłobulin-like recep	ig,Gemini_mov;TM;SS	4.2			
	407588	Z37544	Hs.37121	phospholipase C, beta 3 (phosphatid	C2.PI-PLC-Y,PI-PLC-X;TM				
	407228	M25079	Hs.155376	hemoglobin, beta	globin;TM;	4.2 4.2			
	450900	H61005	Hs.37902	ESTs	none	4.2 4.2			
	410188	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	Ricin_B_lectin,Glycos_tra	4.2			
25	458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	C1g,Collagen;TM;SS				
	403138			NM_006056:Homo sapiens G protein-co	7tm_1,HECT;TM;SS	4.2 4.2			
	432074	AA525248	Hs.149723	ESTs	Y_phosphatase_none	4.2			
	438682	AA354489	Hs.375594	EBP50-POZ interactor of 64 kD	none	4.2			
	401908			C17000154:gi[12003980]gb]AAG43830.1	TM;SS				
30	451287	AK002158	Hs.26194	likely homolog of mouse immunity-as	TM;	· 4.2 4.2			
	407904	W44735	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl	none				
	403694			Target Exon	UDPGT-	4.1			
	423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph		4,1			
	425603	U52219	Hs.158329	G protein-coupled receptor 50	sugar_tr;TM; 7tm_1;TM;SS	4.1			
35	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	TM;SS	4.1			
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	transmembrane4;TM;SS	4.1			
	423313	NM_014269	Hs.126838	a disintegrin and metafloproteinase		4.1			
	432171	AI202503	Hs.343661	ESTs, Weakly similar to ALUB_HUMAN	disintegrin,Reprolysin,Pe WD40	4.1			
	434652	AF148713	Hs.125830	bladder cancer overexpressed protei	WD40,DUF6;	4.1			
40	429592	AB029041	Hs.209646	KIAA1118 protein		4.1 4.1			
	432982	AA531058	Hs.182248	truncated calcium binding protein	Tropanin,Exo_endo_phas,IQ OPR.ZZ;TM;	***			
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protei	TM;SS	4.1			
	441455	AJ271671	Hs.7854	zinchron regulated transporter-lik	Zip:TM;SS	4.1			
	400785			C11000861:gij9938016/refNP_084687.	TM:SS	4.1			
45	447232	AW499834	Hs.327	interleukin 10 receptor, alpha		4.1			
	450785	AA852713	Hs.108885	Homo sapiens, alpha-1 (VI) collagen	TM;SS	4.1			
	424027	AW337575	Hs.201591	ESTs	vwa,Collagen;TM;SS	4.1			
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	7tm_2,HRM,none EGF,DSL,EB;TM;SS	4.1			
	437118	AB037857	Hs.300591	CO9 partner 1		4.1			
50	411410	R20693	Hs.69954	taminin, gamma 3	none laminin_B,laminin_EGF,lam	4.1			
	413902	AU076743	Hs.75613	CO36 antigen (collagen type i recep		4.1			
	428938	AC002425	Hs.194660	ceroid-lipofuscinosis, neuronal 3,	E2F_TDP,CD36;\$\$ CLN3;TM;\$\$	4.1			
	453094	AA740928	Hs.27356	ESTs	none	4.1			
	440811	BE384713	Hs.74655	ESTs, Wealdy similar to T34482 hypo		4.1			
55	407287	AI578812	Hs.345139	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sa	hormone_rec,zf-C4,none	4.0			
	428028	U52112	Hs.182018	Interleukin-1 receptor-associated k	ras,cadherin	4.0			
	428469	BE549205	Hs.184488	flotilin 2	death.pkinase;TM;	4.0			
	423114	AU076497	Hs.1614	cholinergic receptor, nicotinic, at	None Chan I BD Mour chan an	4.0			
	426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	Neur_chan_LBD,Neur_chan_m	4.0			
60	444626	AA320893	Hs.117062	hypothetical protein FLJ14497	DUF232SS	4.0			
			***********	nyperioses protosi i co imor	pyr_redox;TM;SS	4.0			
	TABLE 30	<b>08</b> :							
	Pkey:		ue Fos orobes	et identifier number					
	CAT num		cluster numb						
65	Accession		ank accessio						
	Pkey	CAT Number	Accession						
	458147	1030220_1		AW848490 AW849062 AW752597 AW752699					
	406729	0_0	AA069711	**************************************					
70	410693	1054267_1		AW797320 BE161676 AW797356 AW797352					
	413100	1490226_1		BE065168 BE065313 BE065208					
	432497	852_71		R94134 AA551104 AA777322 Al033094 BE247143					
		, .							
	TABLE 30	C:							
75	Pkey:		in olimber co	rresponding to an Eos probeset					
	Ref:	Som	ence source	The 7 digit numbers in this setums on Carteria to	relifier (CI) combon - C - A				
		Sour	ence of huma	The 7 digit numbers in this column are Genbank Ide n chromosome 22" Dunham, et al. (1999) Nature 40	rruner (GJ) nurrioers, "Dunham, et al." refer 3:490-405	s to the protication entitled "The DNA			
	Strand:	info	ortes DAN etra	n chromosome 22. Donnam, et al. (1999) <u>Nature</u> 40 nd from which exons were predicted.	2:903-430.				
	Nt_positio								
80	Nt_position: Indicates nucleotide positions of predicted exons.								
	Pkey	Ref	Strand	Nt_position		•			
	401699	3176654	Minus	33285-34084					
	404864	5263010	Plus	94495-94661,95055-95195,97396-97508,9760					
				2 2 122222 23.40,0103031300,3100					

	402241	7690131	Minus	125073-125206,130996-131125
	404913	7341740	Ptus	97717-97976
	404854	7143420	Plus	14260-14537
_	403105	8980016	Minus	145287-145744
5	404510	9588566	Minus	89583-89725.90402-90555.91428-91673
	404243	5672609	Plus	74695-75123
	406257	7417784	Plus	55821-56037
	400575	9886575	Ptus	131603-132095
	403138	9211494	Minus	164684-165066,167757-168651
10	401908	8698760	Minus	126888-127024
	403694.	7107765	Plus	142925-143080,165505-166186,167486-16763
	400785	8131682	Plus	43113-43967

TABLE 31A: ABOUT 189 GENES DOWN-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE
Table 31A lists about 189 genes down-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 30A, except that the numerator was set to
the 90th percentile amongst various non-malignant brain specimens, the denominator was set to the 90th percentile value amongst various gliomas, the numerator was greater than
or equal to 50 units, and the ratio was greater than or equal to 2.5 (i.e. 2½-fold downregulation in brain tumor vs. normal brain).

Privey:

ExAcon:

LingenelD:

LingenelD:

Lingene Tita:

Protein Domains:

Rt:

Rt: 15

20

25	NI.		_	oram ussue vs. guoma		
	Pkey	ExAcch	UniGene ID		Protein Domains	R1
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	F420_oxidored;TM;SS	14.5
	432874	W94322	Hs.279651	melanoma inhibitory activity	SH3;TM;SS_	8.3
30	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	SCP,LCCL;TM;SS	8.2
30	426300	U15979	Hs.169228	della-like homotog (Drosophila)	EGF, tarninin_EGF; TM; SS	8.2
	447990	BE048821	Hs.20144	small inducible cytokine subfamily	IL8;SS	7.3
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HU	GONF, TPR	7.1
	411602	L01406	Hs.767	growth hormone releasing hormone re	7tm_2.HRM:TM:SS	6.1
35	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneur	sugar_tr;TM;SS	6.0
33	426488	X03350	Hs.4	alcohol dehydrogenase 18 (class I),	adh_zinc;TM;	5.9
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotei	SH3,PH;TM;	5.3
	436950 406837	L05779	Hs.113	epoxide hydrotase 2, cytoplasmic	abhydrolase,Hydrolase;TM=	5.2
	410387	R70292	Hs.156110			4.9
40	432855	AI277367	Hs.47094	ESTs	C- 1/20 711 00	4.8
70	432033	AF017988	Hs.279565	secreted frizzled-related protein 5	Fz,NTR:TM:SS	4.7
	421481	AW298235 AW391972	Hs.101689	ESTs	T11.00	4.6
	420255	NM_007289	Hs.104696 Hs.1298	KIAA1324 protein	TM;SS	4.5
	420233	AA157857	Hs.182265	membrane metallo-endopeptidase (neu keratin 19	Peptidase_M13:TM;SS	4.5
45	412445	X51362	Hs.73893		filament,bZIP;\$S	4.4
75	413966	AA133935	Hs.173704	dopamine receptor D2	7tm_1;TM;SS	4.3
	415165	AW887604	Hs.78065		AM	4.2
	420103	AA382259	Hs.95197	complement component 7 aldehyde dehydrogenase 1 family, me	kdl_recept_a.sushi.tsp_1,	4.2
	426723	AW003069	Hs.183860	ESTs	aldedh;TM;	4.2
50	409081	AJ010277	Hs.50403	T-box 19	GNT-1;TM;SS	4.1
50	407142	AA412535	HS.30403	gb:zt99b10.s1 Soares_testis_NHT Horn	T-box;TM;	4.0
	414449	AA557660	Hs.76152	decorin	Na_sutph_symp;TM;	4.0
	444784	012485	Hs.11951	ectonucleotide pyrophosphatase/phos	LRRNT,LRR,LRR,LRRNT	4.0
	420321	D78761	Hs.96657	hyothetical protein	Somatomedin_B,Endonucleas	3.9
55	401700	0.0.01	113.30037	Target Exon	tsp_1;SS TM:	3.8 3.8
	418807	NM_004944	Hs.88646	deoxyribonuclease Hike 3	Exo_endo_phos;TM;SS	3.8
	406746	AA580395	Hs.279860		TCTP:TM:	3.7
	449077	AW262836	Hs.252844	ESTs	1011,1m,	3.7
	415718	F30631	Hs.200237	ESTs	isoamytase_N	3.7
60	402449			Target Exon	pkinase,LRR,LRRCT;TM;SS	3.6
	457489	AI693815	Hs.127179		TM:SS	3.6
	406743	AA911568	Hs.279860		TCTP:TM:	3.6
	416950	AL049798	Hs.80552	dermatopontin	, o., , i.m.	3.6
	451554	AJ474866	Hs.193237			3.6
65	440708	AF038962	Hs.7381	voltage-dependent anion channel 3	Euk_parin,Enterotoxin_AP	3.5
	426095	AJ278023	Hs.89986	ESTs	WD40.none	3.5
	406742	AJ458091	Hs.279860	turnor protein, translationally-cont	TCTP:TM:	3.5
	429343	AK000785	Hs.199480		VHS,ENTH,UIM;SS	3.4
	439457	AF086274		gb:Horno sapiens full length insert	,,,	3.4
70	408796	AA588292	Hs.170345		hormone_rec.zt-C4	3.4
	440659	AF134160	Hs.7327	claudin 1	PMP22_Claudin;TM;SS	3.4
	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	UDPGP:SS	3.4
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group	hormone_rec,zf-C4,none	3.3
	445234	AW137636	Hs.146059	ESTs	14-3-3.none	3.3
75	430511	BE018156	Hs.2575	calpain 1, (mu/l) large subunit	efhand, Peptidase_C2, Calpa	3.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effec	7tm_1.CIDE-N;TM;SS	3.3
	413687	AI522318	Hs.103819	ESTs	TM;SS	3.3
	428928	8E409838	Hs.194657	cadherin 1, type 1, E-cadherin (epi	cadherin,Cadherin_C_term,	3.3
00	409738	BE222975	Hs.56205	insulin induced gene 1		3.3
80	442046	AA974575	Hs.287385		zl-C2H2,SET;TM;	3.2
	413127	BE066529		gb:RC3-BT0333-300300-017-a12 BT0333		3.2
	429350	A1754634	Hs.131987	ESTs	MANETINE	3.2
	427980	AA418305	Hs.303205	EST	LRR none	3.2
					- · · ·	

	424498	AB033043	Hs.149377	hypothetical protein OKFZp761L0424	AIP3:TM:SS	3.2
	435684 402632	NM_001290	Hs.4980	LIM domain binding 2	UM_bind;TM;	3.2
	431130	NM_006103	Hs.2719	Target Exon	ig:TM;SS	3.1
5	410636	AA088177	Hs.172870	HE4: epididymis-specific, whey-acid ESTs	wzp;TM;SS TM;SS	3.1
•	452658	N88604	Hs.30212	thyroid receptor interacting protei	PCI:TM:	3.1 3.1
	453180	N46243	Hs.110373	ESTs, Highty similar to T42626 secr	laminin_G.URRCT_none	3.1
	430319	AJ480214	Hs.356075	ninjurin 2	TM:SS	3.1
• •	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	C2:TM:	3.1
10	456063	NM_006744	Hs.76461	retinol-binding protein 4, intersti	ipocafin,TGF-beta,TGFb_p	3.1
	429798	AL11757B	Hs.222909	DKFZP434C128 protein	TM:	3.1
	417677	NM_016055	Hs.82389	CGI-118 protein		3.1
	443792	AI763073	Hs.204873	ESTs		3.1
15	445861	BE293423	Hs.11809	single ig IL-1R-related molecule	TIR:TM;	31
13	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	LRR.none	3.1
	456689 446492	NM_002251	Hs.117780	potassium voltage-gated channel, de	ion_trans,K_tetra;TM;SS	3.1
	427706	AW205115 AW971225	Hs.161287 Hs.293800	ESTs ESTs, Wealthy similar to ALU1_HUMAN	SPRY,zf-B_box,PAAD_D	3.1
	458008	AA809314	Hs.123295	ESTs	SCANZI-C2H2,none	3.0 3.0
20	449708	A1694598	Hs.202126	ESTS	3CSULZI-CZNZIRUR	3.0
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein	TM:SS	3.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	FMO-like.pyr_redox;TM;S	3.0
	425280	U31519	Hs_1872	phosphoenotpyruvate carboxykinase 1	PEPCK:TM:	3.0
25	453177	AW389509	Hs.223747	ESTs	zf-C2H2,none	3.0
25	416781	AF072928	Hs.79877	myotubularin related protein 6		3.0
	447582	BE293520	Hs. 18910	prostate cancer overexpressed gene	sugar_tr;TM;SS	3.0
	417365	050683	Hs.82028	transforming growth factor, beta re	pkinase.WD40;TM;	3.0
	452540 430233	AW161048 AW367902	Hs.150549	ESTs. Wealdy similar to T33997 hypo	August and the second	2.9
30	418127	BE243982	Hs.236443 Hs.83532	Homo sapiens mRNA; cDNA DKFZp564N10	PH,Ets,CH,spectrin,Ca_cha	. 2.9
	404445	06243302	ris.03332	membrane cofactor protein (CD46, tr Target Exon	sushi;TM;SS	2.9
	423323	AI951628	Hs.127007	potassium channel, subfamily K, mem	ion_trans;TM;SS	2.9 2.9
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cONA DKFZp586M07	7tm_1,none	2.9
	427981	BE275986	Hs.181311	asparaginyl-IRNA synthetase	tRNA-synt_2,tRNA_anti,tRN	2.9
35	452242	R50956	Hs.159993	gycosyltranslerase		2.9
	440232	AJ766925	Hs.112554	ESTs	_	2.9
	444634	AW611988	Hs.197813	ESTs	CKS	2.9
	445889	BE465186	Hs.266958	ESTs	TM;	2.9
40	414483	R25513	Hs.10683	ESTs		29
70	453500 419768	A1478427 T72104	Hs.43125	esophageal cancer related gene 4 pr	TMSS	2.9
	427804	AL049654	Hs.93194 Hs.180871	apolipoprotein A-I	Apolipoprotein;SS	2.9
	423753	Y11312	Hs.132463	protein kinase C, alpha binding pro phosphoinositide-3-kinase, class 2,	POZ;SS	2.9
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN	C2,PI3_PI4_kinase,PI3Ka,P lipocalin;SS	2.9 2.9
45	427842	AW936961	10.202110	gb:RC1-DT0029-160200-013-a12 DT0029	efhand,mito_carr,none	2.8
	432834	F06459	Hs.289113	cytochrome b5 reductase 1 (BSR.1)	NAD_binding,FAD_binding_6	2.8
	421435	AW972072	Hs.372167	ESTs		2.8
	402458			C1002064;gij11993050jgbjAAG42574.1j	TM;\$\$	2.8
50	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	Calsequestrin;SS	2.8
50	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, bet	ETF_beta;SS	2.8
	459439	AW402931	Hs.352411	gb:UI-HF-BKO-abd-a-01-0-UI.r1 NIH_M	•	2.6
	438622 417023	L03151	14. 204606	gb:Homo sapiens cell-type T-cell im		2.8
	453281	AA192278 W46280	Hs.301596	ESTs, Moderately similar to S65657		2.8
55	403028	****0200	Hs.55940	ESTs, Wealdy similar to A25704 syna Target Exon	de venin dendati	2.8
	449029	N28989	Hs.22891	solute carrier family 7 (cationic a	trypsin,trefoil	2.8 2.8
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) h	aa_permeases;TM;S\$ EGF,cadherin,Jaminin_G;TM	2.8
	406918	M88357		gb:Homo sepiens ONA-binding protein	zi-C2H2,KRAB,zi-BED;TM;	27
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector protein S	TM;	27
60	443990	AW205085	Hs.39557	ESTs	··· <del>·</del>	27
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	2.7
	431713	AK000388	Hs.267997	EHM2 gene	Band_41;TM;	2.7
	431469	N49424	Hs.124159	ESTs .	SH3	2.7
65	400386 406684	AF075290	11. 50004	gap junction protein, alpha 3, 46kD	connexin;TM;SS	2.7
U.J	449874	X16354 AA135688	Hs.50964	carcinoembryonic antigen-related ce	ig;TM;SS	27
	403213	~~133000	Hs.10083	Homo sapiens, clone IMAGE:4139786, NM_019595:Homo sapiens intersectin	TM:	27
	459665	BE159784	Hs.47647	gb:MR0-HT0408-220300-001-h06 HT0408	SH3,ethand,C2,PH,RhoGEF;T	2.7
	421823	N40850	Hs.28625	ESTs		2.7 2.7
70	422693	BE300073	Hs.279860	tumor protein, translationally-cont	TCTP,none	27
	454906	AI219323	Hs.101077	ESTs, Weakly similar to T22363 hypo	TM:	27
	447075	AV662037	Hs.124740	ESTs, Weakly similar to (38022 hypo	TM;	2.7
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	тплопе	2.7
75	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypo		2.7
13	436972	AA284679	Hs.25640	claudin 3	PMP22_Claudin;TM;SS	2.7
	441379	AW175787	Hs.334841	selenium binding protein 1	TM;	2.7
	421143	AB024536	Hs.102171	immunoglobulin superfamily containi	ig.LRR.LRRNT,LRRCT;TM;S	2.7
	422558 428900	NM_006420			Sec7,none	2.7
80	421153	AA437189 AF009267	Hs.352324 Hs.102238		SS	27
	427074	AA527435	Hs.178589		ofbood-This	27
	448133	AA723157	Hs.73769	folate receptor 1 (aduit)	efhand;TM; Folate_rec,MIP;TM;SS	26 26
	419158	AF031475	Hs.89648	arginine vasopressin (neurophysin I	hormone5,hormone4;SS	26
				=		

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	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B07		26
	437176	AW176909	Hs.42346	calcineum-binding protein calsarc	Galactosyl_T;TM;SS	26
	435075 403153	R51094	Hs.12400	ESTs Tanget Exon		2.6 2.6
5	400387	AF133131		double homeobox, 5		26
•	425940	AB023184	Hs.163990	KIAA0967 protein	PDZ:SS	2.6
	416157	NM_003243	Hs.342874	transforming growth factor, beta re	zona_petlucida:TM;SS	2.6
	452554	AW452434	Hs.58006	ESTs. Wealty similar to ALU5_HUMAN	HLH,PAC,PAS,none	2.6
10	453247	T80198	Hs.111806	ESTS	wwa_Cache.none	2.6
10	407744 432877	AB020629 AW974111	Hs.38095	ATP-binding cassette, sub-family A ESTs	ABC_tran,PRX;TM;SS	2.6 2.6
	450115	AI591038	Hs.292477 Hs.38132	ESTS	Ets,SAM_PNT,none	26
	406337		1.0.00.02	C14000021:gij7242973jdbjjBAA92547.1	Peptidase_M22	2.6
	430877	NM_005269	Hs.2693	glioma-associated oncogene homolog	zi-C2H2:SS	2.6
15	453874	AW591783	Hs.36131	collagen, typo XIV, atpha 1 (unduli		2.6
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelia	NAD_binding,flavodoxin,FA	26
	427620 446585	NM_003705 AV659397	Hs.179866 Hs.299668	solute carrier family 25 (mitochond ESTs, Weakly similar to I38022 hypo	ethand,mito_carr,TM;SS=	2.6 2.6
		BE208189	Hs.174031	cytochrome c oxidase subunit VIb	tubulin,FKBP,COX68,7tm_1,	2.6
20	428111	S76617	Hs.2243	B lymphoid tyrosine kinase	SH2,SH3,pkinase;SS	2.6
	440133	AI056255	Hs.133349	ESTS	•	2.6
	419693	AA133749	Hs.301350	FXYD domain-containing ion transpor	ATP1G1_PLM_MAT8;TM;SS	2.6
	417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR_zI-C3HC4,PHD,TM;SS=	2.6
25	419100 449925	AAA64362 Al342493	Hs.6748 Hs.24192	hypothetical protein PP1665 Homo sapiens cDNA FLJ20767 fis, clo	squash,GDPD;TM;	2.6 2.6
ديد	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastroint	GSHPx;SS	26
	425640	U34051	Hs.158460	cyclin-dependent kinase 5, regulato	CDK5_activator;TM;	26
	409021	AA156640	Hs.49881	fatty acid binding protein 3, muscl	lipocalin,none	2.6
20	400538			ENSP00000239776*:BA425A6.2 (similar	TM;SS	. 2.6
30	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell sur	TM;SS	2.6
	408310 433032	AW179023 AI084066	Hs.191705 Hs.20072	gb:PM3-ST0036-170899-001-e08 ST0036	Band_41;	2.6 2.6
	419389	AI074951	Hs.319095	myosin regulatory light chain inter ESTs	DPPIV_N_term,none	2.6
	453145	R63438	Hs.183454		STT3:TM:SS	2.6
35	443460	AL050275	Hs.9383	DKFZP566D213 protein	EGF,taminin_EGF,EB;TM;S	2.6
	421903	AW079940	Hs.15951	ESTs, Wealdy similar to S32436 coll	\$S	2.5
	421757	Z20897	Hs.296259		Arylesterase;\$\$	25
	428475 424657	AF172940 AA344719	Hs.184542	CGI-127 protein gb:EST50901 Gall bladder II Homo sa		2.5 2.5
40	432862	AW004958	Hs.236720		TM;SS	2.5
, -	427195	W27230	Hs.173912		DEAD,heficase_C;	2.5
	447770	AB032417	Hs.19545	frizzled (Drosophila) homotog 4	Fz,Frizzled,7tm_2;TM;SS	2.5
	456523	AJ083668	Hs.50601	hypothetical protein MGC10986	pkinase,none	2.5
45	451846	T65840	Hs.11762	ESTs	147040-TA4	2.5
73	432906 453876	BE265489 AW021748	Hs.3123 Hs.110406	lethal giant larvae (Drosophila) ho ESTs, Wealdy similar to 138022 hypo	WD40;TM;	2.5 2.5
	441488	AW450935	Hs.7862	hypothetical protein FLJ20312	TM;	2.5
	444669	F18939	Hs.153827			2.5
50	452497	AA732153	Hs.27865	Homo sapiens cDNA; FLJ21333 fis, cl		2.5
50	T.O. C.	40				
	TABLE 3 Pkey:		inna Eas araba	set Identifier number		
	CAT nur		ne clusier num			
	Accessio		nbank accession			
55						•
	Pkey	CAT Numb				
	439457 413127	23338_1		W69434 W69517 BF330853 BF747375 BE066356 BE066292 BF33	0000 DET43440 DE000040 DE240040 DE	MCCCO DEDCESOD DET 12510 DET 16600
	713121	151610_1		BF334312	D300 BF (4) (42 BC0004 13 BF (423 10 BC)	000323 BE000230 BF / 423 (0 BF / 40003
60	427842	1164138_1		AW936961 AA416706 R29415		
	438622	46171_1		3155 L03161		
	424657	896375_1	AW963487	7 AA365077 AA344719		
	TABLE	10.				
65	TABLE 3 Pkey:			orresponding to an Eos probeset		
•••	Ref.			. The 7 digit numbers in this column are Genbank	Identifier (GI) numbers. "Dunham, et al." o	elers to the publication entitled 'The DNA
		se	quence of hum	an chromosome 22" Dunham, et al. (1999) Nature	402:489-495.	
	Strand:			and from which exons were predicted.		
70	Nt_posit	ion: tn	dicates nucleoti	ide positions of predicted exons.		
70	Pkey	Ref	Chand	Att maritime		
	401700	3176654	Strand Minus	Nt_position 35416-35534		
	402449	9796674	Plus	59867-60039,62588-62828,63465-63623,6492	!	
75	402632	9931268	Plus	101166-101419		
75	404445	7596866	Minus	31112-31423		
	402458	9796782	Plus	170479-171134		
	403028 403213	7670577 7630897	Minus Minus	114150-114272 162572-162739,164442-164540		
	403153		Minus	42232-43389		
80	406337	9213455	Plus	90117-90337		
	400538		Plus	8752-9822		

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TABLE 32A: ABOUT 68 GENES UP-REGULATED IN GLIOMA COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT BRAIN TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL, MOLECULES, PEPTIDES, OR ANTIBODIES

Table 32A lists about 68 genes up-regulated in glioma compared to normal adult issues and to non-malignant brain tissues that are fixely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrio/Eos-Hu03 GeneChip® array as follows: the ratio of "average" glioma to "average" normal adult issues was greater than or equal to 2.5, the ratio of "average" glioma to "average" normalignant brain tissues was greater than or equal to 2.0, the "average" normal adult tissue level was set to the 98th percentile value amongst various non-malignant tissues, the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant tissues, the "average" glioma value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an encogenic function or of transducing an intracefular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Predicted protein domains are noted. 5

10

Pkey: ExAccn: Unique Eas probeset identifier number

Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Predicted Protein Domains UnigenelD: Unigene Title: Protein Domains:

15

R1: glioma vs. normal adult lissues and non-malignant brain lissues that are likely to encode proteins

					•	
	Pkey	ExAcon	UniGene ID	Unigene Title	Protein Domains	R1
~ ~	424343	AW956360	Hs.4748	adenytate cyclase activating polype	7tm_2,HRM	8.8
20	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (form		7.8
	456723	243902	Hs.4748	adenylate cyclase activating polype	7tm_2,HRM	7.5
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypo		7.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	ASC;TM;	6.3
25	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322,	TM;	6.0
25	414825	X06370	Hs.77432	epidermal growth factor receptor (a	Furin-like,pkinase,Recep_	6.0
	423779	AW071837	Hs.57971	ESTs	TNFR_c6	5.5
	409638	AW450420	Hs.21335	ESTs	7tm_2,HRM	5.3
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	Neur_chan_LBD,Neur_c	5.2
20	436456	AW292677	Hs.248122	G protein-coupled receptor 24		· 5.1
30	424340	AA339035	Hs.7033	ESTs	fig_chan,ANF_receptor,non	5.0
	425115	R44664	Hs.123956	ESTs	7tm_1	4.7
	446809	AW590171	Hs.101413	ESTs	CaMBD,SK_channel,CaMBD,SK	4.4
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	ubiquitin;SS	4,4
35	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_train,ABC_membrane,PRK	4.2
22	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity I	ig:TM;SS	4.2
	428141	D50402	Hs.182611	solute carrier family 11 (proton-co	· Nramp;TM;	4.1
	435472	AW972330	Hs.283022	triggering receptor expressed on my	ig;TM;SS	4.1
	435615	Y15065	Hs.4975	polassium voltage-gated channel, KQ	ion_trans,KCNQ1_channel;T	3.8
40	448204	AI475124	Hs.170561	ESTs	lig_chan,SBP_bac_3	3.7
40	433290	R20077	Hs.302185	Homo saplens clone 23818 mRNA seque	lig_chan,SBP_bac_3,ANF_re	3.6
	408243	Y00787	Hs.624	interleukin 8	HLH,PAS,IL8;TM;	3.6
	415849	R20529	Hs.6806	ESTs	7tm_2,GPS,Gal_Lectin,HRM,	3.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	fn3;TM;SS	3.4
45	445070	NM_000677	Hs.258	adenosine A3 receptor	7tm_1;TM;SS	3.4
45	428037	N47474	Hs.89230	potassium intermediate/small conduc	CeMBD,SK_channel	3.2
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	kfl_recept_a,PKD,MHC_1;TM	3.1
	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vaso		3.0
	418054	NM_00231B	Hs.83354	lysyl oxidase-like 2	SRCR,Lysyl_oxidase;TM;S	3.0
50	424441 446057	X14850	Hs.147097	H2A histone family, member X	histone,C8FO_NFYB_HMF;TM=	3.0
50	438204	AJ420227	Hs.366053	Trp-p8 transient receptor potential		2.9
	431674	AI589645 AA098901	Hs.128690	ESTs	7tm_1	29
	424028	AF055084	Hs.301642 Hs.153692	G-protein coupled receptor	GCV_H	2.9
	415209	F00183	Hs.172004	Homo sapiens cDNA FLJ14354 fis, clo titin		2.9
55	438537	AK000511	Hs.6294	7	6701A 4.714.	2.8
	431053	\$40369	Hs.249141	hypothetical protein DKFZp434L1435 Glutamate receptor subunit	tRNA-synt_1;TM;	28
	408482	NM_000676	Hs.45743	adenosine A2b receptor	lig_chan_ANF_receptor;TM=	28
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7tm_1;TM;SS	2.8
	426865	D63476	Hs.172813	PAK-interacting exchange factor bet	kringle,trypsin,plant_thi	2.8 2.8
60	430897	U71092	Hs.248122	G protein-coupled receptor 24	SH3,PH,RhoGEF,Terpene_syn	
••	438993	AA828995	113.240122	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	7tm_1;TM;	2.7
	409552	AL119675	Hs.54929	phosphorylase kinase, gamma 1 (musc	EGF,metalthio,integrin_B, pkinase,Bac_ONA_binding;T	2.7 2.7
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S	PC_rep;TM;	27
	429150	AF120103	Hs.197366		COXB,SHMT,MIF,GST_C,EF1G_	2.7
65	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C	ABC_tran_ABC_membrane;TM=	2.7
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion mol	EGF, lectin_c, sushi; TM; S	2.7
	432074	AA525248	Hs.149723		Y_phosphatase	2.6
	402154			NM_031896*:Homo sepiens catcium cha	PMP22_Claudin;TM;SS	2.6
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_pellucida;TM;SS	2.6
70	419913	AW270040	Hs.34455	ESTs	EPH_lbd,fn3.pkinase,	2.6
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integr	MIP.TM:SS	2.6
	412070	AW893260		gb:CM2-NN0010-100300-111-e09 NN0010	7tm_2,HRM	2.6
	422676	D28481	Hs.1570	histamine receptor H1	7tm_1;TM;SS	2.6
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	fn3;TM;	2.6
75	444381	BE387335	Hs.283713		Collagen;TM;SS	2.6
	419972	AL041465	Hs.182982	golgin-67		2.6
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarbo	TM:SS	2.6
	421997	R66740	Hs.110613		aa_permeases.pyridoxal_de	2.6
	430181	AF065314	Hs.234785		cNMP_binding,ion_trans;TM	2.5
80	426318	AA375125	Hs.147112		EPH_lbd.pkinase,fn3,SAM,n	2.5 2.5
	434808	AF155108	Hs.256150		TM;	2.5
	418843	AJ251016	Hs.89230	potassium intermediate/small conduc	CaMBD.SK_channet;TM;SS=	2.5
	410290	AA402307	Hs.322844	hypothetical protein DKFZpS64A176	Sema PSI,TIG,integrin_B;T	2.5
					manufit felt i frammani att.	_,

424909	S78187	Hs.182575	cell division cycle 258	Rhodanese;SS	2.5
408359	R38438		SLC15A2 Solute carrier lamily 15 (H	PTR2;TM;	2.5
414561	Al064813		Homo sapiens emino acid transport s	Aa_trans;TM;	2.5

5 TABLE 328:

Pkey: CAT number: Unique Eos probeset identifier number Gene cluster number

Accession: Genbank accession numbers

10 Pkey 438993

CAT Number Accession
2580163_1 AI926361 AAB34879 AA828996
287551_1 BG820657 AW890808 BF904755 AW893260 BI034684 BF963423 BF961550 M85689

TABLE 32C: 15

Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA Pkey: Ref:

sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.

Strand:

Nt_position: Indicates nucleotide positions of predicted exons. 20

Pkey Ref 402154 8516165 Nt_position 125299-125494 Strand Minus

25 TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER

TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER
Table 33A issts about 798 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-matignant tissues. In order to remove gene-specific before the ratio was evaluated.

Pkey:

Unique Eos probeset identifier number
ExAcon:

Exemplar Accession number, Genbank accession number
Unigene [Tite:
Unigene gene bite
Unigene gene bite
Unigene gene bite

30

Unigene number
Unigene gene title
Ratio of tumor to normal tissue 35 R1:

	Pkev	ExAcon	UniGeneID	Unigene Title	Ri
	421471	U90545	Hs.104635	solute carrier family 17 (sodium phospha	1007.4
	445178	A1792241	Hs.129614	kidney-specific membrane protein	438.0
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	338.4
	421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	323.6
	440304	BE159984	Hs.125395	ESTs	295.0
	436878	BE465204	Hs.47448	ESTs	258.8
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	258.6
45	421155	H87879	Hs.102267	tysyl oxidase	251.8
	426471	M22440	Hs.170009	transforming growth factor, alpha	224.5
	421478	AI683243	Hs.97258	ESTs	212.6
	424086	AI351010	Hs.102267	lysyl oxidase	199.2
	428295	NM_003058	Hs.183572	solute carrier family 22 (organic cation	186.4
50	426890	AA393167	Hs.41294	ESTs	183.4
	441031	AJ110684	Hs.7645	fibrinogen, B beta polypeptide	174.0
	411642	NM_014932	Hs.71132	neuroligin 1	172.4
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	161.4
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	151.0
55	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	135.0
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	134.8
	453160	AI263307	Hs.146228	ESTs	132.6
	452431	U88879	Hs.29499	toll-like receptor 3	130.6
60	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor I	120.4
60	420642	AKD01520	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT	112.6
	407975	X89426	Hs.41716	endothelial cell-specific molecute 1 (NO	111.8
	431708	A1698136	Hs.108873	ESTs	109.8
	446460	AW013999	Hs.150164	ESTs	103.6
65	443450	N66045	Hs.133529	ESTs	103.0
05	432865	AI753709	Hs.152484	ESTs	101.4
	442438	AA995998	11- 2004	gb:os26b03.s1 NCI_CGAP_Kid5 Horno sepiens	98.8
	433447	U29195	Hs.3281	neuronal pentrauin II	98.5
	440311	A1733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN!	98.2
70	415076	NM_000857		guanylate cyclase 1, soluble, beta 3	97.0
, 0	437157 453319	BE048860 AI985369	Hs.120655	ESTs ESTs	94.4
	447046	AA326187	Hs.20117 Hs.17170		91.4
	439169	A4320107 A1912122	Hs.41095	G protein-coupled receptor 4 ESTs	90.2
	431870	AW449902	Hs.105500	ESTS ESTS	86.6
75	438993	AA828995	rts. 103300	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	84.4
, 5	445279	R41900	Hs.22245	ESTs	83.8
	451592	A1805416	Hs.213897		82.4
	422966	AV648419	Hs.122613		79.4
	423109	M59305	Hs.123655		78.8 78.0
80	415989	AJ267700	Hs.111128	ESTs	78.0 77.0
	422544	AB018259	Hs.118140		77.0 74.8
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	74.8 74.8
	429352	AK001512	Hs.200097	hypothetical protein FLJ 10650	73.0
	-23445			rishen marrie hactours on second	73.0

	453300			CON francis is a second of the	
	453392 441665	U23752 Al301355	Hs.32964 Hs.151285	SRY (sex determining region Y)-box 11 ESTs	72.2
	435094	AI560129	Hs.277523	EST	71.6 71.2
	403345	V-1-00 153	113.27 / 323	201	69.6
5	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	69.0
	440482	AA886658	Hs.50873	ESTs	67.6
	457100	AA417878	Hs.48401	ESTs, Weakly similar to ALUS_HUMAN ALU S	67.0
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	65.2
10	407905	AW103655	Hs.252905	ESTs	63.2
10	422998	AK000588	Hs.122939	hypothetical protein FLJ20581	61.8
	432267	AK000872	Hs.274227	Homo sapiens cONA FLJ10010 fis, clone HE	61.2
	449448	D60730	Hs.57471	ESTs	60.6
	431941	AK000106	Hs.272227	Homo saplens cONA FLJ20099 fis, clone CO	59.8
15	419752 449579	AA249573 AW207260	Hs.152618 Hs.134014	ESTs	58.4
13	408609	AA330431	Hs.640	prostate cancer associated protein 6 calcitorsin receptor	58.2 57.4
	451009	AA013140	Hs.115707	ESTS	57.4 57.2
	435610	AI862767	Hs.114157	ESTs, Weakly similar to putative p150 [H	56.4
	411893	R82845	Hs.273789	ESTs	56.2
20	415227	AW821113	Hs.72402	ESTs	55.2
	433859	AW898758	Hs.163925	ESTs	55.0
	450459	AI697193	Hs.299254	ESTs	54.4
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	53.4
25	421831	AA298836	Hs.22026	ESTs	52.8
23	438817	AJ023799	Hs.163242	ESTs	52.1
	449101 410025	AA205847	Hs.23016	G protein-coupled receptor	52.0
	423685	BE220489 BE350494	Hs.113592 Hs.49753	ESTS	51.8
	436751	AA732217	Hs.294054	Homo sapiens mRNA for KIAA1561 protein, ESTs	48.0 46.6
30	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	45.4
• •	444059	R69743	Hs.75442	abumin	44.8
	442671	AI005668	Hs.134779	EST	44.4
	445657	AW612141	Hs.279575	ESTs	44.3
2.5	452891	N75582	Hs.212875	ESTs, Wealdy similar to KIAA0357 [H.sapi	44.0
35	423735	AA330259		gb:EST33963 Embryo, 12 week Il Homo sapi	43.8
	422553	AI697720	Hs.171455	ESTs	43.6
	452461	N78223	Hs.108106	transcription factor	42.8
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	42.6
40	452240	AI591147	Hs.61232	ESTs	41.7
40	445186 452788	AW614544	Hs.123641	protein lyrosine phosphatase, receptor t	41.4
	419287	AW294571 X91906	Hs.135040	ESTS	41.4
	428822	W2841B	Hs.89872 Hs.301148	chloride channel 5 (nephrolithiasis 2, X	40.6 40.2
	412359	AW837985	FIS.301140	potassium voltage-gated channel, lsk-rel gb:CV3-LT0048-140200-083-e05 LT0048 Homo	40.2 40.0
45	434208	T92641	Hs.127648	hypothetical protein PRO2176	39.2
	442168	AJ253165	Hs.146022	ESTs	38.8
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	38.6
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	38.4
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	38.4
50	428795	R45503	Hs.97469	ESTs, Wealdy similar to 149698 alpha-1,3	37.6
	406411				37.6
	423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	37.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	37.2
55	448788	AI570286	Hs.107070	ESTs	37.2
"	441826 409263	AW503603	Hs.129915	phosphotriesterase related	37.0
	425577	AA069573 BE464496	Hs.50319 Hs.280977	ESTs ESTs	36.8
	452249	8E394412	Hs.61252	ESTs	36.2 34.8
	435986	AA703158	Hs.187848	ESTs	34.4
60	417236	AI908497	Hs.170737	Homo sapiens cDNA: FLJ23251 fis, clone C	33.8
	440234	AW117264	Hs.126252	ESTs	33.8
	435334	R94223	Hs.117747	ESTs	33.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	33.1
65	424871	NM_004525		low density lipoprotein-related protein	32.8
65	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	32.4
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (I	32.4
	451050	AW937420	Hs.69662	ESTs	32.0
	449034	A1624049	U- 21/4/A	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sepiens	31.6
70	434539 431595	AW748078 AA508196	Hs.214410		31.0
, ,	449625	NM_014253	Hs.23796	gb:nh60f07.s1 NCI_CGAP_Pr8 Home sapiens	30.6
	448243	AW369771	Hs.77496	odz (odd Oz/ten-m, Drosophila) homolog 1 small nuclear ribonucleoprotein polypept	30.5 30.4
	413573	A1733859	Hs.149089		30.4 30.2
	421037	A1684808	Hs.197653		30.2 30.2
75	449353	AA001220	Hs.271369		30.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	29.6
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	29.6
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superlami	29.6
80	459508	R83265	Hs.205956		29.2
80	414245	BE148072	Hs.75850	WAS protein family, member 1	28.8
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	28.6
	445925	A1733820	Hs.145664		28.4
	412616	AW970584	Hs.291033	ESTs	28.0

	424638	Al472106	Hs.49303	Homo sapiens cDNA FLJ11663 fs, clone HE	27.6
	445885	AJ734009	Hs.127699	IQAA1603 protein	27.6
	410247	AF181721	Hs.61345	RU2S	27.4
5	406414 435951	AF269162	U- 41007	elles Care and	27.2
,	458580	N73773	Hs.41267 Hs.282950	c21orf7 form A-D ESTs	27.2
	419948	AB041035	Hs.93847	NADPH oxidase 4	27.0 26.4
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	26.3
	427457	AW779105	Hs.164682	ESTs, Wealty similar to ORF2 consensus s	26.0
10	446346	AI290205		gb:q/79g06.x1 Soares_NhHMPu_S1 Homo sapi	26.0
	448595	AB014544	Hs.21572	KIAA0644 gene product	25.8
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	25.6
	433242	AB040938	Hs_113940	KIAA 1505 protain	25.6
15	453118	AW195849	Hs.252757	EST ₅	25.6
13	412209	AW901456	14- 440000	gb:RC0-NN1012-270300-031-c07 NN1012 Homo	25.2
	429710 444783	Al337113 AK001468	Hs.146025	Homo sapiens cDNA: FLJ23594 fls, clone L	25.2
	436788	AA766908	Hs.62180 Hs.259047	anillin (Drosophila Scraps homolog), act ESTs	24.6
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	24.4 24.4
20	419172	AW338625	Hs.22120	ESTs	24.3
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 ffs, clone C	24.2
	413623	AA825721	Hs.246973	ESTs	24.0
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247 Homo	23.8
26	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	23.8
25	432809	AA565509	Hs.131703	EST8	23.7
	440102	AI672443	Hs.131190	ESTs	23.6
	451559	AL119980	Hs.128857	ESTs	23.2
	410811 415778	AW805687 M16505	Hs.300648	ESTs	23.0
30	453628	AW243307	Hs.79876 Hs.170187	steroid suffatese (microsomal), erytsulf ESTs	23.0
-	401352	THE TOPPE	16.110101	2318	22.8 22.6
	451561	N52812	Hs.177403	ESTs	22.6
	401976				22.4
~~	410658	AW105231	Hs.192035	ESTs .	22.4
35	416220	N49776	Hs.121773	ESTs	22.2
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	22.0
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	22.0
	444144	BE 159397	Hs.7736	hypothetical protein	21.8
40	438504 439157	AW665281	Hs.224625	ESTs	21.2
40	429006	AA912737 AA443143	Hs.20160 Hs.50929	ESTs	20.8
	442006	AW975183	Hs.292663	Homo sapiens cDNA FLJ 13842 fis, clone TH ESTs	20.5
	409569	AW573153	Hs.256216	EST\$	20.2 19.8
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cONA DKFZp586J0323 (f	19.8
45	404200			the supplied in any object by a change of the	19.6
	446591	H44186	Hs.15456	PDZ domain containing 1	19.2
	420218	AW958037	Hs.22437	Homo sapiens cDNA: FLJ23366 fis, clone H	18.9
	408390	AA054222	Hs.40400	ESTs	18.8
50	444038	AW134509	Hs.135077	ESTs	18.8
50	446443	AV659082	Hs.134228	ESTs	18.8
	442204 451177	AI635450 AI969716	Hs.21914	ESTs	18.4
	453931	AL121278	Hs.13034 Hs.25144	ESTs ESTs	18.2
	437212	AJ765021	Hs.210775	ESTs	18.1 18.1
55	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	18.0
	451659	BE379761	Hs.14248	ESTs. Wealthy similar to ALUS_HUMAN ALU S	17.8
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	17.6
	441082	AW444804	Hs.202655	ESTs	17.6
60	446259	AA425204	Hs.42278	Homo sapiens cDNA FLJ13391 fis, clone PL	17.6
O.	423609 428301	AA328348 AW628666	Hs.218289	ESTs	17.4
	446364	A8006624	Hs.98440 Hs.14912	ESTs	17.4
	419983	W55956	Hs.94030	KIAA0286 protein	17.4
	424929	AI640761	Hs.224988	Homo sapiens mRNA; cDNA DKFZp586E1624 (I ESTs	17.0
65	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	17.0 17.0
	449122	AI631310	Hs.196955	ESTs	17.0
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	16.8
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	16.8
70	418053	AA211493		gb:zn55d06.a1 Stratagene muscle 937209 H	16.8
70	433225	AW816515	Hs.173540		16.8
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ 13103 fis, clone NT	16.6
	421002 419296	AF116030 AA236115	Hs.100932 Hs.120785		16.5
	421659	NM_014459	Hs.120765 Hs.106511		16.2
75	417589	T82075	Hs.13911	protocadherin 17 ESTs	16.0
	446057	AJ420227	Hs.149358		16.0 15.8
	434636	AA083764	Hs.241334		15.6
	446797	AI682536	Hs.163495		15.6
80	443718	A1083580	Hs.221373	ESTa	15.4
οU	409748	A1670776	Hs.20961	ESTs	15.2
	443211	Al128388	Hs.143655		15.0
	428911 444692	Z43846 AW770022	Hs.194478		14.9
	*14072	AW779922	Hs.145047	ESTs	14.8

	445436	AJ224105	Hs.151408	ESTs	14.6
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	14.5
	405943				14.4
5	406291 458679	AW975460	D- 142552	CCT-	14.4
-	450152	A1138635	Hs.143563 Hs.22968	ESTs ESTs	14.4
	403899	~13000	115.22500	2018	14,4
	454490	AW797778		gb:CM2-UM0041-250200-104-d02 UM0041 Homo	14.2 14.2
	451807	W52854	Hs.27099	DKFZP564J0863 protein	14.0
10	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	13.8
	447499	AW262580	Hs.147674	KIAA1621 protein	13.8
	406598			• • •	13.8
	430939	AJ269471	Hs.187018	ESTs	13.4
1.5	443316	AJ478483	Hs.18443	ESTs	13,4
15	408034	N26639	Hs.42192	Human EST clone 251800 mariner transposo	13.2
	428508	BE252383	Hs.184668	SB8i31 protein	13.2
	447934	AW631440	Hs.165596	ESTS	13.2
	406671	AA129547	Hs.285754	met proto-oncogens (hepatocyte growth fa	13.1
20	438199 415511	AW016531 AJ732617	Hs.122147 Hs.182362	ESTS	13.0
20	426920	AA393351	Hs.132121	ESTS ESTS	12.9
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 ffs, clone K	12.8 12.6
	423321	AB013885	Hs.126926	beta-ureidopropionase	12.5
	403622		-10.120020	eca-acaopapoisse	12.4
25	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	12.4
	422317	NM_001147	Hs.115181	angiopoletin 2	12.2
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	12.2
	445717	AW664658	Hs.149332	ESTs	12.2
20	418413	R95735	Hs.117753	ESTs, Wealdy similar to antigen of the m	12.1
30	405336				12.0
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	12.0
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	12.0
	414923 432009	AW445008	Hs.77637	homeo box A4	11.9
35	432309	AL137424 Al379486	LL- 150420	gb:Homo sapiens mRNA; cDNA DKFZp761G2123	11.8
55	453955	AW579207	Hs.159430	ESTs	11.8
	407510	U96191		gb:RC1-DT0029-120100-011-h01 DT0029 Horno	11.8
	433231	AB040926	Hs.143552	gb:Human trophoblast hypoxia-regulated f KIAA1493 protein	11.6
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	11.6 11.6
40	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	11.4
	405609			and the same of the same of the same of	11.4
	418912	NM_000685	Hs.89472	anglotensin receptor 1	11,4
	421306	AA806207	Hs.125889	ESTs	11,4
40	428721	X02158	Hs.2303	erythropoietin	11.4
45	419255	AA235672	Hs.87491	EST8	11.4
	450006	Al241555	Hs.60171	ESTs	11.3
	435420	AJ928513	Hs.59203	ESTs	11.2
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	11.2
50	424647	W67751	Hs.137308	ESTs	11.0
50	435758 404347	A1242163	Hs.22670	chromodomain helicase DNA binding protei	11.0
	438664	AJ911173	Hs.213722	ESTs	10.8
	429125	AA446854	Hs.271004	ESTs	10.8
	416560	R02818	Hs.14102	ESTS	10.7
55	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	10.6 10.6
	435085	AW130284	Hs.192752	ESTs, Moderately similar to NSD1 protein	10.6
	442409	BE208843	Hs.129544	ESTs, Weakly similar to ORF YLL027w [S.c	10.6
	450644	AW505496	Hs.281215	ESTs	10.6
60	448298	AW137134	Hs.187203	ESTS	10.4
60	404115				10.2
	406242	umare e			10.2
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.2
	452588	AA889120	Hs.110637	homeo bax A10	10.2
65	457233	AI355009	Hs.221698	EST ₅	10.2
0,5	416185	AW975861	Hs.291995	ESTS	10.2
	446152 446298	AI292036 AF187813	Hs.150028	ESTs	10.1
	423637	AL137279	Hs.14637 Hs.130187	kidney- and liver-specific gene	10.1
	442405	BE465247	Hs.129530	Homo sapiens mRNA; cDNA DKFZp434O1214 (f ESTs	10.0
70	419213	AW749146	113.123330	gb:PM0-BT0340-170100-004-e03 BT0340 Homo	9.9
	420840	AI915838	Hs.294008	ESTs	9.8 9.8
	423355	AA324856	Hs.257510		9.8
	444929	AI685841	Hs.161354		9.8
7.	423811	AW299598	Hs.50895	homeo box C4	9.8
75	433527	AW235613	Hs.133020		9.6
	429975	A1167145	Hs.165538		9.6
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	9.5
	433703	AA210863	Hs.3532	nemo-like kinase	9.2
80	417404	NM_007350		pleckstrin homology-like domain, family	9.2
90	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	9.2
	406992	\$82472		gb:beta -pol=DNA polymerase beta (exon a	9.2
	419699 443740	AA248998	Hs.31246	ESTS	9.2
	3/40	R56434	Hs.21062	EST6	9.2

				POT-	
	422728 436961	AW937826 AW375974	Hs.103262 Hs.156704	ESTs ESTs	9.2
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	9.2 9.1
_	411411	AA345241	Hs.55950	ESTs. Wealthy similar to KIAA1330 protein	9.1
5	424115	AA335497	Hs.293965	ESTs	9.0
	402045				9.0
	433426	H69125	Hs.133525	ESTs	9.0
	425493 447641	AW363582 BE619186	Hs.75323	prohibijin gb:501472933F1 NIH_MGC_68 Homo sapiens c	9.0
10	403095	DC015100		Animatation Livid woo for unito salvers c	9.0 8.8
	407942	AA378608	Hs.5894	hypothetical protein FLJ 10305	8.8
	423126	AA322245	Hs.290165	ESTs	8.8
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	8.7
15	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.6
13	443647 401439	AV653846	Hs.126261	Homo sepiens Chromosome 16 BAC clone CIT	8.6
	449532	W74653	Hs.271593	ESTs	8.6 8.6
	453197	AI916269	Hs.109057	ESTs. Wealdy similar to ALUS_HUMAN ALU S	8.6
~~	448450	BE612490		gb:601451884F1 NIH_MGC_66 Homo sapiens c	8.5
20	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN T	8.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	8.4
	402921 428133	AW167727	Hs.11873	ESTs	8.4
	419503	AA243642	Hs.137422	ESTs	8.4 8.4
25	452644	AW452616	Hs.212481	ESTs	8.4
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	8.4
	409695	AA296961		gb:EST112514 Adrenal gland tumor Horno sa	8.3
	418076	R61388	Hs.6724	EST8	8.3
30	402695 423099	NM_002837	Hs.123641	amiala hanalaa ahaaahataan aasaataa	8.3
50	413998	AW103807	Hs.243933	protein tyrosine phosphatase, receptor t ESTs	8.3 8.2
	410008	AA079552	113.210000	gb:zm20h12.s1 Stratagene pancreas (93720	8.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	8.2
25	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	8.1
35	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	8.0
	413627 415713	BE182082	Hs.246973	ESTs	8.0
	426695	AW968573 AW118191	Hs.112729	gb:EST380649 MAGE resequences, MAGJ Homo ESTs	8.0 8.0
	452284	AW451426	Hs.252740	EST8	8.0
40	454933	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	8.0
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKF2p566A1046 (f	8.0
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-ternity C (CFTR	8.0
	444107	T46839	Hs.10319	UDP glycosyttransferase 2 family, polype	7.9
45	445740 433190	T78281 M26901	Hs.13226 Hs.3210	Homo sapiens clone 25181 mRNA sequence renin	7.9
	432777	AA564991	Hs.269477	ESTs	7.8 7.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxytic	7.7
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	7.7
50	434032	AW009951	Hs.206892	ESTs .	7.7
30	419750 439024	AL079741	Hs.183114	Homo sapiens cONA FLJ14236 fis, clone NT	7.6
	437205	R96696 AL110232	Hs.35598	ESTs gb:Homo sapiens mRNA; cDNA DKFZp564D2071	7.6 7.4
	446030	AF131805	Hs.13544	Homo sapiens clone 24850 mRNA sequence	7.4
	448311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.4
55	452883	X80031	Hs.150318	ESTs .	7.4
	448253	H25899	Hs.201591	ESTs	7.4
	406030 437084	AI911516	Hs.127811	FOT	7.4
	435013	H91923	Hs.110024	ESTs NACHUINIQUIDODO avidoroductoro MI PO exitu	7.3
60	432143	AL040183	Hs.123484	NADH:ubiquinone oxidoreductase MLRQ subu ESTs, Weakly similar to The KIAA0149 gen	7.3 7.3
-	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (93720	7.2
	425151	AA351814	Hs.298678	ESTs	7.2
	448582	A1538880	Hs.94812	EST6	7.2
65	455068 406504	AI807894	Hs.27910	centrosomal protein 2	7.2
02	428395	AA427992	Hs.104885	ESTE Weakly similar to sing force and	7.2
	421102	AI470093	Hs.89217	ESTs, Wealdy strattar to zinc finger prot ESTs	7.2 7.2
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	7.1
70	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	7.1
70	415084	M19267	Hs.77899	tropomyosin 1 (alpha)	7.0
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	7.0
	439416 420036	W58294 R60336	Hs.56254 Hs.52792	ESTS	6.9
	423349	AF010258	Hs.127428	Homo sapiens mRNA; cDNA DKFZp586(1823 (f homeo box A9	6.8 6.8
75	413070	AA126776	· ······ · · · · · · · · · · · · · · ·	gb:zn88c11.s1 Stratagene lung carcinoma	6.8
	449361	AW207890	Hs.201918	ESTs	6.8
	459309	AA040620	Hs.109144	ESTs	6.8
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.8
80	416462	W92845 AW591623	Un 4E44NA	gb:zh80f05.r1 Soares_fetal_liver_spleen_	6.8
50	447835 403563	W44321073	Hs.164129	ESTs	6.7 6.7
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	6.7 6.5
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	6.6

	455275	AW977806		ab-EST388810 MACS MACO Home	
	441350	AB020690	Hs.7782	gb:EST389810 MAGE resequences, MAGO Homo paraneoplastic antigen MA2	6.6 6.6
	445575	Z25368	Hs.172004	tiin	6.6
_	446075	AW451457	Hs.279179	ESTs	6.6
5	405963				6.6
	423049 436456	X59373	Hs.188023	ESTs cer-	6.6
	420273	AW292677 AI652864	Hs.65909 Hs.197257	ESTs ESTs	6.5 6.5
	420831	AA280824	Hs.190035	ESTs	6.4
10	423739	AA398155	Hs.97600	ESTs	6.4
	441559	AA938448	Hs.259733	ESTs	6.4
	433999	AA778212	Hs.191869	ESTs	6.4
	439703 433757	AF086538 AI949974	Hs.198245 Hs.152670	ESTs ESTs	6.4
15	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.3 6.3
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	6.3
	448515	H68441	Hs.13528	Homo sapiens cDNA FLJ14054 fts, clone HE	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	6.3
20	429357 404939	AA779725	Hs.164589	ESTs	6.3
20	417071	N58820	Hs.275133	ESTs	6.3 6.2
	436209	AW850417	Hs.254020	ESTs. Moderately similar to unnamed prot	8.2
	403111				6.2
25	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	6.2
2,5	442353 451110	BE379594 A1955040	Hs.49136 Hs.301584	ESTs ESTs	6.2
	420092	AAB14043	Hs.88045	ESTs	6.1 6.1
	441801	AW242799	Hs.211874	ESTs	6.0
20	407500	U43279		gb:Human nucleoporin nup 36 mRNA, comple	6.0
30	450864	R64139	Hs.205225	ESTs	6.0
	455711 405394	BE069465		gb:RC2-BT0388-290100-012-a11 BT0388 Homo	6.0
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	6.0 6.0
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sepiens c	6.0
35	414575	H11257	Hs.295233	ESTs	5.9
	435767	H73505	Hs.117874	ESTs	5.9
	445495 428372	BE622641 AK000684	Hs.38489 Hs.183887	ESTs hypothetical protein FLJ22104	5.9
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.9 5.9
40	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.9
	402421				5.8
	417038	T85230		gb:yd33f02.r1 Soares fetal liver spleen	5.8
	438461 440870	AW511956 AJ687284	Hs.293261 Hs.150539	ESTS	5.8
45	452281	T93500	Hs.28792	Homo sepiens cDNA FLJ13793 fis, clone TH Homo sepiens cDNA FLJ11041 fis, clone PL	5.8 5.8
	417280	AW173116	Hs.262206	ESTs	5.7
	437259	Al377755	Hs.120695	EST ₈	5.7
	425717	X07282	Hs.171495	retinoic acid receptor, beta	<b>5</b> .7
50	443614 450625	AV655386 AW970107	Hs.7645	fibrinogen, B beta polypeptide gb:EST382188 MAGE resequences, MAGK Horno	5.7
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	5.6 5.6
	430371	D87466	Hs.240112	KIAA0276 protein	5.6
	430499	AW969408	Hs.231991	ESTs .	5.6
55	427920	Z11502	Hs.181107	annexin A13	5.6
	449318 407864	AW236021 AF069291	Hs.108788 Hs.40539	ESTs, Weakly similar to zeste [D.melanog chromosome 8 open reading frame 1	5.6 5.5
	410754	T63840	16.4000	gb:yc16b10.s1 Strategene lung (937210) H	5.5 5.5
	415286	AW249540	Hs.72548	ESTs	5.5
60	443297	AI049864	Hs.133029	ESTs	5.5
50	440138 441006	AB033023 AW605267	Hs.6982 Hs.7627	hypothetical protein FLJ10201 CGI-60 protein	5.5
	409348	AI401535	Hs.146090	ESTs	5.4 5.4
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 ffs, clone HE	5.4
65	408938	AA059013	Hs.22607	ESTs	5.4
65	456411	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.4
	443756 422232	AW089799 D43945	Hs.153665 Hs.113274	ESTs	5.4
	424574	BE408618	Hs.150748	transcription factor EC malonyl-CoA decarboxylase	5.4 5.3
~~	424834	AK001432	Hs.153408		5.3
70	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKF2p434O1572 (f	5.3
	425782	U66468	Hs.159525		5.3
	450236 418110	AW162998 R43523	Hs.24684 Hs.217754	KIAA1376 protein Homo saplens cDNA: FLJ22202 fis, clone H	5.3
	427061	AB032971	Hs.173392		5.3 5.3
75	413841	M34276	Hs.75578	plasminogen	5.3 5.3
	432358	AI093491	Hs.72830	ESTs	5.2
	416805	F13271 W03856	Hs.79981	Human clone 23560 mRNA sequence	5.2
	438475 443305	WU3856 AI050693	Hs.13188 Hs.133318	ESTs, Highly similar to Gene product wit ESTs	5.2 5.2
80	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.2 5.1
	451859	H44491	Hs.252938	ESTs, Wealthy similar to ALU1_HUMAN ALU S	5.1
	429826	N93266	Hs.40747	ESTs	5.1
	436032	AA150797	Hs.109276	latexin protein	5.1

	447081	Y13896	Hs.17287	potassium inwardly-rectilying channel, s	5.1
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	5.1
5	440238	AW451970	Hs.155644	paired box gene 2	5.1
ر	426651 425813	AU076646 AA364138	Hs.171683 Hs.210553	nuclear receptor subtamily 1, group H, m ESTs, Weakly similar to hypothetical pro	5.0 5.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	5.0
	430682	AW971949	Hs.291252	ESTs	5.0
10	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo	5.0
10	429222 446317	AI457692	Hs.99164 Hs.150906	ESTS	5.0 5.0
	409506	AI287367 NM_006153	Hs.54589	ESTs NCK adaptor protein 1	5.0
	407768	AW002841	Hs.29475	ESTs	5.0
	437938	A1950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	5.0
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	4.9
	426215 448570	AW963419 AI923944	Hs.155223 Hs.30913	stanniocalcin 2 ESTs	4.9 4.9
	445034	AW293376	Hs.160323	ESTs	4.9
~~	410361	BE391804	Hs.62661	guarrylate binding protein 1, interferon-	4.8
20	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	4.8
	438492 446417	AW340048 AI299050	Hs.293188	ESTS	4.8
	409578	BE041386		gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens gb:hk88c02.x1 NCI_CGAP_Lu21 Homo sapiens	4.8 4.8
	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenytylsulfate:g	4.8
25	413795	AL040178	Hs.142003	ESTs	4.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	4.8
	452208 422711	AA024792 D60641	Hs.31895 Hs.21739	ESTs, Weakly similar to 89 [H.saplens] Homo sapiens mRNA; cDNA DKFZpS86I1S18 (f	4.7 4.7
	441392	AW451831	Hs.222119	ESTs. Wealthy similar to K1CQ_HUMAN KERAT	4.7
30	439221	AA737106	Hs.32250	ESTs	4.7
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.7
	417355 414700	D13168 H63202	Hs.82002 Hs.38163	endothelin receptor type 8 ESTs	4,7 4,7
	402739	7100202	113.50105	2318	4.6
35	403170				4.6
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	4.6
	408380 427899	AF123050 AA829286	Hs.44532 Hs.181062	diublquitin serum amyloid A1	4.6 4.5
_	446302	AI285848	Hs.149757	ESTs	4.5 4.5
40	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	4.4
	413384 421298	NM_000401 AW172431	Hs.75334 Hs.13012	exostoses (multiple) 2	4.4
	420789	AW172431 AI670057	Hs.199882	ESTs ESTs	4.4 4.4
45	453558	Al417023	Hs.40478	ESTs	4.4
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	4.4
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	4.4
	410334 457030	AW979261 Al301740	Hs.291993 Hs.173381	ESTs dihydropyrimidinase-like 2	4.4 4.4
50	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	4.3
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.3
	401157	05010202	U- 2004	alamatal annuals fortan annual sanctation	4,3
	432004 426866	BE018302 U02330	Hs.2894 Hs.172816	placental growth factor, vascular endoth neurogutin 1	4.3 4.3
55	446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	4.3
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	4.2
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.2
	433578 407065	BE336886 Y10141	Hs.3416	adipose differentiation-related protein gb:H.sapiens DAT1 gene, partial, VNTR.	4.2 4.2
60	407182	AA312551	Hs.230157	ESTs	4.2
	416565	AW000960	Hs.44970	ESTs	4.2
	442230	8E219088	Hs.279547	ESTs	4.2
	440680 413802	AA903098 AW964490	Hs.32241	gb:ok46f08.s1 NCI_CGAP_Lei2 Horno sapiens ESTs	4.2 4.2
65	438370	AA843242	Hs.48523	ESTS	4.2
-	432731	R31178	Hs.287820		4.2
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	4.2
	441484 411213	AA935481 AA676939	Hs.58972 Hs.69285	ESTs	4.2
70	453045	AW418979	Hs.224502	neuropilin 1 ESTs	4.2 4.2
	407999	Al126271	Hs.49433	ESTs. Wealdy similar to HYPOTHETICAL PRO	4.2
	409770	AW499536		gb:Ul-HF-BROp-aji-c-12-0-Ul.r1 NIH_MGC_5	4.1
	449856	AA203155	Hs.18200	ESTs	4.1
75	430808 412872	S69377 BE006341	Hs.247978	T-cell acute lymphocytic leukemia 2 gb:RC2-BN0127-240300-011-b05 BN0127 Homo	4,1
, 5	430719	AA488988	Hs.293798		4.1 4.1
	409637		Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	4.1
	414696		Hs.76918	Niemann-Pick disease, type C1	4.1
80	444670 448090		Hs.37494 Hs.270289	ESTs ESTs	4.1
50	408830		Hs.48403	hypothetical protein FLJ10847	4.1 4.1
	419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypept	4.1
	416555			BCL2/adenovirus E1B 19kD-interacting pro	4,1

	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	4.1
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	4.1
	459595	AL040421	11- 45-4073	gb:OKFZp434B0714_r1 434 (synonym: htes3)	4.1
5	438859 423279	AI559626 AW959861	Hs.164973 Hs.290943	ESTs, Wealtly similar to AF231024 1 proto	4.0
	441592	AW137071	Hs.127211	ESTs	4.0
	411836	AW901879	113.12/211	gb:QVO-NN1021-280400-212-110 NN1021 Homo	4.0
	426384	AI472078		gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	4.0 4.0
	412494	AL133900	Hs.792	ADP-ribosytation factor domain protein 1	4.0
10	413583	AL120806	Hs.5888	ESTs	4.0
	415610	L44319		gb:HUMEST1D10 Human thymus NSTH II Homo	4.0
	430009	AA894564	Hs.22242	ESTs	4.0
	449539	W80363	Hs.58446	ESTs .	4.0
	438929	AW195515	Hs.253177	ESTs	4.0
15	416000	R82342	Hs.79856	ESTs	4.0
	429616	AI982722	Hs.120845	EŞTs	4.0
	458471	AV648609	Hs.194240	ESTs .	4.0
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	4.0
20	459046	AA910339	Hs.26216	Homo sapiens cDNA: FLJ22811 fis, clone K	3.9
20	438177	BE327015	Hs.281391	ESTs	3.9
	422438	AA445925	Hs.270896	ESTs	3.9
	450382 449611	AA397658 AI970394	Hs.60257	Homo sapiens cDNA FLJ13598 fls, clone PL	3.9
	452030	AL137578	Hs.197075 Hs.27607	ESTs	3.9
25	452881	AW135220	Hs.241921	Homo sapiens mRNA; cDNA DKFZp564N2464 (f ESTs	3.9
	414729	BE466928	Hs.281901	ESTs	3.9
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.9
	405908			Same of the state of the s	3.9 3.8
	445452	H92975	Hs.246046	ESTs, Wealdy similar to RET1_HUMAN RETIN	3.8 3.8
30	447961	W32791	Hs.170405	ESTs	3.8
	446639	AI016826	Hs.132501	ESTs	3.8
	401189				3.8
	429548	AW138872	Hs.135288	ESTs	3.8
26	431523	N55759	Hs.163674	EST ₅	3.8
35	430014	H59354	Hs.182485	actinin, alpha 4	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	3.8
	437939	AW298600	Hs.141840	ESTs. Weakly similar to S59501 interfero	3.8
40	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.8
40	433522	AI821730	Hs.116524	ESTs	3.8
	443843 407305	AW878864	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	3.7
	434613	AA715284 AI821826	No 107700	gb:rv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.7
	410276	A1554545	Hs.187786 Hs.68301	ESTs, Moderately similar to ALUB_HUMAN !	3.7
45	422504	AA311407	715.00301	ESTs gb:EST182167 Jurkat T-cells V Homo sapie	3.7
••	421013	M62397	Hs.1345	mutated in colorectal cancers	3.7 3.7
	437949	U78519	Hs.41654	ESTs	3.7
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.7
	409446	AI561173	Hs.67688	ESTs	3.7
50	415263	AA948033	Hs.130853	ESTs	3.7
	450206	A1796450	Hs.201600	ESTs .	3.7
	439444	AJ277652	Hs.54578	ESTs	3.7
	437828	AW976806	Hs.291805	ESTs	3.7
55	453238	AA033991	Hs.269234	ESTs	3.7
33	420041	AB005142	Hs.94592	kiatho	3.7
	448458 435080	AW614367	Hs.171054	ESTs	3.7
	444249	AI831760 T87398	Hs.155111 Hs.205816	ESTs FCT-	3.7
	426595	AW971980	Hs.62402	ESTs p21/Cdc42/Rac1, activated binaria 1 (waret	3.7
60	417715	AW969587	Hs.86366	p21/Cdc42/Rac1-activated kinase 1 (yeast ESTs	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7 3.6
	440048	AA897461	Hs.158469	ESTs. Weakly similar to envelope protein	
	430091	AB032958	Hs.233023	KIAA1132 protein	3.6 3.6
	438030	X98427	Hs.122634	ESTs	3.6
65	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.6
	446638	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.6
	417860	AW408557	Hs.235498	Homo sapiens cDNA FLJ14075 fis, clone HE	3.6
	435794	H72108	Hs.13704	ESTs	3.6
70	449695	AA164569	Hs.34550	ESTs	3.6
70	411485	AW848125		gb:IL3-CT0214-301299-048-G04 CT0214 Homo	3.6
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	3.6
	458201	A/989961	Hs.233477	ESTs, Moderately similar to A Chain A, S	3.6
	440987 425178	AA911705	Hs.130229	EST ₆	3.6
75	419080	H16097 AW150835	Hs.161027 Hs.18878	ESTs	3.6
	436091	AA704705	Hs.181044	hypothetical protein FLJ21620	3.6
	452671	AW861074	Hs.225833	ESTs, Wealdy similar to A Chain A, Human ESTs	3.6
	437222	AL117588	Hs.299963	EST\$	3.6
00	437809	AL137723	Hs.5855	Homo sapiens mRNA; cDNA DKFZp434D0818 (f	3.6
80	411545	AW850818		gb:IL3-CT0220-091199-026-A03 CT0220 Homo	3.5 3.5
	414799	AJ752416	Hs.77326	insufin-like growth factor binding prote	3.5
	439882	AA847856	Hs.124565	ESTs	3.5
	419229	AJ827237	Hs.282884	ESTs .	3.5
					3.0

	431889	AA521277	Hs.124945	ESTs ESTs	3.5
	422660 415122	AW297582 D60708	Hs.237062 Hs.22245	ESTS	3.5 3.5
_	444127	N63620	Hs.13281	ESTs	3.5
5	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	409044	AI129586	Hs.33033	ESTs ESTs	3.5
	453365 452355	AA035211 N54926	Hs.17404 Hs.29202	G protein-coupled receptor 34	3.5 3.5
	423246	AL119114	Hs.23107	ESTs	3.5
10	434131	AI858275	Hs.143659	ESTs	3.5
	425304	AA463844	Hs.31339	fibroblast growth factor 11	3.5
	453775 426559	NM_002916 AB001914	Hs.35120 Hs.170414	replication factor C (activator 1) 4 (37 paired basic amino acid cleaving system	3.4 3.4
	456311	AA225632	Hs.190016	ESTs	3.4
15	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfami	3.4
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	3.4
	401811 404021				3.4 3.4
	447175	AI365208	Hs.293606	ESTs	3.4
20	453743	AL120480		gb:DKFZp761K098_r1 761 (synonym: hamy2)	3.4
	455070	AW854675		gb:MR1-CT0258-290300-206-a01 CT0258 Homo	3.4
	419548 449441	AA244199 Al656040	Hs.196532	gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sepiens ESTs	3.4 3.4
	441606	R37263	Hs.21065	ESTs	3.4
25	446594	Al311917	Hs.16292	ESTs	3.4
	424664	Al432572	Hs.164221	ESTs	3.4
	413719 427914	BE439580 AA417350	Hs.75498 Hs.20575	small inducible cytokine subfamily A (Cy ESTs	3.4
	438257	AW474419	Hs.224794	ESTs	3.4 3.4
30	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoletin A;	3.4
	454690	AW854639		gb:MR1-CT0258-140100-203-d10 CT0258 Homo	3.3
	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	3.3
	407331 440472	AJ570416 AA886169	Hs.99910 Hs.169071	phosphofructokinase, platelet ESTs	3.3 3.3
35	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.3
	403797				3.3
	417924	AU077231 AW958932	Hs.82932 Hs.293833	cyclin D1 (PRAD1: parathyroid adenomatos	3.3
	410623 449338	H73444	Hs.394	ESTs adrenomedullin	3.3 3.3
40	441024	AW081530	Hs.137088	ESTs	3.3
	405257				3.3
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	3.3
	416892 444471	L24498 AB020684	Hs.80409 Hs.11217	growth arrest and DNA-damage-inducible, KIAA0877 protein	3.3 3.3
45	431589	AA305688	Hs.267695	UOP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.3
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	3.3
	425236	AW067800	Hs.155223	stanniocalcin 2	3.3
	428824 450101	W23624 AV649989	Hs.173059 Hs.24385	ESTs Human hbc647 mRNA sequence	3.2 3.2
50	425260	L47726	Hs.1870	phenylalanine hydroxylase	3.2
	443830	AI142095	Hs.143273		3.2
	415245	N59650	Hs.27252	ESTs	3.2
	405953 430812	L10405	Hs.247992	DNA binding protein for surfactant prote	3.2 3.2
55	418946	A1798841	Hs.132103		3.2
	424750	D29956	Hs.152818		3.2
	435342	AW979168	Hs.163270		3.2
	458860 430172	AW873557 AA468591	Hs.212739 Hs.161889		3.2 3.2
60	431842	NM_005764			3.2
	451221	AI949701	Hs.210589		3.2
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	3.2
	433727 424897	C16221 D63216	Hs.112608 Hs.153684		3.2 3.2
65	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.1
	418030	BE207573	Hs.83321	neuromedin B	3.1
	417919	AP928203	Hs.86379	ESTs	3.1
	430437 409663	AI768801 AI743750	Hs.169943 Hs.65862		3.1
70	454024	AA993527	Hs.16281	ESTs hypothetical protein FLJ23403	3.1 3.1
	424980	L42172	Hs.154078		3.1
	421633	AF121860	Hs.106260	sorting nextin 10	3.1
	436002	R68529	Hs.120967		3.1
75	437682 439451	AA476652 AF086270	Hs.94952 Hs.278554	Homo sapiens cDNA: FLJ23371 fis, ctone H heterochromatin-like protein 1	3.1 3.1
. •	430183			gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.1
	428479	Y00272	Hs.184577	cell division cycle 2, G1 to S and G2 to	3.1
	441285		4 Hs.167	microtubute-associated protein 2	3.1
80	456386 451130		Hs.211347	gb:47e1 Human retina cDNA randomly prime 7 ESTs	3.1
	439702				3,1 3,1
	453331	AJ240665	Hs.6895	ESTs	3.1
	428841	AI418430	Hs.10493	5 ESTs	3.1

	449899	AI610700	Hs.103280	ESTs	3.1
	436009	H57130	Hs.120925	ESTs	3.1
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clone HE	3.1
5	408239 418526	AA053401	Hs.271827 Hs.85838	ESTs. Moderately similar to ALU7_HUMAN A	3.1
,	401260	9E019020	NS.03030	solute carrier tamily 16 (monocarboxylic	3.1 3.1
	450705	U90304	Hs.25351	iroquois-class homeodomain protein	3.1
	447233	AW246333	Hs.17901	Homo sapiens cONA: FLJ21974 fis, clone H	3.1
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	3.0
10	403346			, , , , , , , , , , , , , , , , , , , ,	3.0
	446319	AW207590	Hs.160711	ESTs	3.0
	432757	AF113013	Hs.278919	PRO0806 protein	• 3.0
	407921	AJ378617	Hs.23100	Homo sapiens cDNA FLJ12592 fis, clone NT	3.0
15	414618	AJ204600	Hs.96978	EST6	3.0
13	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	440113 424539	AI916532 L02911	Hs.188272 Hs.150402	ESTs activin A receptor, type I	3.0 3.0
	428945	AW192803	Hs.98974	ESTs	3.0
	458297	R54033	Hs.21245	ESTs	3.0
20	424405	AJ076838	Hs.12967	ESTs	3.0
	411290	AW835544		gb:QV4-LT0016-271299-068-f03 LT0016 Homo	3.0
	459068	BE464396	Hs.118468	EST8	3.0
	459065	AI373532	Hs.157910	ESTs	3.0
25	437693	AJ754443	Hs.185951	ESTs	3.0
23	429418 406117	AJ381028	Hs.99283	ESTa	3.0
	415492	R41674	Hs.16491	ESTs	3.0
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RPS-1087M19 from	3.0 3.0
	453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (f	3.0
30	408119	W26213		gb: 22d 10 Human retina cDNA randomly prim	3.0
	438358	AL035992	Hs.210278	ESTs	3.0
	412372	R65998	Hs.118615	ESTs	3.0
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256022	3.0
35	403782				3.0
23	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.0
	456388 447922	W28557 Z92910	Hs.20019	gb:48d8 Human retina cDNA randomly prime	3.0
	428857	AF008192	Hs.194283	hemochromatosis putetive GR6 protein	3.0 3.0
	406991	582185	14.137200	(NONE)	3.0
40	432596	AJ224741	Hs.278461	matrilin 3	3.0
	453202	AW085781	Hs.26270	Homo sapiens cDNA FLJ11588 fis, clone HE	3.0
	414132	AI801235	Hs.48480	ESTs	3.0
	409122	W07089	Hs.297873	ESTs	3.0
45	405547				3.0
43	422219	AW978073	11-404004	gb:EST390182 MAGE resequences, MAGO Homo	3.0
	417227 448592	T57776 N69546	Hs.191094 Hs.141706	ESTs ESTs	3.0
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.0 3.0
	400368	BE779978	Hs.69149	proline-serine-threonine phosphatase int	3.0
50	455362	AW902635		gb:QV3-NN1024-100500-181-b02 NN1024 Harmo	3.0
	443578	R97191	Hs.134106	ESTs	3.0
	419348	AA236645	Hs.98274	ESTs	3.0
	439138	A1742605	Hs.193696	EST8	3.0
55	449547	H93543	Hs.117963	ESTS	3.0
33	455180 444228	AW863503 AV648612	Hs.282396	gb:MR3-SN0009-180400-110-c12 SN0009 Homo	3.0
	423498	U91963	Hs.129700	ESTs tolloid-like 1	3.0 3.0
	401707	031300	113.123700	wildering i	3.0
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	3.0
60	441677	AW271702	Hs.93739	ESTs	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH .	3.0
	431311	AA502552	Hs.188980	ESTs	3.0
	426326	BE165753	Hs.250528	ESTs, Weakly similar to unnamed protein	3.0
65	412685 414752	BE092186 BE503505	N= 340000	gb:IL2-BT0734-200400-075-H05 BT0734 Homa	3.0
03	403144	05303303	Hs.248689	ESTs	3.0
	407539	X91103		gb:H.sapiens mRNA for Hr44 protein.	3.0 3.0
	412379	AW947581		gb:RC0-MT0004-140300-031-d08 MT0004 Homo	3.0
	407937	AW297944	Hs.242811	ESTs	3.0
70	456976	AI681882	Hs.270428	ESTs	3.0
	417066	AA329572	Hs.172004	tiin	3.0
	406007	177744	11- 4545-	PAT.	3.0
	416940	N75620	Hs.43157	ESTs	3.0
75	433322 406088	H50621	Hs.134156	ESTs	3.0
	416573	R10356	Hs.18865	ESTe Weekly similar to ACCOTTOR 2 DC272	3.0
	423130	AW897586	Hs.21213	ESTs, Weakly similar to AC007228 2 BC372 ESTs	3.0 3.0
	412721	AW183165	Hs.95600	ESTs	3.0
00	418375	NM_003081		synaptosomal-associated protein, 25kD	3.0
80	422992	AF016833	Hs.122785		3.0
	406506				3.0
	413472	BE242870	Hs.75379	solute carrier family 1 (glizi high affi	3.0
	422650	D42055	Hs.1565	neural precursor cell expressed, develop	3.0



	400325	M85292	Hs.247924	Homo sepiens endogenous HIV-1 related	S8	3.0
	401078					3.0
	445645 445704	AI336596 AI337228	Hs.156294 Hs.197083	ESTs ESTs		3.0
5	427072	H38046		gb:yp58c10.r1 Soares fetal liver spleen		3.0 3.0
		_	• •			··
	TABLE 339		- Pao	d Martifes assets		
	Pkey: CAT numb		e Eos proces cluster numb	st identifier number er		
10	Accession:		ank accession			
	Okaz	CAT aumbar	Annerica			
	Pkey 407615	CAT number 1005404_1	Accession AW753085	AW753082 AW054744 AW753107 AW7530	187	
1.0	408119	1040172_1	W26213 HO	8055 Z44031 AW964559 R17434	· <del>··</del>	
15	409519	113722_1	AA075368 A			
	409578 409594	1140976_1 114249_1		.W419449 AW663595 .A975618 AA076220		
	409695	114876_1		A296889 AAD76945 AA077528 AA077497		
20	409745	115237_1				833 AA 150722 BE 152353 AW 188822 BE 152450
20	409770 410008	1154048_1 116812_1		AW499553 AW502138 AW499537 AW502 BE142525 BE142527	136 AW501743	
	410049	1172307_1		AW939654 AW939655		
	410534	1207247_1	AW905138	AW753008 R13818 Z43519		
25	410754 411290	1219733_1 1237738_1		801569 AW801568 AMBRITAN	2012 DEDOOESE DEDOOSSOO AS	4405 1747101 4414040175 414040174 414040777 414040707
22	411230	123/130_1		AW848693 BE350771	103 86092333 86092199 41	1485 1247181_1AW848125 AW848124 AW848203 AW848695
	411545	1249138_1	AW850818	AW850833 AW851100		
	41 1836 41 2209	1260619_1 1283610_1		AW901875 AW866247 BE011294 BE5048	13	
30	412359	129085_1		AW901450 AW901441 AW837938 AA101955 AW837913 AW837!	135	•
	412379	1292479_1	AW947581	AW947546 AW947545 AW947544	•	
	412685 412872	1321663_1		BE092157 AW983859		
	413070	1333898_1 134815_1		BE006307 BE006311 AA133984 BE148613 BE063475 AA35821!	•	
35	415610	1540554_1		2851 T75057		
	415713 416462	154859_1		AA167225 AA491129		
	416548	1595954_1 1600181_1	W92845 H	6608 N72413		
40	416913	163001_1		BE161007 BE162500 AW749902 AW7498	64 BE162498 BE161005 AA	.190449 AW513465 BE161006 BE162499
40	417038	164390_1		192508 T89190		
	418053 419213	171810_1 182860_1		AW817839 AW817836 AW749138 AW749123 AW749130 AA235	142	
	419546	185766_1		AA244272 H57440	146	
45	420637	195241_1		AA278945 AA747691	_	
43	422063 422219	210852_1 213547_1		BE156473 BE156474 BE156475 AA30283 AW978072 AA807550 AA306567	9	
	422504	217160_1		AW958321 N23583 R70050		
	423735	231498_1		AA561806 AA502431 AW974633 AA6494	96	
50	426384 427072	266211_1 274884_1		AA377209 AA865807 69645 AA397968 H38047		
•	428637	293660_1		AA878419 AA431342 AA431628		
	430183	31412_2			84393 BE064394 BE157228	BE183282 AI936370 AA552514 T67280 AA039909
	431595 432009	335512_1 34025_1		BE142920 AI280311 AI205616 D61709 BE007148 T52277		
55	437205	43463_1	AL110232	N94765		
	437938	44573_2	A1950087	N70208 R97040 N36809 Al308119 AW967	677 N35320 Al251473 H593	97 AW971573 R97278 W01059 AW967671 AA908598 AA251875
						AA884922 BE328517 Al219788 AA884444 N92578 F13493 AA927794 283144 Al890387 Al950344 Al741346 Al689062 AA282915 AW102898
<i>c</i> 0						892 Al356394 AW103813 Al539642 AA642789 AA856975 AW505512
60			AI961530	AW629970 BE612881 AWZ76997 AW5136	01 AW512843 AA044209 A	N856538 AA180009 AA337499 AW961101 AA251669 AA251874
						1741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 173032 Al564269 F00531 H83488 W37181 W78802 R66056 Al002839
				A300207 AW959581 T63226 F04005	VV3 1140101 A1141414141414	13002 ABONEUS I (1035) 1100-400 113/101 11/10002 NOOCOOS
65	438966	467436_1		AA834841 AA828650		
05	438993 440680	467651_1 500121_1		AA834879 A1926361 AW836693 BE160824 AW606818 AW582	500 AW836768	
	442438	542469_1		Al916584 R61781 T77332 F07756 F0814		
	446346			AW235762 AI651268		
70	446417 447641	676384_1 73043_1		BE256910 5 BE264952 R26042		
, ,	448450	76399_1		T05205 AA481187		
	449034	794817_1	AJ624049	AW117770 AI858360		
	450625 452453	84032_1 918300_1		7 AA513951 AA010406 AI902518 AI902516		
75	453743	979613_1		AW836448 AW176802		
	453955	989877_1	AW57920	7 AW936883 AW008026 N88905		
	454392 454490	115882_1 1217172_1		) AA078319 R85057 AWB03024 H85811 A 8 AW797781 A <b>W7</b> 97780	A078293	
	454690	1229106_1			4692 BE145866 AW816154	AW854698 AW854654 AW813335 AW854699
80	454933	1245515_1	BE14171	I AW845993 AW845989		
	455070 455180	1252209_1 1258558_1	AW85467	5 AW854685 AW854716 AW854690 AW85 3 AW863362	4515 AW854624 AW85462	AW854641 AW854632 AW854695 AW854661
	455275	1272255_1		3 AW863362 6 AW887923 AW886321		
		-				

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	455362	1284507_1	AW902635 AV	N902574 BE011167 RE	011329 AW902808 AW902651		
	455711	1352369_1			0110LD A1100LL00		
	456386	18426931					
_	456388	18428391	W28557				
5	456411	185688_1		.244095 AA244183			
	459587	94893_1	AA031956				
	459595	969956_1	AL040421				
10	TABLE 330						
10	Pkey:			sponding to an Eos pro		(CI) ambam. Which we start when to the middle control of	D- 014
	Ref:				is column are Gentalik identible: im, et al. (1999) <u>Nature</u> 402:489-	(GI) numbers. "Dunham, et al." refers to the publication entitled "	I MB CAVA
	Strand:			d from which exons were		730.	
	Nt_position			positions of predicted en			
15				p-0 0- p-0 0-			
	Pkey	Ref	Strand	Nt_position			
	401078	3687273	Plus	105052-105171			
	401157	9438289	Minus	114133-114247,11456	7-114645		
20	401189	9690246	Minus	90815-90929			
20	401260	8076883	Minus	86008-86355			•
	401352 401439	9931258	Minus Plus	26064-26208 92993-94026			
	401707	8246737 2951946	Plus	21972-22104			
	401811	6730720	Ptus	107002-107209			
25	401976	3095020	Minus	17594-17709,21068-2	1175		
	402045	7923943	Plus	5964-6128			
	402421	9796341	Minus	46609-46662,46758-4	5811,86293-86346,89776-89829	),90048-90101,102817-102924	
	402696	7328818	Minus	23600-23731			
20	402739	9212192	Plus	60456-61019			
30	402921	7981303	Minus		5858,57124-57309,59633-59761	1,59957-60123	
	403095 403111	8954339	Phrs	150025-150240,15156	4-151690		
	403111	8980970 9454549	Plus Minus	175012-175159 166200-166628			
	403170	9838134	Plus	40955-41356			
35	403345	8569726	Plus	77890-78069			
,	403346	8569726	Plus	92752-93015			
	403563	8101139	Plus	2800-3501			
	403622	8569879	Plus	1941-2388,2580-2761			
40	4037B2	8078608	Plus	41326-41633			
40	403797	8099896	Minus	123065-125008			
	403899 404021	7381715 8655968	Minus	9144-9350			
	404115	9621489	Plus Plus	192534-193489 232707-232982			
	404200	6010176	Minus	7068-7210			
45	404347	9838195	Plus	74493-74829			
	404939	6862697	Plus	175318-175476			
	405257	7329310	Plus	73121-73273			
	405336	6094635	Ptus	33267-33563			
50	405394	6624123	Minus	31900-32373			
30	405547 405609	1054740	Plus	124361-124520,1249		** 47015 40010 40051 50157 51674 51777 51877 51860 57707 6	2010 55400
	400009	5757553	Minus		i8169-58296,6021 <b>5-60332</b> ,6148	i4,47815-48018,49961-50153,51624-51727,51823-51959,52702-5 12.61777	2310,33403-
	405908	6758795	Plus	97969-98715	0105-30250,00213-00332,01-0	2-01727	
	405943	6758796	Plus	20605-20812			
55	405953	7960374	Minus	65101-65574			
	405963	8247786	Plus	4056-4699			
	406007	8247802	Minus	13484-13829		•	
	406030 406088	8312328	Minus	96123-96547			
60	406117	9123919 9142932	Minus Plus	65772-66270 54304-54584			
	406242	7417725	Minus	36736-36951			
	406291	5686274	Phrs	9562-9867			
	406411	9256407	Plus	7400-7527			
	406414	9256407	Plus	49593-49850			
65	406504	7711360		107068-107277			
	406506	7711374		6843-8077			
	406598	8248514	Plus	56373-56849			
70	TADIE	MA. ADOUT	107 CENEC NO	REGULATED IN KIDNEY	CANCED		
, 0						s that are likely to be extracellular or cell-surface proteins. These	wore selected as for
	Table 33	A and the o	redicted orotein co	ntained a structural dom	ain that is indicative of extraceth	der localization (e.g. ig. In3, egf, 7tm domains). Predicted protein	domains are noted.
	Pkey:			sel identifier number		non vacacata (a.g. ig. mat agit tall administration to comme promise	
	ExAccn;			ion number, Genbank at	cession number		
75	Unigene	ID:	Unigene number				
	Unigene	Title:	Unigene gene title				
	PSDom	ain:	Protein Structural				
	R1:		Ratio of tumor to	normal tissue			
80	Di	E 4	6 hala a 10	1 Unione Title	Den'-	•	
60	Pkey 421471	ExAcch U90545			PSDomain TM,SS	R1 1007.4	
	452401	NM_00			TM,SS,XIink,CUB	336.4	
	421727				TM,SS,Monooxygenase		•
				•	204		

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	426471	M22440	Hs.170009	transforming gr	TM,SS,EGF	224.6
	441031	Al110684	Hs.7645	fibrinogen, B b	fibrinogen_C	174.0
	411642	NM_014932	Hs.71132	neuroligin 1	TM,SS,COesterase	172.4
_	452838	U65011	Hs.30743	preferentially	TM	161.4
5	425984	AW836277	Hs.165636	hypothetical pr	TM	151.0
	453165	S74727	Hs.32042	aspartoacylase	TM	134.8
	452431	U88879	Hs.29499	toll-like recep	TIM, SS, TIR, LRRCT	130.6
	423508	AW604297	Hs.129711	hepatitis A vir	TM,SS.ig	120.4
10	407975	X89426	Hs.41716	endothelial cel	SSJGFBP	111.8
10	415076	NM_000857	Hs.77890	guanylate cycla	TM.guanylate_cyc	97.0
	447046	AA326187	Hs.17170	G protein-coupl	TM,7tm_1	90.2
	423109 422544	M59305	Hs.123655	natriuretic pep	TM,SS,ANF_receptor	78.0
	429352	AB018259	Hs.118140	KIAA0716 gene p	TM	74.8
15	453392	AK001512	Hs.200097	hypothetical pr	TM	73.0
15		U23752	Hs.32964	SRY (sex determ	TM.HMG_box	72.2
	403345 430440	X52599	Hs.2561		TM,alpha-amylase	69.6
	408509	AA330431	Hs.640	nerve growth fa	TM,SS,NGF	69.0
	449101	AA205847	Hs.23016	calcitonin rece	TM,SS,7tm_2	57.4
20	423685	BE350494		G protein-coupl	TM,7tm_1	52.0
20	452891	N75582	Hs.49753 Hs.212875	Homo sapiens mR	TM,Myosin_tail	48.0
	408430	S79876	Hs.44926	ESTs, Weakly si	SS	44.0
	419287	X91906	Hs.89872	dipeptidylpepti	TM,SS,DPPIV_N_term,Peptidase_S9	42.6
	428822	W28418	Hs.301148	chloride channe	TM,C8S,vollage_CLC	40.6
25	434208	T92641	Hs.127648	potassium volta	TM TMLSS	40.2
	400792	AA635062	Hs.50094	hypothetical pr Homo sepiens mR		39.2
	444743	AA045648	Hs.11817		TMBIR CARD 21-C3HC4	38.6
	406411	74104040	110.11017	nudix (nucleosi	TM,mut7	38.4
	423657	AL045128	Hs.1691	glucan (1,4-alp	TM, wa.FG-GAP	37.6
30	424871	NM_004525	Hs.153595	low density lip	TM,alpha-amylase TM,SS,EGF,ldl_recept_a,ldl_recept_b	37.5
	449625	NM_014253	Hs.23796	odz (odd Oz/ten	SH2,EGF	32.8
	423020	AA383092	Hs.1608	replication pro	TM	30.5
	422420	U03398	Hs.1524	tumor necrosis	TMTNF	29.6 29.6
	414245	8E148072	Hs.75850	WAS protein fam	TM,WH2	28.8
35	410247	AF181721	Hs.61345	RU2S	TM	
	406414			***************************************	TM, wa, FG-GAP	27.4 27.2
	435951	AF269162	Hs.41267	c21orf7 form A-	TM	27.2
	419948	AB041035	Hs.93847	NADPH oxidase 4	TM,SS,Ferric_reduct	26.4
	448595	AB014544	Hs.21572	KIAA0644 gene p	TM.SS.LRRCT.URR	25.8
40	419569	AJ971651	Hs.91143	jagged 1 (Alagi	TM,SS,OSL,EGF	25.6
	433242	AB040938	Hs.113940	KIAA1505 protei	SS	25.6
	416778	M16505	Hs.79876	steroid sulfata	TM, Sulfatase	23.0
	401352				TM	22.6
	404200				SS	19.6
45	446591	H44186	Hs.15456	PDZ domain cont	TM,POZ	19.2
	431806	AF186114	Hs.270737	tumor necrosis	TMSS	18.0
	423909	AJ223183	Hs.135194	immunoglobulin	TM,SS,ig	17.6
	446364	AB006624	Hs.14912	KIAA0286 protei	TM	17.4
60	425695	NM_005401	Hs.159238	protein tyrosin	TM,Band_41,Y_phosphatase	17.0
50	410947	AK000305	Hs.67055	hypothetical pr	TM	16.8
	421002	AF116030	Hs.100932	transcription f	TM,KRAB,zf-C2H2	16.5
	421659	NM_014459	Hs.106511	protocadherin 1	TM,\$S,cadherin	16.0
	458679	AW975460	Hs.143563	ESTs	SS	14.4
55	406598			_	SS	13.6
33	428508	BE252383	Hs. 184668	SBBIJ1 protein	TM,PX	13.2
	423321	AB013885	Hs.126926	beta-ureidoprop	TM,SS,CN_hydrolase	12.5
	422317	NM_001147	Hs.115181	angiopoletin 2	fibrinogen_C	12.2
	428227	AA321649	Hs.2248	small inducible	IL8	12.0
60	414923	AW445008	Hs.77637	homeo box A4	TM,homeobox	11.9
00	433231 443672	AB040926	Hs.143552	KIAA1493 protei	SS.	11.6
	405609	AA323362	Hs.9667	butyrobetaine (	TM	11.4
	418912	NM_000685	Hs.89472		TM.Myosin_tail,myosin_head	11.4
	449802	AW901804		angiotensin rec	TM,7tm_1	11.4
65	404347	ATTOUR	Hs.23984	hypothetical pr	TM	11.2
Ų,	429945	NM_006729	Hs.226483	diaphanous (Oro	SS	10.8
	435085	AW130284			TM,FH2	10.6
	404115	ATT 100204	Hs.192752	ESTs, Moderatel	TM	10.6
	420757	X78592	Hs.99915		SS	10.2
70	446298	AF187813	Hs.14637	androgen recept kidney- and fiv	TM.Androgen_recep,hormone_rec,zf-C4	10.2
. •	433703	AA210863	Hs.3532	nemo-like kinas	TM_Acetyltransf	10.1
	417404	NM_007350	Hs.82101	pleckstrin homo	TM.pkinase	9.2
	451621	AI879148	Hs.26770	fatty acid bind	TM TM SS licensus	9.2
	402045			any and this	TM.SS.lipocalin	9.2
75	403095				TM,SS SS DAY homoshou	9.0
-	401439				SS.PAX.homeobox TM	8.8
	407721	Y12735	Hs.38018	dual-specificit	7M.pkinase	8.6
	402921				TM	8.4 8.4
	419503	AA243642	Hs.137422	ESTs	TM	8.4 8.4
80	452259	AA317439	Hs.28707	signal sequence	TM ·	8.4
	402696				TM	8.3
	450001	NM_001044	Hs.406	solute carrier	TM,SS,SNF	8.1
	433190	M26901	Hs.3210	renin	SS,æp	7.8
	•					7.0

	449444	AW818436	Hs.23590	solute carrier	TM,MCT	7.7
	444042	NM_004915	Hs.10237	ATP-binding cas	TM_ABC_tran	7.7
	452883	X80031	Hs.150318	ESTs	TM,C4,Collagen	7.4
5	425151 455068	AA351814	Hs.298678	ESTs	TM	7.2
,	406504	AI807894	Hs.27910	centrosomal pro	TMSS	7.2
	410274	AA381807	Hs.61762	because had all	TM	7.2
	423349	AF010258	Hs.127428	hypoxia-inducib homeo box A9	SS TM.horneobox	7.0
	408771	AW732573	Hs.47584	polassium volta	TM,K_tetra.ion_trans	6.8 6.8
10	445575	Z25368	Hs.172004	6tin	TM	6.6
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) ang	TM, SS, fibrinogen_C	6.3
	404939				TM	6.3
15	436209	AW850417	Hs.254020	ESTs, Moderatel	TM,SS	6.2
15	403111				TM	6.2
	405394				TM	6.0
	454392	8E260893	11. 70040	gb:601150677F1	TM,SS	6.0
	415910 402421	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.9
20	425717	X07282	Ma 471400	antinata antid a	TM	5.8
	427920	Z11502	Hs.171495 Hs.181107	retinoic acid r ennexin A13	TM.hormone_rec,zf-C4	5.7
	407864	AF069291	Hs.40539	chromosome 8 op	TM, annexin TM, FHA, BRCT	5.6
	441006	AW605267	Hs.7627	CGI-60 protein	TM	5.5 5.4
	422232	D43945	Hs.113274	transcription f	TMLHLH	5.4
25	425782	U66468	Hs.159525	cell growth reg	SS	5.3
	450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	5.3
	413841	M34276	Hs.75576	plasminogen	SS, trypsin, kringte, PAN	5.3
	436032	AA150797	Hs_109276	latexin protein	TM	5.1
30	447081	Y13896	Hs.17287	potassium inwar	TM,IRK	5.1
30	421126	M74587	Hs.102122	insulin-like gr	SS,thyroglobulin_1,IGFBP	5.1
	426651	AU076646	Hs.171683	nuclear recepto	TM,zf-C4,hormone_rec	5.0
	432328 409506	AI572739	Hs.195471 Hs.54589	6-phosphofructo	TM,6PF2K,PGAM	5.0
	410361	NM_006153 BE391804	Hs.62661	NCK adaptor pro	TM,SH2,SH3	5.0
35	453891	AB037751	Hs.36353	guanytate bindi Homo sapiens mR	TM,SS,GBP TM	4.8
	447269	NM_004861	Hs.17958	cerebroside (3"	TM,SS	4.8 4.8
	422357	AF016272	Hs.115418	cadherin 16, KS	TM.cadherin	4.8
	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zf-C3HC4	4.7
40	402739				SS	4.6
40	443486	NM_003428	Hs.9450	zinc finger pro	TM,KRAB,zf-C2H2	4.6
	408380	AF123050	Hs.44532	diubiquitin	TM.ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	4.6
	414812	X72755	Hs.77367	monokine induce	SS,IL8	4.4
	424063	NM_002019	Hs.138671	fms-related tyr	TM,SS,pkinase,ig	4.4
45	413384	NM_000401	Hs.75334	exostoses (mult	TM	4.4
73	457030 410407	AJ301740 X66839	Hs.173381	dihydropyrimidi	TM,SS,Dihydroorotase	4.4
	401157	V00023	Hs.63287	carbonic anhydr	TM,SS,carb_anhydrase	4.3
	432004	BE018302	Hs.2894	placental growt	TM,citrate_synt SS,POGF	4.3
	424704	AI263293	Hs.152096	cytochrome P450	SS,P450	4.3 4.2
50	407065	Y10141	115.152050	gb:H.sapiens DA	TM,SS,SNF	4.2
	411213	AA676939	Hs.69285	neuropilia 1	TM,CUB,F5_F8_type_C,MAM	4.2
	430806	S69377	Hs.247978	T-cell acute ly	TM.HLH	4.1
	414598	AF002020	Hs.76918	Niemann-Pick di	TM,SS,Patched	4.1
66	408830	AK001709	Hs.48403	hypothetical pr	TM,UPF0013	4.1
55	416655	AW968613	H\$.7942B	BCL2/adenovirus	TM	4.1
	412494	AL133900	Hs.792	ADP-ribosylatio	TM,arf,zf-8_box,zf-C3HC4	4.0
	453195	BE241876	Hs.32352	hypothetical pr	TM	4.0
	428816 401189	AA004986	Hs.193852	ATP-binding cas	TM,ABC_membrane,ABC_tran,COX15-CtaA	3.9
60	451988	AF263928	15- 27410		TM,SET,PHD,HMG_box	3.8
-	421013	M62397	Hs.27410 Hs.1345	papillomavirus mutated in colo	TM TM	3.8
	420041	AB005142	Hs.94592	kietha	TM TM,SS,Glyco_hydro_1	3.7 3.7
	432579	AF043244	Hs.278439	nucleotar prote	TM,33,GyCC_nydrO_1	3.7 3.6
	453496	AA442103	Hs.33084	solute carrier	TMLSS.sugar_tr	3.6
65	446636	AC002563	Hs. 15767	citron (rho-int	TM,CNH,DAG_PE-bind,PH,pkinase,pkinase_C	3.6
	426274	D38122	Hs.2007	tumor necrosis	TM,TNF	3.6
	452355	N54926	Hs.29202	G protein-coupt	TM,7tm_1	3.5
	453775	NM_002916	Hs.35120	replication (ac	TM,SS,AAA	3.4
70	426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S8,P	3.4
70	420737	£08096	Hs.99899	turnor necrosis	TM,TNF	3.4
	448733	NM_005629	Hs.187958	solute carrier	TM.SNF.ABC_tran.isodh.pkinase,Ribosomal_L18ae	3.4
	413719	BE439580	Hs.75498	small inducible	SS,IL8	3.4
	427914 412642	AA417350	Hs.20575	ESTs	TM,GAS2	3.4
75		BE244598	Hs.809	hepatocyte grow	kringle,PAN,trypsin	3.4
	421893 417924	NM_001078 AU077231	Hs.109225	vascular cell a	TM,SS,ig	3.3
	405257	noviizi	Hs.82932	cyclin D1 (PRAD	TM,cyclin	3.3
	450396	AU077002	Hs.24950	regulator of G-	TM TM,RGS	3.3
	416892	L24498	Hs.80409	growth arrest a	TM,Ribosomal_L7Ae	3.3
80	425236	AW067800	Hs.155223	stanniocalcin 2	SS S	3.3 3.3
	430812	L10405	Hs.247992	DNA binding pro	TM,SS	3.2
	431842	NM_005764	Hs.271473	epithelial prot	TMSS	3.2
	424897	D63216	Hs.153684	frizzled-relate	TM,Fz,NTR	3.2

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	414821	M63835	LL 77424	Fc fragment of	THE CC In	34
			Hs.77424		TM,SS,lg	3.1
	418030	BE207573	Hs.83321	neuromedin B	\$\$	3.1
	421633	AF121860	Hs.106260	sorting nexin 1	ТМРХ	3.1
-	441285	NM_002374	Hs.167	microtubule-ass	SS,tubulin-binding	3.1
5	418526	BE019020	Hs.85838	solute carrier	TM,MCT	31
	401260				TMSS	3.1
	450705	U90304	Hs.25351	iroquois-class	TM.homeobox	3.1
	424415	NM_001975	Hs.146580	enolase 2. (gam	TM,SS,enolase	3.0
	403346				TM_atpha-armylase	3.0
10	432757	AF113013	Hs.278919	PRO0806 protein	TM	3.0
• •	434398	AA121098	Hs.3838	serum-inducible	TM.pkinase,POLO_box	3.0
	424539	L02911	Hs.150402	activin A recep		3.0
	406117	LUZSII	ns. 130402	acaviii A resep	TM.Activin_recp.pkinase	
	408119	14100040		ab.22440.11	SS	3.0
15		W26213	14- 277204	gb:22d10 Human	TM,SS	3.0
13	431984	AL080239	Hs.272284	Human DNA seque	TM	3.0
	403782				TM	3.0
	447922	Z92910	Hs.20019	hemochromatosis	TM,SS,ig,MHC_I,histone,SPRY,zf-B_box,zf-C3HC4	3.0
	428857	AF008192	Hs.194283	putative GR6 pr	SS	3.0
20	432596	AJ224741	Hs.278461	matrilin 3	SS	3.0
20	453202	AW085781	Hs.26270	Homo sapiens cD	TM	3.0
	405547				TM,SS,ABC_membrane,ABC_tran	3.0
	423496	U91963	Hs.129700	tolloid-like 1	TM,SS,EGF,CUB,Astacin	3.0
	401707				SS	3.0
	403144				TM,ion_trans,K_tetra	3.0
25	418375	NM_003081	Hs.84389	synaptosomal-as	TM,NA	3.0
	422992	AF016833	Hs.122785	maitase-glucoam	TM,Glyco_hydro_31,trefoil	3.0
	406506				TM	3.0
	413472	BE242870	Hs.75379	solute carrier	TMLSOF	3.0
	410172	55242010	113.13313	SOUTH CARRES	FIRLOUP	3.0
30	TABLE 34	D.				
50	Pkey:		Fan ausbar	at identifies sumbas		
				set identifier number		
	CAT numb		e cluster numb			
	Accession	: Gen	bank accessio	n numbers	,	
35	-					
33	Pkey	CAT number	Accession			
	408119	1040172_1		)8055 Z44031 AW954559 R		
	454392	115882_1	BE260893	AA078319 R85057 AW8030	024 H85811 AA078293	
40	TABLE 34	IC.				
40	TABLE 34 Pkey:		ue number co	rresponding to an Eos prob	eset	
40		Unic				et al." refers to the publication entitled "The DNA
40	Pkey:	Unic Seq	uence source.	The 7 digit numbers in this	column are Genbank identifier (GI) numbers. "Dunham,	et at." refers to the publication entitled "The DNA
40	Pkey:	Unic Seq seq:	uence source. Jence of huma	The 7 digit numbers in this	column are Genbank identifier (GI) numbers. "Dunham, n, et al. (1999) Nature 402:489-495.	et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand:	Unic Seq seq: Indi	uence source. Jence of huma Lates DNA stra	The 7 digit numbers in this in chromosome 22" Dunham and from which exons were	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted.	et al." refers to the publication entitled "The DNA
40 45	Pkey: Ref:	Unic Seq seq: Indi	uence source. Jence of huma Lates DNA stra	The 7 digit numbers in this in chromosome 22" Dunham	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted.	et al.* refers to the publication entitled *The DNA
	Pkey: Ref: Strand: Nt_positio	Unic Seq seq: Indi on: tndi	uence source. Jence of huma Lates DNA stra Lates nucleotic	The 7 digit numbers in this in chromosome 22" Dunham and from which exons were to positions of predicted exo	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted.	et at." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position	Unic Seq seq: Indi on: Indi	uence source. Jence of hums cates DNA stra cates nucleotic Strand	The 7 digit numbers in this in chromosome 22" Dunharr and from which exons were to positions of predicted exo Nt_position	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position Pkey 401157	Unic Seq seq: Indi on: Indi Ref 9438289	uence source. uence of hume cates DNA stra cates nucleotic Strand Minus	The 7 digit numbers in this in chromosome 22" Dunham and from which exons were to positions of predicted exo Nt_position 114133-114247,114567-	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_position Pkey 401157 401189	Unic Seq seq Indi on: tndi Ref 9438289 9690246	uence source. sence of hume cates DNA stra- cates nucleotic Strand Minus Minus	The 7 digit numbers in this in chromosome 22" Dunharr and from which exons were to positions of predicted exo Nt_position 114133-114247,114567- 90815-90929	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et at." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260	Unic Seq seq: Indi on: tndi Ref 9438289 9690246 8076883	uence source. Jence of huma Lates DNA stra- Lates nucleotic Strand Minus Minus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were to positions of predicted exo Nt_position 114133-114247,114567- 90815-90929 85008-86355	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352	Unic Seq seq: Indi on: tndi Ref 9438289 9690246 8076883 9931258	uence source. uence of huma cates ONA str cates nucleotic Strand Minus Minus Minus Minus Minus	The 7 digit numbers in this in and from which exons were to positions of predicted exo Nt_position 114133-114247,114567-90815-90929-86008-86355-26064-26208	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352 401439	Unic Seq seq: Indii on: Indii Ref 9438289 9690246 8076883 9931258 8246737	uence source. uence of huma cates DNA str cates nucleotic  Strand Minus Minus Minus Minus Minus Minus Plus	The 7 digit numbers in this in chromosome 22" Dunhar and from which exons were to position 114133-114247,114567- 90815-90929 65008-66355 26064-26208 92993-94026	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352 401439 401707	Unic Seq seq Indi Indi Ref 9438289 9690246 8075883 9931258 8246737 2951946	uence source.  Jence of hume  cates DNA stre  cates nucleotic  Strand  Minus  Minus  Minus  Minus  Minus  Plus  Plus  Plus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were to positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	et al." refers to the publication entitled "The DNA
45	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260 401352 401439 401707 402045	Unic Seq seq Indi Indi Ref 9438289 9690246 8075883 9931258 8246737 2951946 7923943	uence source. uence of hume cates DNA sire cates nucleotic Strand Minus Minus Minus Minus Plus Plus Plus Plus	The 7 digit numbers in this in this in the remaind from which exons were to positions of predicted exo Nt_position 114133-114247,114567-90815-90929 65008-86355 26064-26208 92933-94025 21972-22104 5964-6128	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45 50	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352 401439 401707 402045 402421	Unix Seq seq Indi Indi Ref 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341	uence source.  uence of hume  cates DNA stra- cates nucleotic  Strand  Minus  Minus  Minus  Minus  Plus  Plus  Plus  Plus  Plus  Minus  Minus  Minus	The 7 digit numbers in this in chromosome 22" Dunhar and from which exons were also positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86355 25064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-468	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Nature</u> 402:489-495. predicted. nns.	
45	Pkey: Ref: Strand: Nt_positio Pkey 401157 401189 401260 401352 401439 401707 402045 402045 402696	Unic Seq seq Indi Indi Ref 9438289 9690246 8076883 9931258 8246737 2951946 7923943 7923943 7723848	uence source. uence of hums attes DNA sirt cates nucleotic  Strand Minus Minus Minus Minus Plus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunham and from which exons were for positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104 5964-6128 45609-46562,46758-468 23600-23731	column are Genbank Identifier (GI) numbers. "Dunham, n, et al. (1999) <u>Natura</u> 402:489-495. predicted. ons.	
45 50	Pkey: Ref: Strand: Nt_position Pkey 401157 401182 401250 401352 401439 401707 402045 402421 402630 402739	Unic Seq Indi Indi P438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192	uence source. Jence of hume Jates DNA stra Jates nucleotic Strand Minus Minus Minus Minus Minus Plus Plus Plus Plus Minus Minus Plus Plus Plus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in this in third the consumers of the consumer	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) <u>Natura</u> 402:489-495. predicted. sns114645	
45 50	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401352 401433 401707 402045 402421 402696 402739 402921	Unix Seq seq indi tndi Raf 9438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303	uence source, uence of hume zites ONA stra zites nucleotic Strand Minus Minus Minus Minus Minus Plus Plus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e positions of predicted exo Nt_position of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-466 23600-23731 60458-61019 52242-52384,55599-556	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260 401352 401433 401707 402045 40245 40245 402739 402901 403095	Unic Seq sequindi India P438289 9690246 8076883 9931258 8246737 2951946 7923943 9723943 9723943 9723943 9723943 9723943 9723943 9723943	uence source. Jence of hums Jates DNA stri Jetes nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Minus Plus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were for positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-468 23600-23731 60458-61019 52242-52384,55599-558 150025-150240,151564	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55	Pkey: Ref: Strand: Nt_position Pkey 401157 401157 401250 401352 401439 401707 402045 402421 402696 402739 402921 403934 40393111	Unix Seq lndi Indi 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8984970	uence source. Jence of hume Jates DNA stra Jates nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this nather 1 digit numbers in this nather 27 Dunhar and from which exons were (e positions of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-466 23600-23731 80458-61019 52242-52384.55599-556 150025-1500240,151564 175012-175159	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50	Pkey: Ref: Strand: NL positio Pkey 401157 401189 401260 401352 401439 401707 4020421 402696 402739 402921 403095 403144	Unix Seq seq indi tridi Raf 9438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8980970 9454849	uence source. Jence of hume Jence of hume Jence of hume Jence of hume Strand Minus Minus Minus Minus Minus Plus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were for positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-468 23600-23731 60458-61019 52242-52384,55599-558 150025-150240,151564	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260 401352 401433 401707 402045 402421 403696 4027739 402931 403095 403111 403144 403345	Unix Seq lndi Indi 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8984970	uence source. Jence of hume Jates DNA stra Jates nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this nather 1 digit numbers in this nather 27 Dunhar and from which exons were (e positions of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-466 23600-23731 80458-61019 52242-52384.55599-556 150025-1500240,151564 175012-175159	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55	Pkey: Ref: Strand: NL positio Pkey 401157 401189 401260 401352 401439 401707 4020421 402696 402739 402921 403095 403144	Unix Seq seq indi tridi Raf 9438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8980970 9454849	uence source. Jence of hume Jence of hume Jence of hume Jence of hume Strand Minus Minus Minus Minus Minus Plus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e positions of predicted exo Nt_position of predicted exo Nt_position of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-466 23600-23731 60458-61019 52242-52384,55599-556 150025-150240,151564 175012-175159 166200-1666228	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260 401352 401433 401707 402045 402421 403696 4027739 402931 403095 403111 403144 403345	Unix Seq sequindi India 9438289 9690246 8075883 9931258 8245737 2951946 7923943 9793343 9793343 9212192 7981303 8980970 9454849 8569726	uence source. Jence of hums Jates DNA stri Jetes nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Minus Plus	The 7 digit numbers in this in chromosome 27 Dunham and from which exons were (e positions of predicted exo Nt_position 114133-114247,114567-90815-9089-86008-86355-26064-26208-92933-94026-21972-22104-5964-6128-46609-46662,46758-46623600-23731-60458-61019-52242-52384-55599-556150025-150245-150246-15024-175159-166200-165628-77890-78609-92752-99015	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60	Pkey: Ref: Strand: NL positio Pkey 401157 401189 401260 401352 401439 401704 402421 402696 402739 402921 4030346 403111 403144 403346	Unix Seq lndi Indi Maix Indi Ref 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8980970 9454649 8559726	uence source. Jence of hume Jates DNA stri Jates nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Plus Minus Plus Plus Plus Plus Minus Plus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunham and from which exons were for positions of predicted exo Nt_position of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 45609-46562,46758-465 23600-23731 60458-61019 52242-52384,55599-555 150025-150240,151564 175012-175159 166200-166628 77890-78069	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55	Pkey: Ref: Strand: NL position Pkey 401157 401189 401260 401352 401439 401707 4020421 402696 402719 402921 403095 403114 403345 403346 4033782	Unix Seq s	uence source. Jence of hume Jence of hume Jence of hume Jence of hume Strand Minus Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunham and from which exons were (e) positions of predicted exo Nt_positions of predicted exo Nt_position of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92933-94026 21977-22104 5964-61260 23731 60458-61019 52242-52394,55599-556150025-150240,151564 175012-175159 166200-165628 77890-78069 92752-99015 41326-41633	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60	Pkey: Ref: Strand: Nt_position Pkey 401157 401189 401260 401352 401433 401707 402045 402421 403696 4027739 402921 403095 403111 403146 403782 403464 403782 404115	Unix Seq sequindin Indix 9438289 9690246 8076883 99311258 8246737 2951946 7923943 7796341 7328818 9212192 7981303 8954339 8980970 9454849 8569726 8569726 8569726 8569726	uence source. Jence of hums Jates DNA stri Jetes nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e positions of predicted exo Nt_position 114133-114247,114567-90815-9089-86008-86355-26064-26208-92933-94026-21972-22104-5964-6128-46609-46662,46758-46624658-61019-52242-52394-55599-556150025-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-150245-1502	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60	Pkey: Ref: Strand: NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position NL_position	Unix Seq sequindin Indix 9438289 9690246 8076883 99311258 8246737 2951946 7923943 7796341 7328818 9212192 7981303 8954339 8980970 9454849 8569726 8569726 8569726 8569726	uence source. Jeence of hume Jeence of hume Jeence of hume Jeence of hume Strand Minus Minus Minus Minus Minus Plus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Minus Plus Plus Minus Plus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e) positions of predicted exo Nt_positions of predicted exo Nt_positions of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-466 23600-23731 60458-61019 52242-52384,55599-556 150025-150240,151564 175012-175159 166200-1666228 77890-78069 92752-93015 41326-41633 232707-232982 77666-7210 74493-74829	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60	Pkey: Ref: Strand: NL_positio Pkey 401157 401189 401250 401439 401707 402045 402421 402695 402739 40291 403346 403782 403115 403346 403782 404115 604200 404393	Unix Seq sequindin India	uence source. Jence of huma- zates DNA stra- zates nucleotic  Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were for positions of predicted exo Nt_position of predicted exo 9293-94026 2993-94026 21972-22104 5964-6128 45609-46562,46758-46524050-23731 60458-61019 52242-52384,55599-555 150025-150240,151564 175012-175159 166200-166528 77890-78069 92752-93015 41326-41633 232707-232982 7066-7210 74493-74829 175318-175476	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60 65	Pkey: Ref: Strand: NL positio NL positio 401157 401189 401260 401369 401439 401707 402045 402421 402696 402739 402921 403095 403111 403146 403162 404150 404347 404347 404347 404347	Unix Sequindin India   Ref 9438289 9690246 8075883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8980970 9454649 8569726 8078608 9621489 6010176 9838195 686597 7328310	uence source. Jernos of hume Jernos of hume Jernos of hume Jernos of hume Jernos Jerno	The 7 digit numbers in this in chromosome 22" Dunham and from which exons were je positions of predicted exo Nt_positions of predicted exo Nt_positions of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26008-86355 26008-86355 26008-86355 26008-86355 26008-86628-86758-46523600-23731 50458-81019 5242-52384,55599-556150025-1500240,151564175012-175159 166200-166628 77890-78069 92752-93015 41328-41633 232707-232982 77066-7210 74493-74829 175318-175476 73121-73273	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. ins114645	
45 50 55 60 65	Pkey: Ref: Strand: Ni_position Ni_position Pkey 401157 401189 401260 401352 401403 401707 4020421 402696 402739 402921 403095 4031144 403345 403146 403146 403146 403147 404939 405594	Unix Seq sequindin India	uence source.  Jeance of hume  Jeance of hume  Jeance of hume  Strand  Minus  Minus  Minus  Minus  Minus  Plus  Plus  Minus  Plus  Minus  Plus  Plus  Minus  Plus  Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) <u>Nature</u> 402:489-495. predicted. sns114645 -111,66293-86346,89776-89829,90048-90101,102817-10 -151890	
45 50 55 60	Pkey: Ref: Strand: NL_positio V01157 401189 401250 401439 401707 402045 402421 40269 402739 40291 403345 403345 403345 403346 403345 404115 40410 40415 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 40414 4041	Unix Sequindin India Sequindin India India India India India Sequindin India I	uence source. Jence of huma- zates Only stra- zates nucleotic  Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunham and from which exons were (e positions of predicted exo Nt_position 114133-114247,114567-90815-90929 85008-86335 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-46523600-23731 60458-61019 52242-52384,55599-555 150025-1590240,151564 175012-175159 166200-166628 77890-78069 92752-89015 41326-41633 232707-232982 7066-7210 74493-74829 175318-175476 73121-73273 31900-32373 124381-1724520,124914	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) Nature 402:489-495. predicted. ins114645	2924
45 50 55 60 65	Pkey: Ref: Strand: Ni_position Ni_position Pkey 401157 401189 401260 401352 401403 401707 4020421 402696 402739 402921 403095 4031144 403345 403146 403146 403146 403147 404939 405594	Unix Seq sequindin India	uence source.  Jeance of hume  Jeance of hume  Jeance of hume  Strand  Minus  Minus  Minus  Minus  Minus  Plus  Plus  Minus  Plus  Minus  Plus  Plus  Minus  Plus  Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were 16 positions of predicted exo Nt_positions of predicted exo Nt_positions of predicted exo Nt_position 114133-114247,114567-90815-90929 86008-86355 26064-26208 92993-94026 21972-22104 5964-6128 46609-46662,46758-465 23600-23731 60458-61019 52242-52384,55599-555 150025-15024-0,151564 175012-175159 166200-166628 77890-78069 92752-93015 41326-41633 232707-232982 7766-7210 74493-74829 175318-175476 73121-73273 31900-32373 124351-12450,124914 42814-43010,43583-43	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65	Pkey: Ref: Strand: Ni_position Ni_position Pkey 401157 401189 401260 401352 401403 401707 4020421 402696 402739 402921 403095 4031144 403345 403146 403146 403146 403147 404939 405547 405609	Unix Seq s	uence source. Jence of hume Jetes OnNa sire Jetes onucleotic Strand Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, n. et al. (1999) Nature 402:489-495. predicted. ins114645	2924
45 50 55 60 65	Pkey: Ref: Strand: NL positio V01157 401189 401250 401439 401704 402421 40264 402739 402921 402921 403045 403146 403346 403144 403346 404115 404105 404105 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 404106 4	Unix Sequindin India Sequindin India	uence source. Jence of huma- zates Only stra- zates nucleotic  Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Minus Plus Minus Plus Minus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e positions of predicted exo Nt_position of predicted	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65 70	Pkey: Ref: Strand: NL position	Unix Sequindin India Sequindin India	uence source. Jeence of hume Strand Minus Minus Minus Minus Minus Plus Plus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65	Pkey: Ref: Strand: Nt_position Nt_position Pkey 401157 401189 401260 401352 401403 401707 4020421 402696 402713 402696 402713 403095 4031144 403345 403146 403146 403147 404939 405547 405609	Unix Seq sequindin India	uence source. Jence of hume Jetes OnNa sire Jetes onucleotic Strand Minus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65 70	Pkey: Ref: Strand: NL positio 401157 401189 401250 401439 401074 402421 40264 402739 402921 402095 403111 403144 403345 404115 404105 404105 404105 40504 40504	Unix Sequindin India Sequindin India	uence source. Jence of Numericates Ohun strates on Leotic Strand Minus Minus Minus Minus Minus Minus Minus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65 70	Pkey: Ref: Strand: Nt_position Nt_position Pkey 401157 401189 401260 401352 401403 401707 4020421 402696 402713 402696 402713 403095 4031144 403345 403146 403146 403147 404939 405547 405609	Unix Seq sequindin India	uence source. Jence of hume Jetes OnNa sire Jetes onucleotic Strand Minus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were jo positions of predicted exo Nt_positions of pr	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924
45 50 55 60 65 70	Pkey: Ref: Strand: NL positio 401157 401189 401250 401439 401074 402421 40264 402739 402921 402095 403111 403144 403345 404115 404105 404105 404105 40504 40504	Unix Sequindin India Sequindin India	uence source. Jence of Numericates Ohun strates on Leotic Strand Minus Minus Minus Minus Minus Minus Minus Plus Plus Minus	The 7 digit numbers in this in chromosome 27 Dunhar and from which exons were (e positions of predicted exo Nt_position of predicted	column are Genbank Identifier (GI) numbers. **Dunham, et al. (1999) Nature 402:489-495. predicted. ins.  -114645  -11186293-86346,89776-89829,90048-90101,102817-10  -151890  -125050  -125050  -133,44863-45033,46429-46554,47815-48018,49961-501	2924

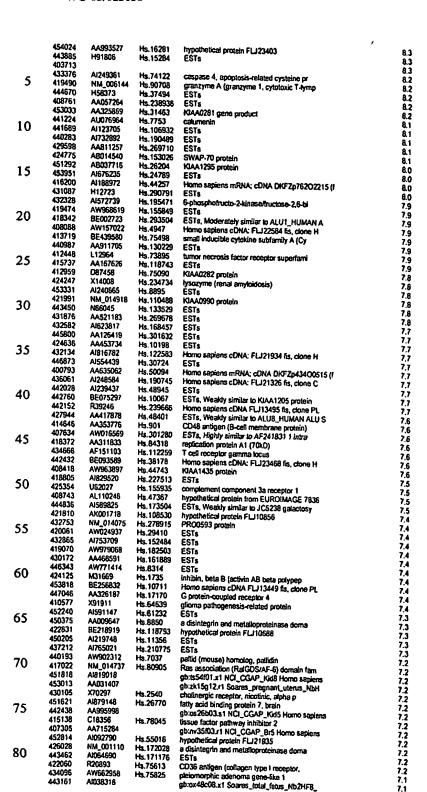
80

TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER
Table 35A lists about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th pecentile for both the numerator and the denominator and using non-matignant kidney specimens in determining the denominator value.

	Pkey:	Unio	e Eos orobese	it klentifier number	
	ExAcon:	Exem	Plar Accession	number, Genbank accession number	
	UnigenelD	: Unige	ine number		
5	Unigene Ti R1:		ne gene title of tumor to no	ernet ficea	
•	•••	14000	OF COLLEGE SECTION	mea m2200	
	Pkey	ExAcen	UnigeneID	UnigeneTide	R1
	424704 426559	AI263293 AB001914	Hs.152096	cytochrome P450, subfamily IU (arachido	40.9
10	458079	AI796870	Hs.170414 Hs.54277	paired basic amino acid cleaving system ESTs	35.6
	433447	U29195	Hs.3281	neuronal pentraxin ()	34.6 32.0
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	29.3
	446921 435359	AB012113 T60843	Hs.16530	small inducible cytokine subfamily A (Cy	25.9
15	450152	AI138635	Hs.189679 Hs.22968	ESTS ESTS	25.4 25.2
	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro	24.8
	440304	B£159984	Hs.125395	ESTs	24.5
	414821 421155	M63835 H87879	Hs.77424 Hs.102267	Fc fragment of IgG, high affinity Ia, re	23.4
20	452795	AW392555	Hs.18878	lysyl oxidase hypothetical protein FLJ21620	22.4 22.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	22.1
	426471	M22440	Hs.170009	transforming growth factor, elpha	21,3
	427897 449523	NM_017413 NM_000579	Hs.181060 Hs.54443	apelin; peptide ligand for APJ receptor chemokine (C-C motif) receptor 5	21.3
25	436961	AW375974	Hs.156704	ESTs	20.7 20.5
	447499	AW262580	Hs.147674	KIAA 1621 protein	20.4
	438817	A1023799	Hs.163242	ESTs .	20.4
	430630 428227	AW269920 AA321649	Hs.2621 Hs.2248	cystatin A (stefin A) small inducible cytokine subfamily B (Cy	19.8 19.5
30	424086	AI351010	Hs.102267	tysyl oxidase	18.7
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	18.7
	438476 415286	AA326108 AW249540	Hs.53631	ESTs, Wealthy similar to enhancer-of-spli	18.7
	428157	A1738719	Hs.72548 Hs.298668	ESTs ESTs	18.2 18.1
35	456804	Al421645	Hs.139851	caveolin 2	17.8
	429490	AJ971131	Hs.293684	ESTs, Weakly similar to alternatively sp	17.5
	429732 433757	U20158 Al949974	Hs.2488 Hs.152670	lymphocyte cytosolic protein 2 (SH2 doma ESTs	17.1
	400419	AF084545	Hs.81800	chondroitin suifate proteoglycan 2 (vers	16.B 16.4
40	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	16.3
	411642	NM_014932	Hs.71132	neurotigin 1	15.2
	444381 435767	BE387335 H73505	Hs.283713 Hs.117874	ESTs, Wealdy similar to CA54_HUMAN COLLA ESTs	16.0
	427581	NM_014788	Hs.179703	KIAAD129 gene product	15.7 15.6
45	448019	AW947164	Hs.195641	ESTs	15.6
	406671 447835	AA129547 AW591623	Hs.285754	met proto-oncogene (hapatocyte growth fa	15.5
	448520	AB002367	Hs.164129 Hs.21355	ESTs doublecortin and CaM kinase-like 1	15,4 14,8
50	417308	H60720	Hs.81892	KIAA0101 gene product	14.8
50	432731	R31178	Hs.287820	fibronectin 1	14.7
	421566 419235	NM_000399 AW470411	Hs.1395 Hs.288433	early growth response 2 (Krox-20 (Drosop neurotrimin	14.6
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.6 14.4
56	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	14.4
55	422603 418110	BE242587 R43523	Hs.118651	hematopoletically expressed homeobox	14.4
	425984	AW836277	Hs.217754 Hs.165636	Homo sapiens cDNA: FLJ22202 fis, clone H hypothetical protein DKFZp761C07121	14.2 14.2
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	14.1
60	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	14.0
v	444989 426890	AI203334 AA393167	Hs.150628 Hs.41294	ESTs ESTs	13.9
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	13.8 13.8
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	13.7
65	446627	AI973016	Hs.15725	hypothetical protein S8BI48	13.6
05	452960 417280	AK001335 AW173116	Hs.31137 Hs.262206	Homo sapiens cDNA: FLJ22681 fis, clone H ESTs	13.3
	422173	8E385828	Hs.250619	phorbolin-like protein MDS019	13.1 13.0
	420552	AK000492	Hs.98806	hypothetical protein	13.0
70	425188 427871	AK002052 AW992405	Hs.155071	hypothetical protein FLJ11190	12.6
. •	446152	AJ292036	Hs.59622 Hs.150028	ESTs, Weakly similar to unknown (H.sapie ESTs	12.6 12.5
	426560	AA381661	Hs.119878	ESTs	12.4
	419034	NM_002110		hemopoietic cell kinase	12.3
75	456508 452281	AA502764 T93500	Hs.123469 Hs.28792	ESTs, Weakly similar to AF208855 1 BM-01	12.3
	442932	AA457211	Hs.8858	Homo sapiens cDNA FLJ11041 fis, clone PL bromodomain adjacent to zinc finger doma	12.3 12.3
	426075	AW513691	Hs.270149	ESTs	12.3
	434398	AA121098	Hs.3838	serum-inducible kinase	12.2
80	450506 425782	NM_004460 U66468	Hs.418 Hs.159525	fibroblast activation protein, alpha cell growth regulatory with EF-hand doma	12.1
	426108	AA622037	Hs.166468		12.0 11.9
	416000	RB2342	Hs.79856	ESTs	11.8
	450236	AW162998	Hs.24684	KIAA1376 protein	11.7
				000	

	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11848 fis, clone HE	11.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	11.4
	442227	AW771958	Hs.175437	ESTs	11.4
5	414004 447056	AA737033	Hs.7155	ESTs, Wealdy similar to 2115357A TYNG or	11.4
,	444863	N67879 AW384082	Hs.157695 Hs.301323	ESTs · ESTs	11.3
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	11.3 11.2
	426780	BE242284	Hs.172199	adenylata cyclase 7	11.1
	453160	AI263307	Hs.146228	ESTs	11.1
10	449539	W80363	Hs.58446	ESTs .	11.1
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	11.0
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	11.0
	408380	AF123050	Hs.44532	dlubiquilln	11.0
1.5	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	11.0
15	451277	AK001123	Hs.26176	hypothetical protein FLJ 10261	10.8
	453165 435380	\$74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	10.8
	447183	AA579001 AI554733	Hs.192221 Hs.173182	ESTs ESTs	10.7
	438330	AW450572	Hs.257316	EST6	10.7 10.6
20	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERAT	10.5
	418036	237976	Hs.83337	latent transforming growth factor beta b	10.5
	452852	AW378065	Hs.8687	ESTs	10.4
	431512	BE270734	Hs.2795	lactate dehydrogenase A	10.3
26	421478	A)683243	Hs.97258	ESTs	10.3
25	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fis, clone H	10.3
	411800	N39342	Hs.5184	TH1 drosophila homolog	10.3
	433862	D86960	Hs.3810	KIAA0205 gene product	10.3
	440594	AW445167	Hs.126036	ESTs	10.2
30	414504 431211	AW069181 M86849	Hs.293523 Hs.5566	ESTs, Wealdy similar to transformation-r	10.2
20	437682	AA476652	Hs.94952	gap junction protein, beta 2, 26kD (conn Homo sapiens cDNA: FLJ23371 fis, clone H	10.2
	430097	AI523245	Hs.127638	ESTs	10.1 10.1
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	10.0
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	9.9
35	424113	AI743880	Hs.12876	ESTs	9.9
	439981	A1348408	Hs.124675	ESTs, Wealdy similar to unnamed protein	9.9
	411937	AW876626		gb:RC3-PT0028-120200-013-d08 PT0028 Homo	9.9
	439653	AW021103	Hs.6631	hypothetical protein Ft J20373	9.9
40	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	9.8
40	424523	AW963062	Hs.165809	ESTs	9.8
	410762	AF226053	Hs.66170	HSKM-B protein	9.8
	433285 413795	AW975944	Hs.237396	ESTs	9.7
	434392	AL040178 AW983709	Hs.142003 Hs.268051	ESTs ESTs	9.6
45	435542	AA687376	Hs.269533	ESTs	9.6
70	430687	N66801	Hs.260287	ESTs, Wealdy similar to ALU7_HUMAN ALU S	9.6 9.5
	410339	AI916499	Hs.298258	ESTs	9.5
	452431	U88879	Hs.29499	toll-like receptor 3	9.5
	405121	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	9.5
50	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	9.4
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	9.4
	449825	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homotog 1	9.4
	441024	AW081530	Hs.137088	ESTs .	9.3
55	445900 433001	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	9.2
"	440074	AF217513 AA863045	Hs.279905	clone HQ0310 PRO0310p1	9.2
	421659	NM_014459	Hs.199057 Hs.106511	ESTs, Weakly similar to T00050 hypothesi protocadherin 17	9.2
	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	9.2 9.1
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	9.1
60	428820	AA436187	Hs.172631	integrin, alpha M (complement component	9.1
	419441	AW023731	Hs.274368	Homo sapians mRNA; cDNA DKFZp586i1524 (f	9.0
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	9.0
	431941	AK000106	Hs.272227	Homo sepiens cDNA FLJ20099 fis, clone CO	9.0
65	446460	AW013999	Hs.150164	ESTs	8.9
05	452598	AI831594	Hs.68647	ESTs, Wealthy similar to ALU7_HUMAN ALU S	8.9
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	8.9
	437259 420235	A1377755 AA256756	Hs.120695 Hs.31178	ESTs ESTs	8.7
	436959	AL133076	Hs.5354	hypothetical protein FLI12716	8.7 8.7
70	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.6
	435894	AI076667	Hs.188011	ESTs	8.6
	418693	AJ750878	Hs.87409	thrombospondin 1	8.6
	425770	NM_014363			8.6
~~	456249	Al206144	Hs.82508	HRIHFB2206 protein	8.6
75	437672	AW748265	Hs.5741	flavohemoprotein b5-b5R	8.6
	430268	AK000737	Hs.237480		8.5
	417225	AA815048	Hs.24078	Homo sapiens cDNA FLJ12649 fis, clone NT	8.5
	435266	AK001942	Hs.4863	Homo saplens cDNA FLJ11080 fis, clone PL	8.4
80	447974 447850	R76886 AB018298	Hs.19822	gb:yi64b03.s1 Soares placenta Nb2HP Homo	8.4
50	429525	N92540	Hs.205353	SEC24 (S. cerevisiae) related gene (amil ectonucleoside triphosphate diphosphohyd	8.4
	435717	AF227905	Hs.105794		8.3 8.3
	445784	AJ253155	Hs.146065	ESTs	8.3
				<del>-</del> ·	<b>U. J</b>





	450700	414-070400			
	458725	AW970192	Hs.171942	ras responsive element binding protein 1	7.1
	426423	NM_012446	Hs.169833	singte-stranded-DNA-binding protein	7.1
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
_	435664	A1032087	Hs.269819	ESTs	7.0
5	431708	AI698136	Hs.108873	ESTs	7.0
	426501	AW043782	Hs.293616	ESTs	7.0
	453548	AL079983	Hs.75442	albumin	7.0
	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	7.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fs, clone H	
10	431556	AF016028	Hs.260039	sarcospan (Kras oncogene-associated gene	7.0
	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	6.9
	418986	AJ123555	Hs.81796	ESTs	6.9
	430290	AJ734110	Hs.136355	ESTs	6.9
	427472	AA522539	Hs.131250		8.9
15	444042	NM_004915	Hs.10237	transposon-derived Buster3 transposase-i	6.9
	414737	AI160386		ATP-binding cassette, sub-family G (WHIT	6.9
	420479		Hs.125087	ESTs	6.9
	432656	AW183695	Hs.186572	ESTs	6.9
	414217	NM_000246	Hs.3076	MHC class II transactivator	6.9
20		Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.9
20	431870	AW449902	Hs.105500	ESTs	6.9
	415788	AW628686	Hs.78851	KIAA0217 protein	6.9
	430066	AI929659	Hs.237825	signal recognition particle 72kD	6.9
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	6.8
25	401539				6.8
25	412782	AI189211	Hs.173044	ESTs	6.8
	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2	6.8
	437205	AL110232		gb:Homo saplens mRNA; cDNA DKFZp554D2071	6.7
	458814	A1498957	Hs.170861	ESTS	6.7
20	452106	Al141031	Hs.21342	ESTs	6.7
30	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	6.7
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	6.7
	445527	W39694	Hs.83286	ESTs	6.7
	424063	NM_002019	Hs.138671	fins-related tyrosine kinase 1 (vascular	
	421977	W94197	Hs.110165	ribosomal protein L26 homotog	6.7
35	430280	AA361258	Hs.237868	interleukin 7 receptor	6.7
	415989	AJ267700	Hs.111128	ESTs	6.7
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	6.7
	425295	AA431366	Hs.37251	ESTs	5.6
	438619	AB032773	Hs.6341		6,6
40	424916	AW887440	Hs.23096	TU1281-TY protein	6.6
	429697	AW296451	Hs.24605	ESTs	6.6
	408741	M73720		ESTs .	6.6
	403549	WITSTZU	Hs.646	carboxypeptidase A3 (mast cell)	6.6
	449008	AMERICA			6.6
45		AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	6.6
73	435798	BE395289	Hs.12720	elF4E-transporter	6.6
	447217	BE465754	Hs.17778	neuropilin 2	6.6
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	6.6
	410276	AI554545	Hs.68301	ESTs	6.6
50	435391	AA704588	Hs.58934	ESTs	6.6
20	421878	AA299652	Hs.111496	Homo sepiens cDNA FLJ11643 fis, clone HE	6.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	6.5
	448789	BE539108	Hs.22051	Homo sapiens mRNA; cDNA DKFZp434O119 (fr	6.5
	425331	AW96212B		gb:EST374201 MAGE resequences, MAGG Homo	6,5
55	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	6.5
55	444880	AW118683	Hs.154150	ESTs	6.5
	434131	A1858275	Hs.143659	ESTs	6.5
	446658	AI440137	Hs.164989	ESTs	6.5
	408150	BE620274	Hs.43112	Homo sapiens mRNA; cONA DKFZp434B1520 (f	6.5
60	403790			· · · · · · · · · · · · · · · · · · ·	6.5
60	417129	AI381800	Hs.143275	Homo sapiens cDNA FLJ13233 fis, clone OV	6.5
	452119	A1656378	Hs.33461	ESTs	6.4
	437396	BE140396	Hs.21621	hypothetical protein OKFZp7620076	6.4
	458946	AA009716	Hs.42311	ESTs	6.4
15	452110	T47667	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G2463 (f	6.4
65	449318	AW236021	Hs.108788	ESTs. Weakly similar to zeste [O.melanog	6.4
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.4 6.4
	402474			,, p	
	430712	AW044647	Hs.196284	ESTs	6.4 6.4
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	6.4
70	432683	AW995441	Hs.10475	ESTs	6.4
	423764	AF054589	Hs.132739	ESTs	6.4
	409571	AA504249	Hs.187585	ESTs	6.4
	401600	BE247275	Hs.151787	US snRNP-specific protein, 116 kD	6.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.4
75	432925	AA878324	Hs.192734	ESTs	6.4
	427528	AU077143	Hs.179565		6.4
	453894	AW937825	Hs.56847	minichromosome maintenance deficient (S.	6.4
	430335	D80007	Hs.239499	Homo sepiens cDNA FLJ12874 fis, clone NT KIAA0185 protein	6.4
	453370	AJ470523	Hs.182356		6.3
80	421327	AA837295		ESTs, Moderately similar to translation	6.3
	450654	AJ245587	Hs.188802	ESTs	6.3
	413497	BE177661	Hs.25275	Kruppel-type zinc finger protein	6.3
	445279	R41900	U+ 22246	gb:RC1-HT0598-020300-011-h02 HT0598 Homo ESTs	6.3
			Hs.22245	E013	6.3

	45034-				
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	6.3
	421252 432140	AA765930	Hs.130878	ESTs	6.3
	434203	AK000404 BE262677	Hs.272688 Hs.283558	hypothetical protein FLJ 20397	6.3
5	419436	AA991639	Hs.15036	hypothetical protein PRO1855	6.2
_	430287	AW182459	Hs.125759	ESTs, Highly similar to AF161358 1 HSPC0 ESTs, Wealdy similar to tumor suppressor	6.2
	409690	W45393	Hs.94642	ESTs, Highly similar to ATFa (H.sapiens)	6.2
	420101	AW500529	Hs.95180	Homo sapiens mRNA; cDNA DXFZp434A205 (fr	6.2 6.1
10	435889	AJ249107	Hs.269901	ESTs	6.1
10	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	6.1
	448030	N30714	Hs.20161	HDCME31P protein	6.1
	442571 421202	C06338	Hs.165464	ESTs	6.1
	415558	AF193339 AA885143	Hs.102506	eukaryotic translation initiation factor	6.1
15	408042	AL049233	Hs.125719 Hs.42244	ESTS	6.1
	438086	AA336519	Hs.301167	Homo sapiens mRNA; cDNA DKFZp564A023 (fr Homo sapiens cDNA: FLJ21545 fis, clone C	6.1
	427390	AJ432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	6,1
	440749	W22335	Hs.7392	Homo sapiens mRNA; cDNA DKFZp761E0323 (f	6.0 6.0
20	448822	BE149845	Hs.289038	Homo sapiens cONA: FLJ20994 fis, clone C	6.0
20	424806	AA382523	Hs.105689	ESTs .	6.0
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrotase	6.0
	452235 432415	AL039743 T16971	Hs.28514	Homo sapiens mRNA: cDNA DKFZp434H092 (fr	6.0
	436345	AA873008	Hs.289014 Hs.121572	ESTs ESTs	6.0
25	439451	AF086270	Hs.278554	heterochromatin-like protein 1	6.0
	434674	AA831879	Hs.136985	ESTs	6.0
	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	6.0 6.0
	445822	AB037794	Hs.16229	KIAA1373 protein	6.0
30	423590	AW952412	Hs.65874	ESTs	6.0
30	424026	A1798295	Hs.123218	ESTs	5.9
	423246 420982	AL119114 AW576160	Hs.23107	EST ₈	5.9
	435008	AF150262	Hs.100729 Hs.162898	KIAA0692 protein ESTs	5.9
	420092	AA814043	Hs.88045	ESTs	5.9
35	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	5.9 5.9
	450534	AJ570189	Hs.25132	KIAA0470 gene product	5.9
	440146	AW014231	Hs.90790	Homo sepiens cDNA: FLJ22930 ffs, clone K	5.9
40	425361	AA355933	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	5.9
40	425174 458287	D87450 AA987556	Hs.154978	KIAA0261 protein	5.9
	433793	AW975959	Hs.12867 Hs.107513	ESTs Madagatah similarka 1914 a 1959 a sa	5.9
	443228	W24781	Hs.293798	ESTs, Moderately similar to KIAA1058 pro ESTs	5.8
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	5.8
45	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.8 5.8
	415714	NM_002290	Hs.78672	laminin, alpha 4	5.8
	421689	N87820	Hs.106826	hypothetical protein	5.8
	431176 443837	A1026984	Hs.293662	ESTs	5.8
50	410623	A1984625 AW958932	Hs.9884 Hs.293833	spindle pole body protein	5.8
	421298	AW172431	Hs.13012	ESTs ESTs	5.8
	449052	AW029507	Hs.161102	ESTs	5.8
	433043	W57554	Hs.125019	ESTs, Highly similar to KIAAD886 protein	5.8 5.8
55	439444	AI277652	Hs.54578	ESTs	5.7
55	428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypotheti	5.7
	411928	AA888624	Hs. 19121	adaptor-related protein complex 2, alpha	5.7
	442242 417315	AV647908 AI080042	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	5.7
	422544	AB018259	Hs.180450 Hs.118140	ribosomal protein \$24	5.7
60	412584	X54870	Hs.74085	KIAA0716 gene product DNA segment on chromosome 12 (unique) 24	5.7
	433505	AW504027	Hs_15301	Homo sapiens NY-REN-25 antigen mRNA, par	5.7 5,7
	410425	BE278367	Hs.63510	KIAA0141 gene product	5,7 5,7
	457292	Al921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	5.7
65	457100 436995	AA417878	Hs.48401	ESTs, Weakly similar to ALUB_HUMAN ALU S	5.7
05	426283	AI160015 NM_003937	Hs.118112	ESTs	5.7
	441518	AW161697	Hs.169139 Hs.294150	kynureninase (L-kynurenine hydrotase)	5.7
	448807	Al571940	Hs.7549	ESTs ESTs	5.7
70	449656	AA002008	Hs.188633	ESTs	5.7 5.7
70	439211	A1890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	5.7 5.7
	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	5.7
	413551	BE242639	Hs.75425	ubiquitin associated protein	5.7
	441633 427093	AW958544 AA398118	Hs.112242	ESTs COT	5.7
75	427093	U29926	Hs.97579	ESTs	5.6
	432267	AK000872	Hs.83918 Hs.274227	adenosine monophosphate deaminase (isofo	5.6
	419839	U24577	Hs.93304	Homo sapiens cDNA FLJ 10010 fis, ctone HE phospholipase A2, group VII (platelet-ac	5.6
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	5.6 5.6
90	450447	AF212223	Hs.25010	hypothetical protein P15-2	5.6 5.6
80	434823	AB023163	Hs.4014	KIAA0946 protein: Huntingtin interacting	5.6
	420642	AK001520	Hs.99545	nomo sapiens con Fl. 110658 fs. clone NT	5.6
	414020 420825	NM_002984 AI656727	Hs.75703	SITIAL INDUCIDIO CYTORIDO AA (homologous	5.6
	720023	M000121		gb:ti53f12.x1 NCI_CGAP_GC6 Homo sapiens	5.6

	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	5.6
	452046	AB018345	Hs.27657	KIAA0802 prolein	5.6
	408911	AW294772	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	5.6
5	414844 416498	AA296874 U33632	Hs.77494	deoxyguanosine kinase	5.6
-	430512	AF182294	Hs.79351 Hs.241578	potassium channel, subfamily K, member 1 U6 snRNA-associated Sm-like protein LSm8	5.6
	430339	W28608	Hs.239625	integral membrane protein 28	5.6 5.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	5.6
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	5.6
10	441568	AJ733322	Hs.127176	ESTs	5.5
	414575	H11257	Hs.295233	ESTs	5.5
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	5.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	5.5
15	453064	R40334	Hs.301395	Homo sapiens cDNA: FLJ21204 fs, clone C	5.5
13	433409	AJ278802	Hs.25661	ESTs	5.5
	407094 425234	AF000574 AW152225	Hs.22405 Hs.165909	leukocyte immunoglobulin-like receptor. ESTs	5.5
	447644	AW861622	Hs.108648	Homo sapiens cONA FLJ12534 ffs. clone NT	5.5
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	5.5 5.5
20	446534	Al307356	Hs.175225	ESTs	5.5
	452355	N54926	Hs.29202	G protein-coupled receptor 34	5.5
	434715	BE005346	Hs.116410	ESTA	5.5
	440486	BE243513	Hs.7212	hypothetical protein PP1044	5.5
25	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase	5.5
23	419172	AW338625	Hs.22120	ESTs	5.4
	444931 413940	AV652066	Hs.75113	general transcription factor IIIA	5.4
	410480	A1633205 R97457	Hs.159914	ESTs	5.4
	447072	D61594	Hs.63984 Hs.17279	cadherin 13, H-cadherin (heart) tyrosyfprotein suffotransferase 1	5.4
30	434361	AF129755	Hs.117772	ESTs	5.4 5.4
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	5.4
	445175	AV652851	Hs.300848	ESTs	5.4
	411213	AA676939	Hs.69285	neuropitin 1	5.4
26	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	5.4
35	422667	H25642	Hs.133471	EST ₅	5.4
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	5.4
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	5.4
	452060 419093	W26980 AI804054	Hs.153612 Hs.112885	ATP-binding cassette, sub-family F (GCN2	5.4
40	436267	AW450938	Hs. 180115	ESTs ESTs	5.4
, 0	405257	A11-130330	14.100113	E318	5.4
	431154	AW971228	Hs.290259	ESTs	5.4 5.4
	415511	AJ732617	Hs.182362	ESTa	5.4
	419175	AW270037	Hs.179507	KIAA0779 protein	5.3
45	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	5.3
	423720	AL044191	Hs.23388	Homo seplens cDNA: FLJ21310 fis, clone C	5.3
	409995	AW960597	Hs.30164	ESTs	5.3
	414911	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4	5.3
50	455718 430598	8E070263 AK001764	Un 247442	gb:QV4-BT0407-280100-090-e07 BT0407 Homo	5.3
50	419985	H66373	Hs.247112 Hs.15973	hypothetical protein FLJ10902	5.3
	428753	AW939252	Hs.192927	ESTs, Highly similar to bA393J16.3 [H.se hypothetical protein FLJ20251	5.3
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	5.3 5.3
	404176			protein grace prospriotos, receptor (	5.3
55	431475	AI567669	Hs.287316	ESTs .	5.3
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delia-9-desatur	5.3
	405475				5.3
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	5.3
60	446183 417381	AA354991 AF164142	Hs.14222 Hs.82042	Home sapiens mRNA; cDNA DKFZp761P019 (fr	5.3
-	433029	NM_014322		solute carrier family 23 (nucleobase tra opsin 3 (encephalopsin)	5.3
	442837	AI022082	Hs.50492	ESTs	5.3 5.3
	437140	AA312799	Hs.283689	activator of CREM in testis	5.3 5.3
	408989	AW361666	Hs.49500	KIAA0746 protein	5.3
65	417355	D13168	Hs.82002	endothelin receptor type B	5.3
	407361	AA744622	Hs.292645	ESTs, Weskly similar to ALU5_HUMAN ALU S	5.3
	437734	AA693951	Hs.180284	ESTs	5.3
	452234	AW084176	Hs.223296	ESTs .	5.3
70	423057	AW961597	Hs.130816	ESTs	5.3
, 0	439593 446501	8E073597 Al302616	Hs.124863	ESTs .	5.3
	416406	D86961	Hs.150819	ESTs	5.3
	427164	AB037721	Hs.79299 Hs.173871	fipoma HMGIC fusion partner-like 2 KIAA1300 protein	5.2
_	416815	U41514	Hs.80120	UDP-N-acetyl-atpha-D-galactosamine:polyp	5.2
75	448212	AJ475858	1-0.00120	gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sepiens	5.2 5.2
-	412420	AL035668	Hs.73853	bone morphogenetic protein 2	5.2 5.2
	416975	NM_004131		granzyma B (granzyme 2, cytotoxic T-lymp	5.2
	406815	AA833930	Hs.288036	tRNA isopentenytpyrophosphata transferas	5.2
80	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.2
φV	425322	U63630	Hs.155637		5.2
	451156 415910	A1983569 U20350	Hs.232042		5.2
	415910 423024	AA593731	Hs.78913	chemokine (C-X3-C) receptor 1	5.2
	757044		Hs.75613	CD36 antigen (collagen type I receptor,	5.2

	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.2
	451149	AL047586	Hs.10283	ESTs .	5.2
	429458	BE161832	Hs.292689	ESTs	5.2
5	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.2
J	432383	AK000144	Hs.274449	Homo sapiens cONA FLJ20137 fis, clone CO	5.2
	417696 442991	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	5.2
	426711	BE281238 AA383471	Hs.8886 Hs.180669	hypothetical protein FLJ20424 conserved gene amplified in osteosarcoma	5.2 5.2
	438995	AI277986	Hs.164875	ESTs	5.2
10	438582	AI521310	Hs.283365	ESTs, Weakly similar to ALUS_HUMAN ALU S	5.1
	424859	U92014	Hs.153527	Homo saplens pTM5 mariner-like transposo	5.1
	445563	AW873506	Hs.149006	ESTs	5.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	5.1
• •	420567	AK000812	Hs.98874	similar to proline-rich protein 48	5.1
15	420630	AL133101	Hs.99508	Homo sepiens mRNA; cDNA DKFZp43400921 (f	5.1
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	5.1
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	5.1
	438146 423430	Z36842	Hs.57548	ESTS  BADEA & compinion because of B	5.1
20	421633	AF112481 AF121860	Hs.128501 Hs.106260	RAD54, S. cerevisiae, homolog at, B sorting nexts 10	5.1 5.1
20	447197	R36075	FIS. 100200	gb:yh88b01.s1 Soares placents Nb2HP Homo	5.1
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine p	5.1
	456210	N49729	Hs.156875	EST8	5.1
	411893	R82845	Hs.273789	ESTs	5.1
25	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586i1524 (f	5.1
	414696	AF002020	Hs.7691B	Niemann-Pick disease, type C1	5.1
	426822	W78950	Hs.220823	ESTs	5.1
	444269	AI590348	Hs.146220		5.1
30	437204	AL110216	Hs.12285	ESTs	5.1
30	443180	R15875	Hs.70945	ESTs	5.1
	431510 446312	AA580082 BE087853	Hs.112264	ESTS	5.0
	449870	AI672487	Hs.15423	gb:QV1-BT0581-290400-181-h05 BT0681 Homo hypothetical protein HDCMC04P	5.0 5.0
	430462	AI584156	Hs.105640	ESTs	5.0
35	457452	AW972675	14,103040	gb:EST384766 MAGE resequences, MAGL Homo	5.0
-	420397	NM_007018	Hs.97437	centrosomal protein 1	5.0
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.0
	426874	N67325	Hs.247132	ESTs	5.0
40	419746	AW867943	Hs.127216	Homo sapiens cDNA FLJ13465 fs, clone PL	5.0
40	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	5.0
				.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	3.5
				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	5.0
	TABLE 35	i <b>8</b> :			<b>3.0</b>
45	TABLE 35 Pkey:	iB: Uniq	ue Eos probes	et Idenlifier number	
45	TABLE 35	i8: Uniq ber: Gen	ue Eos probes o cluster numb	et Identifier number er	
45	TABLE 35 Pkey: CAT numi	i8: Uniq ber: Gen	ue Eos probes	et Identifier number er	
45	TABLE 35 Pkey: CAT numi	i8: Uniq ber: Gen	ue Eos probes o duster numb bank accessio	et Identifier number er	
	TABLE 35 Pkey: CAT numi Accession Pkey 411937	iB: Uniq ber. Gen u: Gen CAT number 1266219_1	ue Eos probes o cluster numb bank accession Accession AW876826	et Identifier number er n numbers AW876622 AW876624	
45 50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497	B: Unique Communication (CAT number 1266219_1 1373771_1	ue Eos probes o cluster numb bank accession Accession AW876826 BE177661	et Identifier number er n numbers AW876822 AW876624 406215 BE144709 BE144829	
	TABLE 35 Pkey: CAT numi Accession Pkey 411937	iB: Uniq ber. Gen u: Gen CAT number 1266219_1	aue Eos probes e duster numb bank accession Accession AW876826 BE177661 AI656727 A	el Identifier number er n numbers AW876622 AW876624 406215 BE 144709 BE 144829 1697887 AI802122 AA910877 Z28718 T16711 AA6S1731 AL047264	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497	B: Unique Communication (CAT number 1266219_1 1373771_1	aue Eos probes e cluster numb bank accession Accession AW876826 BE177661 AI656727 A	el Identifier number er n numbers AW876622 AW876624 408215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL04726A W055146 R93609 AW467031 Al096866 Al371871 Al126182 Al5647	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
	TABLE 35 Pikey: CAT numi Accession Pikey 411937 413497 420825	.8: Unique der Gen CAT number 1266219_1 1373771_1 196769_1	ue Eos probes o duster numb bank accession AW876826 BE 177661 AI506727 A AI308951 A	et Identifier number er n numbers AW876622 AW876624 406215 BE144709 BE144829 1697887 AI802122 AA910877 Z2871B T16711 AA6S1731 AL047264 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Picey: CAT numi Accession Picey 411937 413497 420825	B: Unique Cere Generic Generic Generic Generic Generic 1266219_1 1373771_1 196769_1 250199_1	aue Eos probes o cluster numb bank accession Av876826 BE 177661 At856727 A AU889510 AW982128	let kientifier number er n numbers AW876622 AW876624 406215 BE 144709 BE 144829 1697887 AI802122 AAS10877 Z28718 T16711 AA651731 AL047264 W055146 R93609 AW467031 A1096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825 425331 437205	B: Unique ber: Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1	ue Eos probes e cluster numb bank accession Accession AW876626 BE177661 AI556727 A AI308951 A AW968970 AL110232	et Identifier number er n numbers AW876622 AW876624 H06215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA355353 AA427363	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Picey: CAT numi Accession Picey 411937 413497 420825	B: Unique der Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1	Accession AW876626 BE177661 AIS08951 A AW089970 AW962128 AL110232 AW979074	let Identifier number er n numbers AW876622 AW876624 106215 BE144709 BE144829 1697887 AI802122 AA910877 Z2871B T16711 AA651731 AL047264 W055146 R93609 AW467031 AL096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA356353 AA427363 V947655 AA834841 AA828650	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825 425331 437205 438966	B: Unique ber: Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1	Accession Avassion Avassion Authorit Alsosop Awassion Authorit Alsosop Awassion	et Identifier number er n numbers AW876622 AW876624 H06215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA355353 AA427363	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966 442161 44312	B: Unique Gen Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 542465_1	Accession Avassion Avassion Authorit Alsosop Awassion Authorit Alsosop Awassion	let Identifier number er n numbers AW876622 AW876624 +06215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA6S1731 AL047264 WW55146 R93609 AW467031 A1096866 A1371871 A1126182 A15647 AW008695 R68682 A1719136 R97752 AW196262 AA356353 AA427363 Y94765 AA834841 AA628650 AI916584 R61781 T77332 F07756 F08149 F07647	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825 425331 437205 425331 437205 442438 443161 448312 447197	B: Unique Carl number Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 571114_1 711623_1	ue Eos probes o duster numb bank accession Avva76616 BE177661 Al556727 A AVV88970 AV962128 AL 110232 AL 110232 AV879074 AA995998 Al038316 A BE087853 BE087853	el Identifier number er n numbers AW876622 AW876624 106215 BE 144709 BE 144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA355353 AA427363 947765 AA834841 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647 1344631 AI261663 AI286184 AI286184	BE000621 R68735 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 436966 442438 44316 44312 447197 447974	B: Uniquer: Generic Ge	ue Eos probes o duster numb bank accession Accession AW876626 BE177661 AI508951 A AU308951 A AW088970 AW956212 AW979074 AA956998 AI 10232 AW979074 ABE087853 R35075 AI	et Identifier number er n numbers AW876622 AW876624 406215 BE144709 BE144829 1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 WW55146 R93609 AW467031 A1096866 A1371871 A1126182 A15647 AW008695 R68682 A1719136 R97752 AW196262 AA356353 AA427363 994765 AA834841 AA828650 A1916584 R61781 T77332 F07756 F08149 F07647 IJ344631 A1261653 A1286184 B66546 R36167	BE000621 R68735 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT numk Accession Pkey 411937 420825 425331 437205 438966 442438 443161 447197 44797 44797 44784 448212	B: Unique Carlo Ca	ue Eos probes o duster numb bank accession Avv876628 BE1776611 AI556727 A AV088970 AW962128 AL 110232 AV979074 AA995998 AI038316 A BE087853 R36075 AI R76885 AI A447888 A	let Identifier number er n numbers er n numbers  AWB76622 AWB76624  106215 BE 144709 BE 144829  1697887 AIB02122 AA910877 Z2871B T16711 AA651731 AL047264  WU55146 R93609 AW467031 AL096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  U344631 AI261653  AI268184  166546 R36167  153674 R77049  W969013	BE000621 R68735 AW992695 AJ768764 AW271284 AW974553
50	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825  425331 437205 438966 442438 443161 448312 447197 447974 448212 451818	B: Unique Gen Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 671114_1 711623_1 745643_1 755099_1 887271_1 887271_1	Accession Av876626 BE 177661 AI556727 AI308951 AW988970 AW962128 AL 110232 AW97998 AI038316 AB99898 AI038316 AR75888 AIA475888 AIA475888 AIA475888 AIA475888 AIA41988	el Identifier number er n numbers AW876622 AW876624 106215 BE 144709 BE 144829 1697887 A1802122 AA910877 Z28718 T16711 AA651731 AL047264 W055146 R93609 AW467031 A1096866 AI371871 AI126182 AI5647 AW008695 R68682 AI719136 R97752 AW196262 AA355353 AA427363 194765 AA834841 AA828650 AI916584 R61781 T77332 F07756 F08149 F07647 1344631 AI261663 AI286184 866546 R36167 153674 R777049 1W969013 805492 W27615	BE000621 R68736 AW992695 AJ768764 AW271284 AW974553
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50 55 60	TABLE 35 Pkey: CAT numk Accession Pkey 411937 420825 425331 437205 438966 442438 443161 447197 447974 448212 451818 453013 453013 455716	B: Unique Carlo Gen CAT number 1266219_1 196769_1 196769_1 250199_1 43463_1 457438_1 542469_1 561305_1 671114_1 71523_1 745643_1 745643_1 745643_1 74569_1 887271_1 94390_1 1352595_1	ue Eos probes o duster numb bank accession Av876626 BE1776611 AI556727 A AI856727 A AV088970 AW962128 AL 110232 AV979074 AA995998 AI033316 A BE087853 R36075 AI R76886 AI AI475858 A AI819018 f AA031407 BE070263	let Identifier number er n numbers er n numbers  AWB76622 AWB76524  106215 BE 144709 BE 144829  1697887 AIB02122 AA910877 Z2871B T16711 AA651731 AL047264  WU555146 R93609 AW467031 AI096866 AI371871 AI 126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  N94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AI261653  AI286184  166546 R36167  153674 R77049  W969013  W969013  W959015  BE070205 BE070205 BE070203 BE070399 BE070203	BE000621 R68735 AW992695 AJ768764 AW271284 AW974553
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50 55 60	TABLE 35 Pkey: CAT numi Accession Pkey 411937 420825 425331 437205 439966 442438 443161 447197 44797 44797 44791 45013 45013 45013 45013 45013 45013 45013	B: Unique Gen Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 542469_1 561305_1 711623_1 745643_1 755099_1 887271_1 94390_1 1352695_1 339381_1 312557	ue Eos probes o duster numb bank accession Avva7666 BE 17766 1 Al556727 A Al308951 A AWW88970 AW962128 AL 110232 A AL 110232 A AW979074 AA995998 Al03316 A BE087853 R36075 Al R76886 Al Al475858 A Al819018 I AA031407 BE07023 AA715284	et Identifier number er n numbers er n numbers  AW876622 AW876624  H06215 BE 144709 BE 144829  1697887 AI802122 AA910877 Z28718 T16711 AA6S1731 AL047264  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA355353 AA427363  Y94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07847  IJ344631 AI261653  AI266184  866546 R36187  IS3674 R77049  W959013  205492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039	BE000621 R68735 AW992695 AJ768764 AW271284 AW974553
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50 55 60 65	TABLE 35 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 4424361 443161 448312 447197 448212 451816 453013 455716 457452 407305  TABLE 3 Pkey: Ref: Strand:	8: Unique Car Gen Car number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 561305_1 671114_1 711623_1 755099_1 887277_1 1352695_1 339381_1 332695_1 550:	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI556727 A AU308951 A AW088970 AW9962128 AL 110232 AW979074 AA995998 AI038316 A BE087853 R36075 AII R76886 AI AI475858 A AIB19018 I AA031407 BE070283 AW972675 AA715284	et Identifier number er n numbers er n numbers  AW876622 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264  W055146 R93609 AW467031 Al096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  994765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AJ261653  AI286184  365546 R36187  S3674 R77049  W969013  W9499013  W9499013  W9499013  W9499013  W9499013  W5492 W27615  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  Deresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) number and from which exons were predicted.	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
50 55 60 65 70	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825  425331 437205 438966 44243 447197 448212 447197 448212 451818 453013 455716 457452 407305  TABLE 3 Pkey: Ref:	8: Unique Car Gen Car number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 561305_1 671114_1 711623_1 755099_1 887277_1 1352695_1 339381_1 332695_1 550:	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI556727 A AU308951 A AW088970 AW9962128 AL 110232 AW979074 AA995998 AI038316 A BE087853 R36075 AII R76886 AI AI475858 A AIB19018 I AA031407 BE070283 AW972675 AA715284	let Identifier number er n numbers  AW876622 AW876624  H06215 BE144709 BE144829  H697887 AI802122 AA910877 Z28718 T16711 AA6S1731 AL047264  WW0S5146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  H94765  AA834811 AA828650  AH916S84 R61781 T77332 F07756 F08149 F07647  H344631 AI261653  AI266184  B66546 R36187  H35674 R77049  W9599013  R05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  AMESPORIAIN OF HISTORY AND HISTOR	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
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50 55 60 65 70	TABLE 35 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 442438 443161 448312 447197 448212 451818 453013 455716 457452 407305 TABLE 3 Pkey: Ref: Strand: NL_position	8: Unique Carlo Gen CAT number 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 561305_1 671114_1 711623_1 745643_1 745643_1 745643_1 745643_1 312557 5C: Unit Section: Indirect Carlo Gen Car	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI556727 A AU308951 A AW088970 AW9962128 AL 110232 AW979074 AA995998 AI038316 A BE087853 R36075 AI3 R76886 AI AI475858 A AI819018 I AA031407 BE070283 AW972675 AA715284  que number co quence source quence source quence of hum icases DNA str icases mucleofi Strand	et Identifier number er n numbers er n numbers  AW876622 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  994765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  IJ34631 AI261653  AI286184  66546 R36187  IS3674 R77049  IW969013  R05492 W27615  R87751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  AM5491 Rumbers In this column are Genbank Identifier (GI) number and from which exons were predicted.  de positions of predicted exons.  Nt_position	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
50 55 60 65 70	TABLE 35 Pkey: CAT numk Accession Pkey 411937 413497 420825 425331 437205 438966 442438 443161 448212 447197 44797 44797 44797 44797 85716 457452 407305 TABLE 3 Pkey: Ref: Strand: NLpositi	8: Unique Carlo Gen CAT number Gen 1266219_1 196769_1 196769_1 196769_1 250199_1 43463_1 4542469_1 561305_1 671114_1 711623_1 745643_1 194390_1 1352695_1 339381_1 312657  5C: Unit Carlo Gen Carlo	ue Eos probes o duster numb bank accession AW876628 BE1776611 AI556727 A AI308951 A AW988970 AW962128 AL 110232 AW979074 AA995998 AI033316 A BE087853 R36075 AI R76886 AI B19018 I AA031407 BE070263 AW972675 AA715284  que number ce quence of hum icates DNA str icates nucleofi Strand Minus	et Identifier number er n numbers  AWB76622 AWB76524  106215 BE 144709 BE 144829  1697887 AIB02122 AA910877 Z2871B T16711 AA651731 AL04726A  WU55146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  V94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  U344631 AI261653  AI268184  166546 R36167  153674 R777049  W969013  305492 W27615  NB5751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  Deresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) number and from which exons were predicted.  de positions of predicted exons.  NL_position  62028-62608	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
50 55 60 65 70	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825  425331 437205 438966 442438 443161 448312 447197 448212 451818 453013 455716 457452 407303  TABLE 3 Pkey: Ref: Strand: NL_position	8: Unique Car Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 67114_1 711623_1 715099_1 332381_1 332381_1 332381_1 312657	ue Eos probes o duster numb bank accession Accession AW876626 BE177661 i At565727 A AU308951 A AW082970 AW962128 AW979074 AA995998 AI 10232 AW979074 AA955998 AI 10232 AW979074 AA955998 AJ038316 A BE087853 R36075 Ai R76886 Ai A4475856 A AB19018 ft AA031407 BE070263 AW972675 AA715284  que number or quence source quence source quence source guence of hum icates DNA str icates nucleofi Strand Minus Minus	et Identifier number er n numbers er n numbers  AW876822 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  949765  AA834841 AA828650  AI95634 R61781 T77332 F07756 F08149 F07647  13944831 AI261653  AI268184  866546 R36167  153674 R77049  W969013  R05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  AR541366 AA523039	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
50 55 60 65 70	TABLE 35 Pkey: CAT num Accession Pkey 411937 420825  425331 437205 438966 4424361 448312 447197 448212 451818 453013 455716 457452 407305 TABLE 3 Pkey: Ref: Strand: NL_position Pkey 401539 402549 403549	8: Unique Central Service Serv	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI556727 A AU308951 A AW088970 AW9962128 AL 110232 AW979074 AA995998 AI AI38316 A BE087853 R36075 AI3 R76886 AI AI475858 A AI819018 I AA031407 BE070283 AW972675 AA715284 que number ci quence source quence source quence of hum- icases DNA str icases mucleofi Strand Minus Minus Minus	el Identifier number er n numbers er n numbers  AW876622 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  Y94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AJ261653  AI286184  366546 R36187  S3674 R77049  W969013  N05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  AA541366 AA523039  AA541366 AA523039  AIRCHOMMERS In this column are Genbank Identifier (GI) number chromosome 22** Dunham, et al. (1999) Nature 402:489-495.  de positions of predicted exons.  N1_position  62028-62608  S3526-53628,55755-55920,57530-57757  137150-137362	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825  425331 437205 438966 442438 443161 448312 447197 448212 451818 453013 455716 457452 407303  TABLE 3 Pkey: Ref: Strand: NL_position	8: Unique Car Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 67114_1 711623_1 715099_1 332381_1 332381_1 332381_1 312657	ue Eos probes o duster numb bank accession AW876628 BE177661 AI656727 A AI308951 A AW988970 AW962128 AL 110232 AW979074 AA995998 AI033316 A BE087853 R36075 AI R76886 AII A4475886 A AB19018 I AA031407 BE070263 AW972675 AA715284  que number co quence of hum icates DNA str icates nucleofi Strand Minus Minus Minus Minus Minus	et Identifier number er n numbers er n numbers  AW876622 AW876624  H06215 BE 144709 BE 144829  H697887 AI802122 AA910877 Z28718 T16711 AA6S1731 AL047264  WW0S5146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA355353 AA427363  94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07847  IJ344631 AI261653  AI266184  B66546 R36187  IS3674 R77049  W969013  D05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  D076850 AA541366 AA523039  D076850 AIS68 AA572965  D076850 AIS68 AA572965  D076850 AA541366 AA523039  D0	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825 425331 437205 438966 442438 443161 448212 447197 448212 447197 448212 447197 448212 47305 TABLE 3 Pkey: Ref: Strand: NL_position Pkoy 401539 402474 403594 403713	B: Unique Gen CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467438_1 71623_1 715099_1 1352695_1 339381_1 339285_1 339381_1 312657  SC: Unique Gen Canada Gen Can	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI556727 A AU308951 A AW088970 AW9962128 AL 110232 AW979074 AA995998 AI AI38316 A BE087853 R36075 AI3 R76886 AI AI475858 A AI819018 I AA031407 BE070283 AW972675 AA715284 que number ci quence source quence source quence of hum- icases DNA str icases mucleofi Strand Minus Minus Minus	el Identifier number er n numbers er n numbers  AW876622 AW876624  406215 BE144709 BE144829  1697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264  W055146 R93609 AW467031 AI096866 AI371871 AI126182 AI5647  AW008695 R68682 AI719136 R97752 AW196262  AA356353 AA427363  Y94765  AA834841 AA828650  AI916584 R61781 T77332 F07756 F08149 F07647  J344631 AJ261653  AI286184  366546 R36187  S3674 R77049  W969013  N05492 W27615  N85751 AW974119 AA031408 AA572965  BE070195 BE070265 BE070202 BE070233 BE070399 BE070203  AA541366 AA523039  AA541366 AA523039  AA541366 AA523039  AIRCHOMMERS In this column are Genbank Identifier (GI) number chromosome 22** Dunham, et al. (1999) Nature 402:489-495.  de positions of predicted exons.  N1_position  62028-62608  S3526-53628,55755-55920,57530-57757  137150-137362	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TABLE 35 Pkey: CAT num Accession Pkey 411937 413497 420825  425331 437205 438966 442438 44316 448212 447197 448212 451818 453013 455716 457452 407303  TABLE 3 Pkey: Ref: Strand: NL position Pkey 401539 402474 403549 403730	8: Unique CAT number: Gen 1266219_1 1373771_1 196769_1 250199_1 43463_1 467436_1 561305_1 671114_1 711622_1 745643_1 755099_1 887271_1 339381_1 332655_1 561305_1 67114_1 687271_1 687271_1 6887271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687271_1 687	ue Eos probes o duster numb bank accession Accession AW876626 BE177661   AI508951 A AX088970 AW9962128 AL 10232   AW979074 AA995998 AL 10232   AW979074 AA955998 AJ038316 / BE087853 R36075 AL R76886 AI AJ475856 / AJ819018 f AA031407 BE070263 AW972675 AA715284  que number or quence of hum icates DNA str icates nucleofi Strand Minus Minus Minus Minus Minus Minus Minus	el Identifier number er n numbers er n numbers  AW876622 AW876624	BE000621 R68735 AW992695 A1768764 AW271284 AW974553 56 A1381460 A1358914 A1419231 AW439733 R87059 AA628064



405475 1931025 Ptus 1548-1702

TABLE 38A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER
Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 36A and the predicted protein contained a structural domain that is indicative of surface or extracessular localization (e.g. ig, In3, egi. 7tm domains). Predicted protein domains are 5

10

35A and the pred noted. Plkey: ExAcon: UnigenetO: Unigene Title: PSOomain: R1:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigena number Unigena gene tide Protein Structural Domain Ratio of turnor to normal tissue

15	Pkey	ExAcon	UnigenelD	Unigene Title	PSDomain	R1
••	424704	AI263293	Hs. 152096	cytochrome P450	SS.0450	40.9
	426559	AB001914	Hs. 170414	paired basic am	TM,Peptidase_S8,P	35.6
	458079	A1796870	Hs.54277	ESTs	TM	33.6 34.6
	446921	AB012113	Hs.16530	small inducible	SS.IL8	25.9
20	452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,XEnk,CUB	
	414821	M63835	Hs.77424	Fc fragment of	TM,SS,AIIIA,COB	24.8
	414812	X72755	Hs.77367	monokine induce		23.4
	426471	M22440	Hs.170009	transforming gr	SS,IL8 TM,SS,EGF	22.1
	449523	NM 000579	Hs.54443	chemokine (C-C	TM,7tm_1	21.3
25	428227	AA321649	Hs.2248	small inducible	ILB	20.7
	456804	AI421645	Hs.139851	caveolin 2	TM,Caveatin	19.5
	411642	NM_014932	Hs.71132	neuroligin 1	TM,SS,COesterase	17.8
	427581	NM_014788	Hs.179703	KIAA0129 gene p	TM	16.2
	448520	AB002367	Hs.21355	doublecorfin an	TM,pkinase	15.6
30	417308	H60720	Hs.81892	KIAA0101 gene p	TM	14.8
• •	421566	NM_000399	Hs.1395	early growth re	TMLzf-C2H2	14.8
	422603	BE242587	Hs.118651	hematopoietical	TM,SS,homeobox	14.6
	425984	AW836277	Hs.165636	hypothetical pr	TM	14.4
	432606	NM_002104	Hs.3066	granzyme K (ser	TM,SS,trypsin	14.2
35	458809	AW972512	Hs.20985	sin3-associated	SS	14.1
	446627	AI973016	Hs.15725	hypothetical pr	TM	13.7 13.6
	452960	AK001335	Hs.31137	Homo sapiens cD	TM,Y_phosphatase	
	420552	AK000492	Hs.98806	hypothetical pr	TM,SS	13.3
	425188	AK002052	Hs.155071	hypothetical pr	TM	13.0
40	419034	NM_002110	Hs.89555	hemopoletic cel	TM,pkinase,SH2.SH3	12.6 12.3
	442932	AA457211	Hs.8858	bromodomain adi	TM,bromodomain,PHD	
	434398	AA121098	Hs.3838	serum-inducible	TM.pkinase,POLO_box	12.3
	450506	NM_004460	Hs.418	fibroblast acti	SS,OPPIV_N_term_Peotidase_S9	12.2 12.1
	425782	U66458	Hs.159525	cell growth reg	SS	12.0
45	426108	AA622037	Hs.166468	programmed cell	TM,OUF122	11.9
	450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	11.7
	452838	U65011	Hs.30743	preferentially	TM	11.7
	426780	BE242284	Hs.172199	adenylate cycla	TM,guanylate_cyc	11.1
	415323	BE269352	Hs.949	neutrophil cyto	TM,SH3,TPR	11.0
50	423508	AW604297	Hs.129711	hepatitis A vir	TM,SS,ig	11.0
	408380	AF123050	Hs.44532	diubiquitin	TM,ubiquitin.7tm_3,ANF_receptor,sushi,7tm_1	11.0
	448410	AK000227	Hs.21126	hypothetical pr	TM	11.0
	451277	AK001123	Hs.26176	hypothetical pr	TM	10.8
	453165	\$74727	Hs.32042	aspartoacytase	TM	10.8
55	418036	Z37976	Hs.83337	latent transfor	SS.TB.EGF	10.5
	431512	BE270734	Hs.2795	factate dehydro	TM.ldh	10.3
	433862	D86960	Hs.3610	KIAA0205 gene p	TMLSS	10.3
	431211	M86849	Hs.5566	gap junction or	TM.connexin	10.2
<b>~</b>	432579	AF043244	Hs.278439	nucleolar prote	TM	10.0
60	439653	AW021103	Hs.6631	hypothetical pr	TM.SS	9.9
	428862	NM_000345	Hs.2316	SRY (sex-determ	TM,HMG_box	9.8
	410762	AF226053	Hs.66170	HSKM-B protein	SS,zf-MYND	9.8
	452431	U88879	Hs.29499	toff-like recep	TM,SS,TIR,LRRCT	9.5
~-	405121	AB028989	Hs.88500	mitogen-actival	SS,vwa,vwd,TIL_Cys_knot,vwc	9.5
65	449625	NM_014253	Hs.23796	odz (odd Oz/ten	SH2,EGF	9.4
	421659	NM_014459	Hs.106511	protocadherin 1	TM,SS,catherin	9.2
	427283	AL119796	Hs.174185	ectonucleotide	TM,SS,Phosphodiest,Somatomedin_B	9.1
	407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	8.9
70	413554	AA319146	Hs.75426	secretogranin I	TM,SS,Granin	8.6
70	418693	A1750878	Hs.87409	thrombospondin	EGF.TSPN.tsp_1,tsp_3,vwc	8.6
	437672	AW748265	Hs.5741	flavohemoprotei	TM,heme_1,oxidored_fad,Cyt_reductase	8.6
	430268	AK000737	Hs.237480	hypothetical pr	TM,SS	8.5
	447850	AB018298	Hs.19822	SEC24 (S. cerev	TM .	8.4
75	435717	AF227905	Hs.105794	UDP-glucose:gly	TM,Glyco_transi_8	8.3
75	433376	AI249361	Hs.74122	caspase 4, apop	TM,ICE_p20,ICE_p10,CARD	8.2
	419490	NM_006144	Hs.90708	granzyme A (gra	TM,SS,trypsin	8.2
	453033	AA325869	Hs.31463	KIAA0281 gene p	TM	8.2
	432328	AJ572739	Hs.195471	6-phosphotructo	TM,6PF2K,PGAM	7.9
80	413719	BE439580	Hs.75498	small inducible	SS,IL8	7.9
٥U	412448	L12964	Hs.73895	tumor necrosis	TM,SS,TNFR_c6	7.9
	424247	X14008	Hs.234734	lysozyme (renal	SS,tys	7.8
	421991	NM_014918	Hs.110488	KIAA0990 protei	SS	7.8
	400793	AA635062	Hs.50094	Homo sapiens mR	TM,BIR,CARD,zf-C3HC4	7.7

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	414646	AA353776	Hs.901	CD48 antigen (B	TMig	7.6
	418372	AA311833	Hs.84318	replication pro	TM	7.6
	408418	AW963897	Hs.44743	KIAA1435 protei	TM,WD40,FYVE	7.6
-	425354	U62027	Hs.155935	complement comp	TM,7tm_1	7.5
5	432753	NM_014075	Hs.278915	PRO0593 protein	TM_pkinase	7.4
	447045	AA326187	Hs.17170	G protein-coupt	TM,7tm_1	7.4
	410577	X91911	Hs.64839	glioma pathogen	TM,SOP	7.4
	422631	BE218919	Hs.118793	hypothetical pr	TM	7.3
10	417022	NM_014737	Hs.80905	Ras association	TM,RA	7.2
10	430105	X70297	Hs.2540	cholinergic rec	TM,neur_chan	7.2
	451621	AJ879148	Hs.26770	fatty acid bind	TM,SS,Ilpocatin	7.2
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	7.2
	426028	NM_001110	Hs.172028	a disintegrin a	TM, SS, disintegrin, Reprotysin	7.2
15	434098	AW662958	Hs.75825	pleiomorphic ad	TM_zFC2H2	7.1
13	426423	NM_012446	Hs.169833	single-stranded	TM	7.1
	412783 431556	BE276738	Hs.74578	DEAD/H (Asp-Glu	TM,dsm,helicase_C	7.1
	420018	AF016028 U56387	Hs.260039	sarcospan (Kras	TM	6.9
	444042	NM_004915	Hs.94376	proprotein conv	TM,SS,Peptidase_S8,P	6.9
20	432656	NM_000246	Hs.10237	ATP-binding cas	TM_ABC_tran	6.9
~~	430066	A1929659	Hs.3076 Hs.237825	MHC class II tr	TMLRR	6.9
	401539	NI323033	15.23/023	signal recognit	TM,TPR	6.9
	416058	L08895	Hs.78995	MADS box transc	TM,SS,zf-8_box,zf-C3HC4,Lysyl_oxidase	6.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu	TM,SRF-TF	6.8
25	424063	NM_002019	Hs.138671	fms-related tyr	TM SS stingen in	6.7
	418026	BE379727	Hs.83213	fatty acid bind	TM,SS,pkinase,ig	6.7
	438619	AB032773	Hs.6341	TU12B1-TY prote	TM,SS,fipocafin TM	6.6
	408741	M73720	Hs.646	carboxypeptidas		6.6
	403549		15.010	rea now hebanes	SS,Zn_carbOpept,Propep_M14 TM,pkinase	6.6
30	435798	BE395289	Hs.12720	elF4E-transport	TM	6.6
	453070	AK001465	Hs.31575	SEC63, endoptas	TM.SS.DnaJ	6.6
	452092	BE245374	Hs.27842	hypothetical pr	TM,SS,Acyltransferase	6.6
	437396	BE140396	Hs.21621	hypothetical pr	TM	6.5 6.4
	402474			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	TM,Peptidase_C1	6.4 6.4
35	401600	BE247275	Hs.151787	U5 snRNP-specif	TM,SS,HECT	6.4 6.4
	415076	NM_000857	Hs.77890	guanylate cycla	TM.guanylate_cyc	6.4
	430335	D80007	Hs.239499	KIAA0185 protei	TM.S1	6.3
	434203	BE262677	Hs.283558	hypothetical pr	TM	6.2
40	430287	AW182459	Hs.125759	ESTs, Weakly si	TM,SS	6.2
40	417259	AW903838	Hs.81800	chandraitin sul	TM,Xlink,lectin_c,sushi,EGF,ig	6.1
	421202	AF193339	Hs.102506	eukaryotic tran	TM,SS	6.1
	452235	AL039743	Hs.28514	Homo saplens mR	TM	6.0
	429653	NM_005955	Hs.211581	metal-regulator	TM.zi-C2H2	6.0
4.5	444484	AK002126	Hs.11260	hypothetical pr	TM	5.9
45	410193	AJ132592	Hs.59757	zinc finger pro	TM,zf-C2H2	5.9
	425361	AA355933	Hs.132221	Homo sapiens cD	TM	5.9
	410361	BE391804	Hs.62661	guanylate bindi	TM,SS,G8P	5.8
	415714	NM_002290	Hs.78672	laminin, alpha	TM,SS,taminin_G,taminin_EGF	5.8
50	421689	N87820	Hs.106826	hypothetical pr	TM,SS,PHD	5.8
50	443837	AJ984625	Hs.9884	spindle pole bo	SS	5.8
	422544	AB018259	Hs.118140	KIAA0716 gene p	TM	5.7
	412584	X54870	Hs.74085	DNA segment on	TM,tectin_c	5.7
	410425	BE278367	Hs.63510	KIAA0141 gene p	TM	5.7
55	426283 430440	NM_003937	Hs.169139	kynureninase (L	TM	5.7
55	413551	X52599	Hs.2561	nerve growth fa	TM,SS,NGF	5.7
	418250	BE242639	Hs.75425	ubiquitin assoc	TM,SS,UBA	5.7
	419839	U29926 U24577	Hs.83918	adenosine monop	TMA_deaminase	5.6
	430253	AK001514	Hs.93304 Hs.236844	phospholipase A	SS	5.6
60	450447	AF212223	Hs.25010	hypothetical pr	TM	5.6
•	414020	NM_002984	Hs.75703	hypothetical pr	TM,ANF_receptor,guarrylate_cyc,pkinase	5.6
	414844	AA296874	Hs.77494	smafi inducible	SS.IL8	5.6
	416498	U33632	Hs.79351	deoxyguanosine potassium chann	SS,dNK	5.6
	430512	AF182294	Hs.241578	U6 snRNA-associ	TM	5.6
65	419929	U90268	Hs.93810	cerebral cavern	SS SS and Seed 44	5.6
• •	407094	AF000574	Hs 22405	leukocyte immun	SS,ank,Band_41	5.5
	411653	AF070578	Hs.71168	Homo sapiens d	TM,SS,Ig	5.5
	452355	N54926	Hs.29202	G protein-coupl	TM,SS,Aa_trans TM,7tm_1	5.5
	440486	BE243513	Hs.7212	hypothetical pr	TM	5.5
70	444825	AW167613	Hs.248	mitogen-activat	TM,SS.pkinase	5.5
-	447072	D61594	Hs.17279	tyrosylprotein	SS SS	5.5
	453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	5.4
	411213	AA676939	Hs.69285	neuropiän 1	TM.CUB,F5_F8_type_C,MAM	5.4
	429688	8E245169	Hs.211610	CUG triplet rep	TM,rm	5.4
75	405257				TM	5.4
-	414911	NM_000107	Hs.77602	damage-specific	TM,WD40	5.4
	430598	AK001764	Hs.247112	hypothetical or	TM	5.3
	428753	AW939252	Hs.192927	hypothetical pr	TMSS	5.3 5.3
00	406625	Y13647	Hs.119597	stearoyl-CoA de	TM,Desaturase	5.3 5.3
80	405475				TM.sugar_tr	5.3 5.3
	430180	AA331406	Hs.75456	A kinase (PRKA)	TM	5.3 5.3
	417381	AF164142	Hs.82042	sotute cerrier	TM_xan_ur_permease	5.3
	433029	NM_014322	Hs.279926	opsin 3 (enceph	TM,7tm_1	5.3
					4.6	<b>5.5</b>

	4	043460					
	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zl-C3HC4	5.3	
	412420	AL035668	Hs.73853	роив шольроденя	SS,TGFo_propeptide,TGF-beta	5.2	
	416975	NM_004131	Hs.1051	granzyme B (gra	SS,trypsin	5.2	
_	451418	BE387790	Hs.26369	hypothetical pr	TM	5.2	
5	425322	U63630	Hs.155637	protein kinase,	TM,MCM,FAT,FATC,PI3_PI4_kinase	5.2	
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.2	
	428593	AW207440	Hs.185973	degenerative sp	TM	5.2	
	417696	BE241624	Hs.82401	CD69 antigen (p	TM,lectin_c	5.2	
	442991	BE281238	Hs.8886	hypothetical pr	TM	5.2	
10	420567	AK000812	Hs.98874	similar to prof	TM	5.1	
	412676	NM_000165	Hs.74471	gap junction pr	TM.connexin	5.1	
	423430	AF112481	Hs.128501	RAD54, S. cerev	TM,SNF2_N,helicase_C	5.1	
	421633	AF121860	Hs.106260	sorting nextin 1	TMPX		
	436943	AA773838	Hs.5353	caspase 10, apo		5.1	
15	414696	AF002020	Hs.76918	Niemann-Pick di	TM,ICE_p10,ICE_p20,DED	5.1	
	446312		113.70315		TM,SS,Patched	5.1	
	420397	BE087853	U. 02422	gb:QV1-BT0681-2	TM	5.0	
	410274	NM_007018	Hs.97437	centrosomal pro	TM	5.0	
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	5.0	
20	TAD: 5 000						
20	TABLE 368						
	Pkey:			et identifier number			
	CAT number		duster numbe				
	Accession:	Gent	ank accession	numbers			
25							
25	Pkay	CAT number	Accession				
	446312	671114_1	BE087853 A	J286184			
	TABLE 360	3:					
_	Pkey:		ue number con	responding to an Eos probes	zet .		
30	Ref:	Sea	ROCE SOUTE	The 7 digit numbers in this e	column are Genbank Identifier (GI) number	Tuebon of all more to the auti	Service antiford (The DAIA
• •		SACI	ence of human	chromosome 22° Dunham	et al. (1999) Nature 402:489-495.	s. Duthant, et al. Teleta to the poor	acabon enques The ONA
	Strand:	India	otos PNA etros	nd from which exons were p	61 81 (1999) (181018 402.405-455.		
	Nt_position			positions of predicted exon			
			ales Huckbulk	positions of predicted exon	3.		
35	Pkey	Ref	Strand	AM			
33	401539	8072433		Nt_position			
	402474	7547175	Minus	62028-62608			
			Minus	53528-53628,55755-5592	0,57530-57757		
	403549	8081591	Minus	137150-137362			•
40	405257	7329310	Plus	73121-73273			
40	405475	1931025	Plus	1548-1702			
	TABLE 37	A: ABOUT 280	GENES DOW	N-REGULATED IN KIDNEY	CANCER		
	TABLE 37	A: ABOUT 280 lists about 280	GENES DOW!	N-REGULATED IN KIDNEY	CANCER	oca wara salamad de for YoNa 354 d	evened that the numerator and
45	Table 37A	lists about 280	genes significa	N-REGULATED IN KIDNEY antly down-regulated in kidn	CANCER by cancer compared to normal kidney The	sse were selected as for Table 35A, o	except that the numerator and
45	Table 37A denominat	lists about 280 or were switch:	genes significa id.	ently down-regulated in kidn	CANCER ey cancer compared to normal kidney The	ase were selected as for Yable 35A, o	except that the numerator and
45	Table 37A denominat Pkey:	lists about 280 or were switch: Unit	genes significa d. ue Eos probes	ently down-regulated in kidn at identifier number	ey cancer compared to normal kildney The	ese were selected as for Table 3SA, o	except that the numerator and
45	Table 37A denominat Pkey: ExAccn:	lists about 280 or were switch Unic Exe	genes significa d. ue Eos probes nplar Accessio	ently down-regulated in kidn	ey cancer compared to normal kildney The	ise were selected as for Table 35A, o	except that the numerator and
45	Table 37A denominat Pkey: ExAccn: UnigenelD	lists about 280 or were switch Unio Exe : Unio	genes significa ed. ue Eos probes nplar Accessio ene number	ently down-regulated in kidn at identifier number	ey cancer compared to normal kildney The	ise were sciected as for Table 35A, o	except that the numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T	lists about 280 or were switch Unio Exe : Unio itle: Unio	genes significa d. ue Eos probes nplar Accessio ane number ene gene title	ently down-regulated in kidn et Identifier number n number, Genbank access	ey cancer compared to normal kildney The	ase were selected as for Table 35A, o	except that the numerator and
45 50	Table 37A denominat Pkey: ExAccn: UnigenelD	lists about 280 or were switch Unio Exe : Unio itle: Unio	genes significa ed. ue Eos probes nplar Accessio ene number	ently down-regulated in kidn et Identifier number n number, Genbank access	ey cancer compared to normal kildney The	ise were selected as for Table 35A, o	except that the numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelO Unigene T R1:	lists about 280 or were switch Unit Exe t: Uniq itle: Uniq Rati	genes significated.  UE Eos probes  Inplar Accessio  ene number  iene gene title  to of normal to t	antly down-regulated in kidn et identifier number n number, Genbank access numor tissue	ey cancer compared to normal kildney The		except that the numerator and
	Table 37A denominat Pkey: ExAccn: Unigene10 Unigene T R1:	lists about 280 or were switch Unic Exe b: Uniq itle: Uniq Rati	genes significated.  Ue Eos probes  Inplar Accessio  ene number  iene gene title  o of normal to t  UnigeneID	antly down-regulated in kidn et identifier number in number, Genbank access numor tissue UnigeneTide	ey cancer compared to normal kidney The	RI	except that the numerator and
	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T R1: Pkey 425260	lists about 280 or were switch Unic Exe b: Uniq itle: Uniq Rati  ExAccn L47726	genes significated.  ue Eos probes implar Accessio ene number ene gene title of normal to the UnigenelD Hs.1870	antly down-regulated in kidni et Identifier number in number, Genbank access urnor tissue UnigeneTide phenylatanine hydroxytas	ey cancer compared to normal kidney. The ion number	R1 50.20	except that the numerator and
50	Table 37A denominat Pkey: ExAccn: Unigene1D Unigene T R1: Pkey 425260 445835	lists about 280 or were switch Unite Exe b: Unite lite: Unite Rati  ExAcon L47726 A1769774	genes significated.  Jue Eos probes inplar Accessio ene frumber iene gene title of normal to the UnigeneID Hs. 1870 Hs. 209831	antly down-regulated in kidn- et identifier number in number, Genbank access turnor tissue Unigene Title phenylatanine hydroxylas ESTs, Weakly similar to A	ey cancer compared to normal kidney. The ion number	R1 50.20 48.14	except that the numerator and
	Table 37A denominat Pkey: ExAccn: Unigened Unigene T R1: Pkey 425260 445835 440243	lists about 280 or were switch Unic Exect: Unic Rati  ExAcon L47726 A1769774 BE301029	genes significated.  June Eos probes propes per	antly down-regulated in kidniet identifier number in number, Genbank access turnor tissue  UnigeneTitle phenylatanine hydroxytas ESTs, Weakly similar to A ESTs	ey cancer compared to normal kidney The ion number e e iLU1_HUMAN ALU S	R1 50.20 48.14 42.54	except that the numerator and
50	Table 37A denominat Pkey: ExAcon: UnigenelD Unigene T R1: Pkey 425260 445835 440243 431657	lists about 280 or were switch Unit Exe it: Unit iller: Unit Rati  ExAcon L47726 A1769774 BE301029 A1345227	genes significad.  Jule Eos probes replar Accessionen number eene gene title to of normal to the UnigeneID Hs. 1870 Hs. 209831 Hs. 226422 Hs. 105448	antly down-regulated in kidniet Identifier number on number, Genbank access numor tissue  UnigeneTide phenylatanine hydroxylas ESTs, Weakly similar to AESTs Weakly similar to ESTs.	ey cancer compared to normal kidney The ion number e e iLU1_HUMAN ALU S	R1 50.20 48.14 42.54 40.14	except that the numerator and
50	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T R1: Pkey 425260 445835 440243 431657 441120	lists about 280 or were switch Unic Exe t: Unic itle: Unic Reti  ExAcon L47726 A1769774 BE301029 A1345227 A1632015	genes significadd.  ue Eos probes  nplar Accessio  ene number  ene gene title  o of normal to t  UnigeneID  Hs. 1870  Hs. 209831  Hs. 226422  Hs. 105448  Hs. 164492	antly down-regulated in kidnet identifier number on number, Genbank access numor tissue  UnigeneTide phenylatanine hydroxylas ESTs, Weakly similar to AESTs, Weakly similar to EESTs, Weakly similar to EESTs.	ey cancer compared to normal kidney The ion number e e iLU1_HUMAN ALU S	R1 50.20 48.14 42.54 40.14 34.56	except that the numerator and
50	Table 37A denominat Pkey: ExAcon: UnigenelD Unigene T R1: Pkey 425260 445835 440243 431657 441120 432488	lists about 280 or were switch Unit Exe Exe I Unit III III III III III III III III III I	genes significadd.  ue Eos probes inplar Accessio ene number ene gene title to of normal to to Unigenel DHs. 1870 Hs. 208311 Hs. 226422 Hs. 105448 Hs. 164492 Hs. 216640	antly down-regulated in kidniet identifier number on number, Genbank access numor tissue  UnigeneTitle phenytalanine hydroxytas ESTs, Weakly similar to AESTs ESTs ESTs	ey cancer compared to normal kidney The ion number e e iLU1_HUMAN ALU S	R1 50.20 48.14 42.54 40.14 34.56 33.16	except that the numerator and
50 55	Table 37A denominat Pkey: ExAccn: UnigenelD Unigene T R1: Pkey 425260 445835 440243 431657 441120 432488 416854	lists about 280 or were switch Unit Unit Exe Unit itle: Unit Rati ExAcon L47726 AI769774 BE301029 AI345227 AI632015 AA551010 H40164	genes significa- due Eos probes nplar Accessio ene number ene gene title o of normal to t UnigenelD Hs. 1870 Hs. 208301 Hs. 226422 Hs. 164492 Hs. 164492 Hs. 216640 Hs. 80296	antly down-regulated in kidniet identifier number on number, Genbank access numor tissue  UnigeneTide phenylatanine hydroxylas ESTs, Weakly similar to AESTs ESTs ESTs ESTs Purkinje cell protein 4	ey cancer compared to normal kidney The ion number e iLU1_HUMAN ALU S i34087 hypotheti	R1 50.20 48.14 42.54 40.14 34.56 33.16 32.06	except that the numerator and
50	Table 37A denominat Pkey: ExAccn: Unigenel D Unigenel T R1: Pkey 425260 445835 440243 431657 441120 432488 415854 438452	lists about 280 or were switch Unite Exercities: Unite Retirement L47726 A1769774 BE301029 A1345227 A1632015 AA551010 H40164 A1220911	genes significado, ue Eos probes aplar Accessio ene number ene gene title o of normal to t UnigeneID Hs. 1870 Hs. 226422 Hs. 105448 Hs. 164492 Hs. 216640 Hs. 80296 Hs. 2288559	antly down-regulated in kidniet Identifier number on number, Genbank access numor tissue  UnigeneTide phenylatanine hydroxylas ESTs, Weakly similar to AESTs ESTs, Weakly similar to EESTs Purkinje cell protein 4 Homo sapiens cDNA: FL.	ey cancer compared to normal kidney The for number e  LU1_HUMAN ALU S  J34087 hypotheti  J20920 fis, clone A	R1 50.20 48.14 42.54 40.14 34.56 33.16 32.06 29.54	except that the numerator and
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	418021 410681	M15881 AW246890	Hs.1137 Hs.65425	uromodulin (uromucoid, Tamm-Horsfall gly calbindin 1, (28kD)	16.11
	443324	R44013	Hs.164225	ESTs	15.84 15.68
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	15.46
5	436637	AI783629	Hs.26766	ESTs	15.18
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	14.52
	434874	N62448	Hs.135906	ESTs	14.46
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-tamity A (ABC1	13.84
10	453685 451939	AL110309 U80456	Hs.27311	gb:DKFZp564L0278_r1 564 (synonym; hfbr2) single-minded (Drosophila) homolog 2	13.48
10	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	13.24 13.05
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, no	12.97
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	12.66
16	431713	AK000388	Hs.267997	EHM2 gene	12.66
15	436679	AJ127483	Hs.120451	ESTs, Weakly similar to unnamed protein	12.36
	413859 425707	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	12.32
	440504	AF115402 AI948966	Hs.11713 Hs.130017	E74-like factor 5 (ets domain transcript ESTs, Weakly similar to VATX_HUMAN VACUO	11.92 11.66
	417275	X63578	Hs.81849	parvalbumin	11.48
20	410929	H47233	Hs.30643	ESTs	11.40
	427167	A1239507	Hs.99196	ESTs	11.34
	445591	AJ471866	Hs.149095	ESTs	11.30
	443622 438935	AI911527	Hs.11805	ESTs .	11.23
25	438461	H40665 AW075485	Hs.31564 Hs.286049	ESTs phosphoserine aminotransferase	11.16 11.00
20	415539	AI733881	Hs.72472	ESTs	10.84
	438081	H49546	Hs.298964	ESTs	9.76
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	9.74
20	407280	AJ241296	Hs.145609	ESTs	9.71
30	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	9.61
	442448 442308	A1733144 AA989402	Hs.129611 Hs.45194	ESTs ESTs	9.52
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	9.51 9.35
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	9.32
35	418068	AW971155	Hs.293902	ESTs, Weakly similar to protyl 4-hydroxy	9.31
	459247	N46243	Hs.110373	ESTs	9.20
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	9.16
	410247 430573	AF181721 AA744550	Hs.61345 Hs.136345	RU2S ESTs	9.10
40	457411	AW085961	Hs.130093	ESTs	9.08 8.99
, ,	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	8.92
	435024	AI863518	Hs.127743	ESTs, Wealdy similar to V-ATPase G-subun	8.76
	435058	AW023337	Hs.5422	glycoprotein M6B	8.74
45	426451	AI908165	Hs.169946	GATA-binding protein 3	8.50
45	450648 426255	A1703366 BE262530	Hs.26766 Hs.2006	ESTS	8.38
	431820	AW410408	Hs.271167	glutathione S-transferase M3 (brain) L-pipecolic acid oxidase	8.31 8.28
	451027	AW519204	Hs.40808	ESTs	8.10
	435823	R07856	Hs.16355	ESTs	8.06
50	429269	AA449013	Hs.99203	ESTs	8.02
	438199	AW016531	Hs.122147		7.94
	442176 450164	AA983764 AI239923	Hs.128910		7.94
	445627	AW818475	Hs.30098 Hs.7363	ESTs ESTs	7.86 7.85
55	445779	AJ253104	Hs.189267		7.82
	407178	AA195651	Hs.104106		7.68
	426966	AM93134	Hs.159125		7.68
	445659	AW300508	Hs.149229	ESTs	7.50
60	403204	AWIGECZA	Un 170401	FCT-	7.46
50	448037 413589	AW195634 AW452631	Hs.170401 Hs.258811		7.30 7.26
	446063	AJ720140	Hs.151079		7.26 7.26
	424626	AA344308	Hs.128427		7.25
	403381				7.16
65	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	7.12
	432102	AW015506	Hs.130730		7.12
	442315 453698	AA173992 AA037615	Hs.7956 Hs.42746	ESTs ESTA	7.10
	415003	M11437	Hs.77741	ESTs kininggen	7.02 6.95
70	426418	M90464	Hs.169825		6.92
	452883	X80031	Hs.150318		6.88
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8	6.76
	410781	AI375672	Hs.165028		6.74
75	424596	AB020639	Hs.151017		6.66
, ,	441031 451099	AI110684 R52795	Hs.7645 Hs.25954	fibrinogen, B beta polypeptide interleukin 13 receptor, alpha 2	6.66 6.64
	437553	A1829935	Hs.130497		6.63
	445285	U03886	Hs.264	GS2 gene	6.54
00	408427	AW194270	Hs.177236	B ESTs	6.52
80	410442	X73424	Hs.63788		6.46
	457001 420205	J03258 AA256395	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	6.46
	420205		Hs.88156 Hs.126830	ESTS DESTS	6.42 6.35
	771007		115.120036		6.36

	425649	U30930	Hs.158540	UDP giycosyltranslerase 8 (UDP-galactose	6.34
	405373 431322	AW970622		ab-EST382704 MACE	6.32
	440094	AI651558	Hs.270372	gb:EST382704 MAGE resequences, MAGK Horno ESTs	6.32 6.27
5	442764	AI762254	Hs.131122	ESTs	6.21
	424433	H04607	Hs.9218	ESTs	6.20
	415025	AW207091	Hs.72307	ESTs 4	6.16
	428927	AA441837	Hs.90250	ESTs SET	6.16
10	439145 424683	H67348 N87519	Hs.269187 Hs.27196	ESTs ESTs	6.06
10	415314	N88802	Hs.5422	glycoprotein MSB	6.04 5.94
	424025	AJ701852	Hs.301296	ESTs	5.90
	445911	A1985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	5.89
16	417332	AW972717	Hs.288462	Homo sapiens cONA: FLJ21511 fis, clone C	5.86
15	440102	A1672443	Hs.131190	ESTs	5.84
	429609 411666	AF002246 AF106564	Hs.210863 Hs.71346	cell adhesion molecule with homology to	5.82
	446224	AW450551	Hs.13308	neurofilament 3 (150kD medium) ESTs	5.82 5.74
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	5.72
20	436802	N34486	Hs.170504	ESTs	5.72
	412452	AA215731	Hs.283446	ESTs. Weakly similar to ALAT_HUMAN ALANI	5.70
	445611	AW41B497	Hs.145583	ESTs	5.66
	440038 424028	AA881627 AF055084	Hs.243989 Hs.153692	ESTs KIAA0686 protein	5.66
25	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUO	5.61 5.60
	425907	AA365752	Hs.155965	ESTs	5.60
	428523	AW974540	Hs.98626	ESTs	5.58
	429918	AW873986	Hs.119383	ESTs	5.58
30	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	5.56
30	446163 427398	AA026880 AW390020	Hs.25252 Hs.20415	Homo sapiens cDNA FLJ 13603 fs., clone PL	5.56
	418504	BE159718	Hs.85335	chromosome 21 open reading frame 11 Homo sapiens mRNA; cDNA DKFZp564D1462 (f	5.52 5.51
	440666	AA902650	Hs.192742	Homo sapiens cDNA FLJ 12785 fis, clone NT	5.50
25	432286	AW327432	Hs.255843	ESTs	5.48
35	451236	A1767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	5.46
	422746	NM_004484	Hs.119651	glypican 3	5.43
	416426 414449	AA180256 AA557660	Hs.210473 Hs.76152	ESTs, Weakly similar to GELS_HUMAN GELSO	5.37
	445898	AF070623	Hs.13423	decorin Homo sapiens clone 24468 mRNA sequence	5.36 5.34
40	451835	T63643	Hs.209715	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.32
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	5.22
	408604	D51408	Hs.21925	EST ₅	5.18
	456576	AA287443		gb:zs52c10.r1 NCI_CGAP_GC81 Homo sapiens	5.18
45	433212 452114	BE218049 N22687	Hs.121820 Hs.8236	ESTs ESTs	5.16
7.5	458072	AJ890347	Hs.271923	Homo sepiens cDNA: FLJ22785 fis, clone K	5.14 5.14
	443005	AI027184	Hs.200918	ESTs	5.14
	408554	AA836381	Hs.7323	ESTs	5.12
50	438609	T62870	Hs.291991	ESTs	5.10
50	429343	AK000785	Hs.199480	epsin 3	5.10
	452223 44 <del>69</del> 25	AA425467 AW974605	Hs.8035 Hs.176669	ESTs ESTs	5.10
	407664	AW063476	Hs.279080	ESTS	5.09 5.08
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	5.06
55	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	5.04
	435343	AW194962	Hs.199028	ESTs	5.04
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothellal (venous	5.04
	442317 404319	AI915599	Hs.129225	ESTs	5.02
60	433637	AW024214	Hs.135405	ESTs .	5.02 4.92
••	440205	T86950	Hs.188465		4.84
	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	4.83
	453125	AW779544	Hs. 115497	Homo sapiens cDNA: FLJ22655 fis, clone H	4.80
65	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	4.78
05	439750 443633	AL359053 AL031290	Hs.57664	Homo sapiens mRNA full length insert cDN	4.75
	449050	AW302858	Hs.9654 Hs.187333	similar to pregnancy-associated plasma p ESTs	4.74
	422237	M13149	Hs.1498	histidine-rich glycoprotein	4.69 4.67
70	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	4.64
70	431130	NM_006103		epididymis-specific, whey-acidic protein	4.58
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	4.58
	403046 450838	R65841	FF 20003	ECT-	4.51
	455887	BE154173	Hs.28653	ESTs gb:PM1-HT0340-201299-004-f12 HT0340 Homo	4.48 4.47
75	453500	A1478427	Hs.43125	go.PM1-1110340-201299-004-112 H10340 H0m0 ESTs	4.47 4.40
-	405701			<del></del>	4.37
	426657	NM_015865			4.37
	451032	W03692	Hs.25832	Homo sapiens mRNA; cDNA OKFZp564P116 (fr	4.37
80	426200	AA371876	Hs.234786		4.35
QQ.	418836 447754	AI655499 AW073310	Hs.161712		4.34
	438209	AL120659	Hs.163533 Hs.6111	Homo sapiens cDNA FLJ14142 fis, clone MA KIAA0307 gene product	4.32 4.23
	404559			Roun bunner	4.22
					****

	413272	AA127923	Hs.293256	ESTs	4.21
	423068 416982	M25629	Hs.123107	kalikrein 1, renal/pancreas/salivary	4.19
	445512	J05401 A1241246	Hs.80691 Hs.148903	creatine kinase, mitochondrial 2 (sarcom EST	4.18 4.17
5	445177	AI215070	Hs.16135	ESTs	4.16
	448475	BE613134	Hs.247474	Homo sapiens cDNA: FLJ21032 fis, clone C	4.14
	402072			•	4.09
	439285	AL133916	Hs.298998	ESTs	4.02
10	429621 450273	AI823386	Hs.130874	Homo sapiens cDNA FLJ14181 fis, clone NT	3.99
10	453511	AW296454 AL031224	Hs.24743 Hs.33102	hypothetical protein FLJ20171 transcription factor AP-2 beta (activati	3.97 3.94
	452620	AA436504	Hs.119286	ESTs	3.92
	425642	X91220	Hs.158462	solute carrier family 12 (sodium/chlorid	3.91
16	435884	AA701443	Hs.192868	ESTs	190
15	416889	AW250318	Hs.80395	mat, T-cell differentiation protein	3.89
	419677 431958	N77342 X63629	Hs.21851 Hs.2877	Homo sapiens cDNA FLJ12900 ffs, clone NT	3.88
	456844	AI264155	Hs.152981	cadherin 3, type 1, P-cadherin (placenta CDP-diacytglycerol synthase (phosphatida	3.84 3.82
	442306	AI820660	Hs.129205	ESTs	3.82
20	438453	D17056	Hs.288959	Homo sapiens cDNA: FLJ20920 fis, clone A	3.81
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.80
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	3.79
	413841 431161	M34276 AA493591	Hs.75576	plasminogen	3.77
25	428544	AA430034	Hs.191611	gb:nh01a12.s1 NCI_CGAP_Thy1 Homo sepiens ESTs	3.76 3.74
	453903	AW299606	Hs.232777	ESTs	3.74
	434061	AW024973	Hs.283675	NPD009 protein	3.73
	444805	AB007899	Hs.12017	KIAA0439 protein; hornolog of yeast ubiqu	3.73
30	440080 440230	AW051597	Hs.143707	ESTA	3.71
50	428735	A1732970 AJ279246	Hs.126246 Hs.192657	ESTs NPHS2 gene (padocin)	3.70
	421832	NM_016098	Hs.108725	HSPC040 protein	3.68 3.66
	430135	NM_000035	Hs.234234	adolase B, tructose-bisphosphate	3.65
25	453055	AW291436	Hs.31917	ESTs	3.65
35	450696	A1654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	3.59
	440232 432099	A1766925 U20760	Hs.112554 Hs.272429	ESTs	3.57
	445924	AI264671	Hs.164166	calcium-sensing receptor (hypocalcluric ESTs	3.57 3.56
	411356	H45377	110.101100	gb:yn99h03.r1 Soares adult brain N2b5HB5	3.56
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.55
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	3.53
	416298	NM_003891	Hs.1011	protein Z. vitamin K-dependent plasma gi	3.53
	423603 436610	AB007880 AW611912	Hs.129883 Hs.120414	KIAA0420 gane product ESTs	3.53
45	425905	AB032959	Hs.161700	KIAA1133 protein	3.50 3.48
	403625			THE STATE OF POLICE	3.47
	425210	AA054679	Hs.155150	ribonuclease P (14kD)	3.45
	430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113 1 promi	3.42
50	448877 456686	AI583696 AI554303	Hs.253313	ESTs	3.40
	414725	AA769791	Hs.35982 Hs.120355	Homo sapiens cDNA FLJ12776 fis, clone NT Homo sapiens cDNA FLJ13148 fis, clone NT	3.38 3.37
	453574	AI767947	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	3.32
	438535	L09078		gb:Homo sapiens mRNA fragment	3.31
55	414040	N58513	Hs.32171	ESTs	3.30
33	451416 444564	AW631469	Hs.203213	EST8	3.30
	408001	AI167877 AA046458	Hs.143715 Hs.95296	ESTs ESTs	3.29
	406666	V00495	Hs.75442	afbumin	3.27 3.24
<i>c</i> 0	421750	AK000768	Hs.107872		3.24
60	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.23
	423968	AF098277	Hs.136529		3.21
	427209 403442	H06509	Hs.92423	KIAA1566 protein	3.20
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate finked moi	3.20 3.19
65	425548	AA890023	Hs.1906	protectin receptor	3.17
	414502	AL133721	Hs.224680	ESTS	3.16
	427811	M81057	Hs.180884		3.14
	436330	NM_004413		dipeptidase 1 (renal)	3.11
70	433942 408692	AW272166 AL040127	Hs.123465 Hs.34074	ESTs dipeptidylpeptidasa VI	3.11
. •	448819	AI589190	Hs.188372		3.10 3.10
	423041	BE170842	Hs.123123		3.10
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	3.10
75	405664	L34041	Hs.25478	glycerol-3-phosphate dehydrogenase 1 (so	3.10
, 5	449850	AW206292	Hs.199751		3.08
	427450 454788	AB014526 AWB20691	Hs.178121	KIAA0626 gene product gb:RC5-ST0300-300100-012-H06 ST0300 Horno	3.08
	444895	AI574383	Hs.301192		3.06 3.06
00	457782	N54493		gb:yv40g05.s1 Soares fetal liver spleen	3.05
80	429023	NM_000312		protein C (inactivator of coagulation (a	3.05
	427041 434788	AJ693661 AF154121	Hs.97557	ESTs	3.01
	434788 419003	AF154121 T78640	Hs.102867 Hs.268595		3.01
			1 1012 000 300	ESTs .	3.01

	TABLE 37B	:				
	Pkey:			identifier number		
5	CAY numbe Accession:		ctuster number ank accession r			
•	MOOGGARAI.	Genu	OUR SUCCESSION I	immer?		
	Pkey	CAT number	Accession			
	411356	1240273_1		37 AW838640		
10	413752 431161	1386338_1 328713_1		161584 BE 161700 BE 161748 829120 AAS33792		
••	431322	331543_1		A503009 AA502998 AA502989 AA502805 T92188		
	438535	45946_1		IS L09094 L09098 L03165 L09102		
	442476	543547_1		069477 AF069476		
15	453685 454554	977734_1 1223842_1		/088119 H22881 WB11702 BENE1442 BENE1422 AMPAZENE AMPACEN	00 AMIDNEONE DEN	1470 DE001470 DE147400 DE147000 AMPROCOCA AMPROCACA
	101001	1220042	AW806991 A	W814082 AW806992 BE061669 AW807002 BE1466	59 AW806995 AW8	1436 BE061430 BE142460 BE146499 AW806994 AW809156 07000 AW845743 AW845747 AW847504 BE142458 BE061431
			BE061435 AV	V847507 BE146650 BE142470 AW814096 AW80701	12 BE061438 AW80	7011 AW806993 BE142465 BE142459 BE142462 AW854330
		•	AW854331 B	E061434 BE061731 BE142464 AW847501 AW80700	)1 BE142463 AW81	1800 BE061437 AW811802 BE061440 AW806997 AW806998
20	454788	12346941	BE061745 BE AW820691	:061753		
	455887	1380836_1		154098 BE154096		
	456576	201378_1		M 19385 BE084078 AJ478347		
	457782 407198	405265_1		79039 N76605		
25	407150		H91679			
	TABLE 370	>				
	Pkey:			t identifier number		
	Ref: Strand:		ence gi ID d identification			
30	Nt_position		nosomal nucleo	olide position		•
	_					
	Pkey 402072	Ref 8117363	Strand Plus	Nt_position 71983-72128		
	403046	3540153	Minus	55707-55859,56369-56511		
35	403204	7622392	Plus	16214-16439		
	403381	9438267	Minus	26009-26178		
	403442 403625	7210003 8569879	Ptus Plus	174560-175270 6551-7111		
40	404319	9211467	Plus	54436-54608		
40	404559	8748893	Minus	73499-73651,89575-89739		
	405373 405701	2076718 4263751	Plus Plus	21294-21575 93243-93384		
	100/01	4200701	F 1425	53245-53304	•	
45	<del></del>					
43	Table 38	A: ABOUT 850	GENES UP-RE	GULATED IN KIDNEY CANCER COMPARED TO N	ORMAL ADULT TIS	SUES
	array such	that the ratio of	genes up-regu l'averace" kidr	iated in litting cancer compared to normal adult tissu nev cancer to "average" normal adult tissues was ore:	es. These were set eter than or acual to	acted from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip 3.0. The "average" kidney cancer level was set to the 90th
	percentile	amongst variou	s kidney cance	rs. The "average" normal adult tissue level was set k	the 70th percentile	amongst various non-malignant tissues. In order to remove gene-
50	specific ba	ckground levels	s of non-specific tio was evaluat	c hybridization, the 15th percentile value amongst vari	ious non-malignant	issues was subtracted from both the numerator and the
50	Pkey:			eo. At identifier number		
	ExAcon:	Exer		n number, Genbank accession number		
	Unigenel D		ene number			
55	Unigene T R1;		ene gene title n of tumor to oc	rmal adult tissues		
				with both books		
	Pkey	ExAcca	UnigenelD	Unigene Title		RI
	435013 447768	H91923 X88400	Hs.110024 Hs.19520	No 10520-EVVD domaio contribiro inches		15.71
60	445178	AJ792241	Hs.129614	Hs.19520:FXYO domain-containing ion tran Hs.129614:kidney-specific membrane prote		14.07 12.56
	432542	AW083920	Hs.16098	Hs.16098:ctaudin 2		12.41
	443595 413719	AF169312	Hs.9613	NM_016109:Homo saplens angiopoletin-like		11.77
	436878	8E439580 8E465204	Hs.75498 Hs.47448	NM_004591:Homo sapiens small inducible c Hs.47448:ESTs		10.39 10.18
65	440304	BE159984	Hs.125395	Hs.125395:ESTs		9.95
	407065	Y10141				9.58
	413049 425983	NM_002151 AK000226	Hs.823 Hs.165619	NM_002151:Homo sapiens hepsin (transmemb		9.51
	423161	AL049227	Hs.124776	Hs.165619:mucin and cadherin-like Hs.124776:Homo sapiens mR; cD DKFZo564N1		8.88 8.77
70	430569	AF241254	Hs.178098	Hs.178098:angiotensin I converting enzym		8.45
	416768	AA363733	Hs.1032	NM_002909:Homo sapiens regenerating isle		7.94
	422357 420737	AF016272 L08096	Hs.115418 Hs.99899	NM_004062:Homo sapiens cadherin 16, KSP- NM_001252:Homo sapiens tumor necrosis fa		7.78 7.78
26	409745	AA077391		AA077391:7814E12 Chromosome 7 Fetal Brai		7.74
75	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei		7.32
	426682 406851	AV560038 AA509784	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family		7.20
	419508	AW997938	Hs.352392 Hs.90785	Hs.352392:major histocompatibility compl Hs.90786:ATP-binding cassette, sub-famil		7.03 6.57
00	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa		6.36
80	436895 431842	AF037335	Hs.5338	NM_001218:Homo sapiers carbonic anhydras		6.31
	431042	NM_005764 H59354	Hs.271473 Hs.374303	NM_005764:Homo saplens epithelial protei Hs.374303:hypothetical protein MGC20576		6.20 6.20
	423803	NM_005709		NM_005709:Homo sapiens PDZ-73 protein (P		6.20 6.19
				41		

	434779	AF153815	Hs.50151	the EDIFF	
	435767	H73505	Hs.117874	Hs.50151:potassium inwardly-rectifying c Hs.117874:ESTs	6.11
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.08
	425280	U31519	Hs.1872		6.02
5	426559	AB001914	Hs.170414	Hs.1872:phosphoenolpyruvate carboxykise NM_002570:Homo sapiens paired basic amin	5.81 5.73
_	451564	AU076698	Hs.132760	NM_001467:Homo sapiens glucose-6-phospha	5.69
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier ta	5.68
	444151	AW972917	Hs.128749	Hs.128749:alpha-methylacyl-CoA racemase	5.66
	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
10	432579	AF043244	Hs.278439	NM_003946:Homo sapiens nucleolar protein	5.45
	448733	NM_005629	Hs.187958	NM_005629:Homo sapians solute carrier fa	5.42
	446650	AB016625	Hs.15813	NM_003060:Homo sapiens solute carrier fa	5.36
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cD: FLJ21909 fis,	5.35
1.5	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamytransferase 1	5.32
15	423081	AF262992	Hs.123159	Hs.123159:sperm associated antigen 4	5.30
	421893	NM_001078	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
	435886 410276	BE265839	Hs.12126	Hs.12126:hepatocellular carcinoma-associ	5.20
	429451	AI554545 BE409861	Hs.359201	Hs.359201:ESTa	5.20
20	446404	AA019961	Hs.202833 Hs.26216	NM_002133:Homo sapiens heme oxygese (dec Hs.26216:Homo sapiens cD: FLJ22811 fis,	5.14
20	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens du PCJ22811 hs,	5.13
	449444	AW818436	Hs.351306	NM_004698:Homo sapiens solute carrier fa	5.09 5.05
	438105	BE245551	Hs.6079	NM_014863:Homo sapiens B cell RAG associ	5.02
	400419	AF084545	1.00.0	AF084545:Homo sapiens versican Vint isof	5.01
25	453920	Al133148	Hs.36602	NM_000204:Homo sapiens I factor (complem	4.99
	447881	BE620886	Hs.355279	Hs.355279:Homo sapiens cD FLJ23711 fis.	4.97
	422253	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
	439024	R96696	Hs.35598	Hs.35598:ESTs	4.88
20	414799	AJ752416	Hs.77326	NM_000598:Homo sapiens insufin-like grow	4.80
30	426530	U24578	Hs.278525	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
	404240				4.71
	414617	AI339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.68
35	448249 447818	AW855331	Hs.337124	Hs.337124:ESTs	4.67
55	449057	W79940 AB037784	Hs.21906 Hs.22941	Hs.21906:Homo saplens clone 24670 mR seq	4.66
	422424	AB037764 AI186431	Hs.296638	Hs.22941:KIAA1363 protein	4.66
	417338	R70429	Hs.81988	NM_004864:Homo sapiens prostate differen NM_001343:Homo sapiens disabled homolog	4.62 4.62
	425873	NM_013390	Hs.160417	NM_013390:Homo sapiens transmembrane pro	4.58
40	444700	NM_003645	Hs.11729	NM_003645:Homo sepiens fatty-acid-Coenzy	4.58
_	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.56
	414763	U97276	Hs.77266	NM_002926:Homo saplens quiescin Q6 (QSCN	4.48
	443358	H65417	Hs.17757	Hs.17757:pleckstrin homology domain-cont	4.45
4.5	440091	A1767388	Hs.37890	Hs.37890:Homo sapiens, clone IMAGE:48275	4.43
45	447131	NM_004585	Hs.17466	NM_004585:Homo sapiens retinoic acid rec	4.43
	405973	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.42
	427740	BE242604	Hs.180616	NM_005505:Homo sapiens CO36 antigen (col	4.40
	436258	AW867491	Hs.107125	Hs.107125:plasmalemma vesicle associated	4.38
50	452884	C05964	Hs.31841	Hs.31841:ESTs	4.37
50	444006 422627 _	BE395085 BE336857	Hs.10086	NM_016639:Homo sapiens type I transmembr	4.36
	418054	NM_002318	Hs.118787 Hs.83354	NM_000358:Homo sapiens transforming grow	4.35
	419011	H56244	Hs.89552	NM_002318:Horno sapiens lysyl oxidase-lik NM_000846:Horno sapiens glutathione S-tra	4,34 4.34
	404277		10.00002	Tim_oood of total papers glatablesia 3-8a	4.33
55	435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
	431779	AW971178	Hs.268571	NM_001645:Homo sapiens apolipoprotein C-	4.29
	406645	M57466	Hs.814	Hs.814:major histocompatibility complex,	4.28
	421485	AA243499	Hs.104800	Hs.104800:hypothetical protein FLJ10134	4.26
<b>~</b> ^	426812	AF105365	Hs.172613	NM_006598:Homo sapians solute carrier fa	4.25
60	407910	AA650274	Hs.41298	NM_013281:Homo sapiens fibronectin leuci	4.22
	438030	X98427	Hs.122634	Hs.122634:ESTs	4.22
	430661	AC005551	Hs.130714	Hs.130714:ESTs, Moderately similar to AF	4.21
	444381	BE387335	Hs.283713	Hs.283713:hypothetical protein BC014245	4.20
65	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	4.16
05	411358 418323	R47479 NM_002118	Hs.94761 Hs.1162	Hs.94761:KIAA1691 protein	.4.15
	449853	AF006823	H5.24040	NM_002118:Homo sapiens major histocompat	4.12
	415198	AW009480	Hs.943	NM_002246:Homo sapiens potassium channel NM_004221:Homo sapiens tural killer cell	4.11
	418751	BE389014	Hs.372548	Hs.372548:phosphoinositide-3-kise, regul	4.11 4.09
70	414166	AW888941	Hs.75789	NM_006096:Homo sapiens N-myc downstream	4.07
	424125	M31669	Hs.1735	Hs. 1735.inhibin, beta B (activin AB beta	4.00
	416926	H03109	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.92
	419175	AW270037	Hs.362996	Hs.362996:KIAA0779 protein	3.92
7-	424218	AF031824	Hs.143212	NM_003650:Homo sapiens cystatin F (leuko	3.91
75	412870	N22788	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.88
	452203	X57522	Hs.352018		3.87
	446872	X97058	Hs.16362	NM_004154:Homo sapiens pyrimidinergic re	3.87
	449961	AW265634	Hs.133100	Hs.133100:ESTs	3.87
80	424517	AI539443	Hs.137447	Hs.137447:Homo sapiens cD FLJ12169 ffs,	3.86
ou	425262	D87119	Hs.155418		3.83
	443639 448133	BE269042	Hs.9661 Hs.73769	NM_002801:Homo sapiens proteasome (proso	3.82
	418030	AA723157 BE207573	Hs.83321	NM_000802:Homo sapiens folate receptor 1 Hs.83321:neuromedin B	3.81
		00001313	110.0004	1 12.000E LITEURUROUN U	3.81

	*****	*****		MA 007404	
•	412939 409162	AW411491 H25530	Hs.75069 Hs.50868	NM_005412:Homo sapiens serine hydroxymet NM_002555:Homo sapiens solute carrier fa	3.80
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.79 3.78
_	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.77
5	430413	AW842182	Hs.241392	NM_002985:Homo saplens small inducible c	3.76
	422282	AF019225	Hs.114309	Hs.114309:apolipoprotein L, 1	3.76
	420747 414875	BE294407 H42679	Hs.99910 Hs.77522	Hs.99910:phosphofructokise, platelet	3.76
	418793	AW382987	Hs.88474	NM_006120:Homo saplens major histocompat Hs.88474:prostaglandin-endoperoxide synt	3.75 3.74
10	446291	BE397753	Hs.14623	NM_006332:Homo sapiens interferon, gamma	3.71
	417289	D86962	Hs.81875	Hs.81875:growth factor receptor-bound pr	3.69
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	3.58
	448569 437270	8E382657 R18087	Hs.21486 Hs.323769	NM_007315:Homo sapiens sigl transducer a	3.68
15	408452	AA054683	Hs.192455	Hs.323769:cisplatin resistance related p Hs.192455:ESTs, Moderately similar to by	3.67 3.67
	443986	Al381750	Hs.283437	Hs.283437:HTGN29 protein	3.66
	418869	AW516565		AW516565:xq01d05.x1 Soares_NHCeC_cervica	3.65
	425998	AU076629	Hs.165950	NM_002011:Homo sepiens Ebroblast growth	3.62
20	428699 418299	AW578252 AA279530	Hs.190161 Hs.83968	NM_014020:Horno sapiens LR8 protein (LR8)	3.62
20	432593	AW301003	Hs.51483	NM_000211:Homo sapiens integrin, beta 2 Hs.51483:Homo sapiens, Similar to RIKEN	3.61 3.59
	415765	NM_005424	Hs.78824	NM_005424:Homo sepiens tyrosine kise wit	3.58
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.57
25	424893	AW295112	Hs.153848	Hs.153648:protein tyrosine phosphatase,	3.57
23	426046 424415	AA833655 NM_001975	Hs.206868 Hs.146580	Hs.206868:Homo sapiens cD FLJ14056 fts, NM_001975:Homo sapiens enclase 2, (gamma	3.57
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	3.57 3.56
	443834	AI741510	Hs.173548	Hs.173548:ESTs	3.54
20	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53
30	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838 449378	AV651680 AW664026	Hs.208558 Hs.59892	Hs.208558:ESTs Hs.59892:ESTs, Wealdy similar to alpha 5	3.52
	411393	AW797437	Hs.69771	NM_001710:Homo saplens B-factor, properd	3.52 3.50
2.5	414311	A1693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50
35	415149	X12451	Hs.78056	NM_001912:Homo saplens cathepsin L (CTSL	3.50
	424321 414825	W74048 X06370	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
	408194	AA601038	Hs.77432 Hs.191797	NM_005228:Homo saplens epidermal growth Hs.191797:ESTs	3.48 3.48
	410600	AW575742	Hs.351676	Hs.351676:ESTs, Weakly similar to T02670	3.47
40	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47
	436856	AJ469355	Hs.127310	Hs.127310:hypothetical protein BC014917	3.47
	419660 413566	8E280337 AW604451	Hs.194693 Hs.285814	NM_003982:Homo sapiens solute carrier fa	3.47
	412104	AW205197	Hs.240951	Hs.285814:growth factor receptor-bound p Hs.240951:ked cuticle homolog 2 (Drosoph	3.47 3.46
45	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
	412276	BE262621	Hs.73798	NM_002415:Homo sapiens macrophage migrat	3.45
	449338 430304	H73444 AL122071	Hs.394 Hs.238927	NM_001124:Homo sapiens adrenomedutlin (A	3.44
50	415388	AF018081	Hs.78409	Hs.238927:Homo sapiens mR; cD DKFZp434H1 (locuslink)NM_030582:Homo sapiens colleg	3.43 3.43
	432210	AI567421	Hs.273330	Hs.273330:agrin	3.43
	418177	N44967	Hs.351554	Hs.351554:Homo sepiens cD FLJ32092 fis,	3.42
	414888 452445	AL039185 AB002438	Hs.77558 Hs.29596	Hs.77558:thyroid hormone receptor intera	3.42
55	414803	X03100	Hs.914	Hs.29596:Homo sapiens mR from chromosome Hs.914:major histocompatibility complex,	3.41 3.41
	419201	M22324	Hs.1239	NM_001150:Homo sepiens alanyi (membrane)	3.41
	445139	AB037848	Hs.12365	Hs.12365:syptotagmin XIII	3.41
	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41
60	417259 439737	AW903838 AI751438	Hs.81800 Hs.41271	Hs.81800:chondroitin sulfate proteoglyca	3.40
•	410636	AA088177	Hs.172870	Hs.41271:Homo saplens mR full length ins Hs.172870:KIAA1913 protein	3.39 3.39
	431590	AB037789	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.38
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.36
65	416700 440516	AW498958	Hs.343475 Hs.161	NM_001909:Homo sapiens cathepsin D (lyso	3.36
0,5	423720	\$42303 AL044191	Hs.23388	NM_001792:Homo sapiens cadherin 2, type Hs.23388:hypothetical protein DKFZp434F0	3.35
	421902	BE392717	1.0.2000	BE392717:601307571F1 NIH_MGC_44 Home sap	3.32 3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
70	421502	AF111856	Hs.105039		3.32
70	416729 430302	U46165 AL137502	Hs.1027 Hs.238679	NM_004165:Homo sapiens Ras-related assoc	3.30
	445084	H38914	Hs.250848		3.30
	406825	A1982529	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.29 3.29
76	446272	BE268912	Hs.14601	NM_005335:Homo sapiens hematopoietic cet	3.28
75	437145	AF007216	Hs.5462	NM_003759:Homo sapiens solute carrier fa	3.27
	444071 414662	A1627808 AL036058	Hs.110524 Hs.76807	Hs.110524:ESTs Hs.76807:major histocompatibility comple	3.27
	436576	AI458213	Hs.77542	Hs.77542:ESTs, Weakly similar to S26650	3.27 3.26
60	424675	NM_005512		NM_005512:Homo sapiens glycoprotein A re	3.25
80	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.25
	449703 414788	H61001 X78342	Hs.171802 Hs.77313		3.25
	414249	A1797994	Hs.279929	NM_003674:Homo sepiens cyclin-dependent Hs.279929:gp25L2 protein	3.25 3.24
				· · · · · · · · · · · · · · · · · · ·	J. <b>2</b> 4

	430396	D49742	Hs.241363	NM_004132:Homo sapiens hyaturon binding	3.23
	424456	AA341017	Hs.25549	Hs.25549:hypothetical protein FLJ20898	3.23
	452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor kise	3.22
5	425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
J	416033 450931	NM_012201 N25158	Hs.78979 Hs.25648	NM_012201:Homo sapiens golgi apparatus p Hs.25648:tumor necrosis factor receptor	3.19 3.19
	428065	AI834046	Hs.157313	Hs.157313:ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
10	439318	AW837046	Hs.6527	Hs.6S27:G protein-coupled receptor 56	3.17
10	427640	AF058293	Hs.180015	NM_001355:Homo sepiens D-dopachrome taut	3.17
	409936 436001	AK001691 AW903849	Hs.57655 Hs.173840	Hs.57655:dudulin 2 Hs.173840:similar to endothelial cell-se	3.16 3.16
	451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
1.5	420256	U84722	Hs.76206	NM_001795:Homo sepiens cadherin 5, type	3.16
15	407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.15
	428593 410026	AW207440 AI912061	Hs.185973 Hs.55016	NM_003676:Homo sapiens degenerative sper Hs.55016:EPS8-retated protein 2	3.15 3.15
	445333	8E537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
	448143	AF039704	Hs.20478	NM_000391:Homo saplens ceroid-lipofuscin	3.14
20	423007	AA320134	Hs.196029	Hs. 196029: Homo sapiens mR for KIAA1657 p	3.14
	416511 439237	NM_006762	Hs.79356	NM_006762:Homo sapiens Lysosomal-associa	3.14
	446899	AW408158 NM_005397	Hs.318893 Hs.16426	Hs.318893:ESTs, Weatly similar to Z195_H NM_005397:Homo saptens podocalyxin-like	3.13 3.13
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.13
25	434398	AA121098	Hs.3838	NM_006622:Homo saplens serum-inducible k	3.12
	441283	AA927670	Hs.131704	Hs.131704:ESTs	3.12
	418945 418458	BE246762 AA332941	Hs.89499 Hs.85226	NM_000698:Homo sapiens arachidote 5-lipo NM_000235:Homo sapiens lipase A, lysosom	3.12 3.12
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.11
30	436905	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11
	411089	AA456454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
	432990 425009	AL036071 X58288	Hs.279899 Hs.154151	NM_003820:Homo saplens tumor necrosis fa NM_002845:Homo saplens protein tyrosine	3.11 3.10
	443601	AI078554	Hs.42658	Hs. 42658: Homo sapiens cD FLJ30167 fis, c	3.10
35	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	3.10
	413672	BE156536	Hs.353632	Hs.353632:ESTs, Moderately similar to hy	3.09
	407786 414586	AA687538 AA306160	Hs.38972 Hs.16488	NM_005727:Homo sepiens tetrespen 1 (TSPA	3.09
	423712	W45802	Hs.81988	NM_002298:Homo sapiens lymphocyte cytoso Hs.81988:disabled homolog 2, mitogen-res	3.08 3.08
40	438552	AJ245820	Hs.6314	NM_012410:Homo sapiens type I transmembr	3.06
	448364	T08958	Hs.297214	Hs.297214:HSPC141 protein	3.06
	426437 437679	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
	422262	NM_014214 AL022315	Hs.5753 Hs.113987	NM_014214:Homo sapiens inositol(myo)-1(o NM_006498:Homo sapiens lectin, galactosi	3.06 3.06
45	410480	R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs:368614	Hs.368614:ESTs	3.05
	418883	BE387036 F06838	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
	453613 408051	AI623351	Hs.374476 Hs.172148	Hs.374476:ESTs Hs.172148:ESTs	3.05 3.05
50	432278	AL137506	Hs.274256	Hs.274256:hypothetical protein FLJ23563	3.04
	407949	W21874	Hs.247057	Hs.247057;ESTs, Weakly similar to 210926	3.04
	418090	U57059	Hs.83429	NM_003810:Homo sapiens tumor necrosis fa	3.04
	433165 425809	AA578904 AA370362	Hs.292437 Hs.57958	Hs.292437:ESTs Hs.57958:EGF-TM7-latrophilin-related pro	3.03 3.03
55	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447831	Al433293	Hs.164115	Hs.164115:ESTs	3.02
	413278	BE563085	Hs.833	NM_005101:Homo saplens Interferon-stimul	3.01
	418870 456376	AF147204 AA663904	Hs.89414 Hs.89862	Hs.89414:chemokine (C-X-C motif), recept Hs.89862:TNFRSF1A-associated via death d	3.00 3.00
60	439738	BE246502	Hs.9598	Hs.9598:sema domain, immunoglobulin doma	3.00
	444416	AW288085	Hs.11156	NM_016494:Homo sapiens hypothetical prot	3.00
	406656	M16714	Hs.89643	Hs.89643:transketolase (Wernicke-Korsako	3.00
	406826 418707	AW516005 U97502	Hs.84298 Hs.87497	Hs.84298:CD74 antigen (invariant polypep Hs.87497:butyrophilin, subfamily 3, memb	2.99 2.99
65	421742	AW970004	Hs.107528	NM_016108:Homo saplens androgen induced	2.99
	406824	AW515961	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	435605	AF151815	Hs.4973	NM_015680:Homo saplens hypothetical prot	2.98
	410491 427648	AA465131	Hs.64001	Hs.64001:Homo saplens clone 25218 mR seq	2.98
70	411125	AI376722 AA151647	Hs.180062 Hs.68877	NM_004159:Homo sepiens protessome (proso NM_000101:Homo sepiens cytochrome b-245,	2.98 2.98
. •	435550	Al224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.98
	429373	NM_014694		NM_014694:Homo sapiens KIAA0605 gene pro	2.98
	445701	AF055581	Hs.13131	NM_005475:Homo sapiens lymphocyte adapto	2.97
75	414649 444207	A1672727 A1565004	Hs.76753 Hs.374415	NM_000118:Homo sapiens endoglin (Oster-R Hs.374415:ESTs	2.97 2.97
, ,	423225	AA852604	Hs.125359		2.97 2.97
	407792	AI077715	Hs.39384	NM_014344:Homo saptens four jointed box	2.97
	445707	AJ248720	Hs.114390	Hs.114390:ESTs	2.96
80	452888 418478	AW955454 U38945	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
30	411441	AL042355	Hs.1174 Hs.70202	Hs.1174:cyclin-dependent kise inhibitor Hs.70202:WO repeat domain 10	2.95 2.95
	443426	AF098158	Hs.9329	Hs.9329:chromosome 20 open reading frame	2.94
	450876	AF189062	Hs.285976	Hs.285976:LAG1 longevity assurance hornol	2.94

	426359	AA376409	Hs.10862	Hs.10862:Homo sapiens cD: FLJ23313 fis.	2.94
	425421	L11669	Hs.157145	NM_001120:Homo sapiens tetracycline tran	2.93
	449879 454075	H03573 R43826	Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93
5	421595	AB014520	Hs.16313 Hs.301685	Hs.16313:Kruppel-like zinc finger protei Hs.301685:KIAA0620 protein	2.93 2.93
_	457949	W69171	Hs.334814	Hs.334814:hypothetical protein FLJ14868	2.92
	443987	AW163123	Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
	430259 415906	BE550182 AJ751357	Hs.375142 Hs.288741	Hs.375142:Re/GEF-tike protein 3, mouse h	2.92
10	429762	A1346255	Hs.216354	Hs.288741:Homo sapiens cD: FLJ22256 ffs, NM_006913:Homo sapiens ring finger prote	2.91 2.91
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.91
	427080 426432	AW068287 AF001601	Hs.301175 Hs.169857	NM_002872:Homo sapiens ras-retated C3 bo NM_000305:Homo sapiens paraoxose 2 (PON2	2.91 2.90
15	431476	BE612705	Hs.256697	Hs.256697:histidine triad nucleotide bin	2.89
	406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
	451144 456362	AW956103 AW973003	Hs.61712	Hs.61712:Homo sapiens cO FLJ31548 fis, c	2.89
	426440	BE382756	Hs.179909 Hs.169902	Hs.179909:nuclear receptor coactivator 6 NM_006516:Homo sapiens solute carrier fa	2.88 2.88
20	456974	M12529	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.88
	418174	1.20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88
	446055 423184	AI815981 NM_004428	Hs.12909 Hs.1624	Hs.12909:mucolipin 1 NM_004428:Homo saplens ephrin-A1 (EF1),	2.88
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87 2.87
25	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143 407151	AW747996 H25836	Hs.160999	Hs.160999:ESTs, Wealthy similar to 178885	2.87
	449349	A1825386	Hs.301527 Hs.352579	Hs.301527:ESTs, Moderately similar to un Hs.352579:Homo sapiens, chromosome 20 op	2.86 2.86
••	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
30	445143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86
	417355 431685	D13168 AW296135	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B	2.86
	408877	AA479033	Hs.130315	NM_006113:Homo sapiens vav 3 oncogene (V Hs.130315:ESTs	2.86 2.85
26	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
35	412014	AI620650	Hs.43761	Hs.43761:gap junction protein, alpha 7,	2.84
	436749 419625	AA584890 U91616	Hs.5302 Hs.182885	NM_006149:Homo sapiens tectin, galactosi NM_004556:Homo sapiens nuclear factor of	2.84 2.84
	439941	Al392640	Hs.18272	Hs. 18272:solute carrier family 38, membe	2.84
40	436496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84
40	422100 439730	AI096988 AF035292	Hs.111554 Hs.6654	NM_005737:Homo saplens ADP-ribosylation	2.83
	447217	BE465754	Hs.17778	Hs.6654:KIAA0657 protein NM_003872:Homo sapiens neuropilin 2 (NRP	2.83 2.83
	428343	AL043021	Hs.12705	Hs. 12705: similar to HYPOTHETICAL 43.1 KD	2.82
45	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mR; cD DKFZp564O24	2.82
43	415523 439668	ALD42003 Al091277	Hs.296847 Hs.302634	NM_003119:Homo sapiens spastic paraplegi	2.81 2.81
	414570	Y00285	Hs.76473	Hs.302634:frizzted homotog 8 (Drosophila NM_000876:Homo sapiens insulin-like grow	2.80
	426535	AU077012	Hs.288582	NM_006287:Homo sapiens tissue factor pat	2.80
50	409649 406655	AA159216 M21533	Hs.55505	Hs.55505:hypothetical protein FLJ20442	2.80
50	415323	BE269352	Hs.277477 Hs.949	Hs.277477:major histocompatibility compt NM_000433:Homo sapiens neutrophil cytoso	2.79 2.79
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cD FLJ14201 fls,	2.78
	451356	AA748418	Hs.164577	Hs.164577:ESTs	2.78
55	450708 433681	AA376654 AJ004377	Hs.350065 Hs.200360	Hs.350065:Homo sapiens cD FL/30634 fis, Hs.200360:Homo sapiens cD FL/13027 fis,	2.78 2.77
	442599	AF078037	Hs.324051	NM_006663:Homo sapiens RelA-associated I	2.76
	414509	AW161311	Hs.76294	NM_001780:Homo sapiens CD63 antigen (mel	2.76
	431394 417331	AK000692 AW411297	Hs.252351 Hs.81972	Hs.252351:HERV-H LTR-associating 2 Hs.81972:SHC (Src homology 2 domain cont	2.76
60	415995	NM_004573	Hs.355888	NM_004573:Homo sapiens phospholipase C,	2.76 2.75
	414911	NM_000107	Hs.77602	NM_000107:Homo sapiens damage-specific D	2.75
	425976 407893	C75094	Hs.334514	Hs.334514:chromosome 6 open reading fram	2.75
	407903	BE408359 AI287341	Hs.43621 Hs.154029	Hs.43621:hypothetical protein MBC3205 Hs.154029:bHLH factor Hes4	2.75 2.75
65	415052	AA724811	Hs.334791	Hs.334791;similar to neurol tetraspanin	2.75
	428494	AA233439	Hs.184634	Hs.184634:hypothetical protein FLJ20005	2.75
	421506 427581	BE302796 NM 014788	Hs.105097 Hs.179703	NM_003258:Homo sapiens thymidine kise 1, NM_014788:Homo sapiens tripartite motif-	2.74 2.74
=-	424527	AW138558	Hs.334873		2.74
70	439578	AW263124	Hs.350547	Hs.350547:nuclear receptor co-repressor/	2.74
	425188	AK002052 AF151020	Hs.155071		2.74
	428013 439333	AP151020 AW384710	Hs.181444 Hs.132986		2.73 2.73
36	450935	BE514743	Hs.355753		2.73
75	421532	AW138207	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.73
	440502 444981	AI824113 AW855398	Hs.78281 Hs.12210	Hs.78281:regulator of G-protein sigfling	2.73
	439219	N33883	Hs.41322	Hs.12210:tumor endothelial marker 6 Hs.41322:ESTs	2.72 2.72
90	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
80	433179 424528	AW362945 AW073971	Hs.162459		2.72
	411213	AA676939	Hs.238954 Hs.69285	Hs.238954:ESTs, Wealtly similar to putati NM_003873:Homo saplens neuropilin 1 (NRP	2.71 2.70
	433012	NM_004045			2.70



	425345	AU077297	Hs.155894	NM_002827:Homo sapiens protein tyrosine	2.69
	428923 427923	BE047698 AW274357	Hs.188785 Hs.301406	Hs.188785:ESTs Hs.301406:hypothetical protein PP3501	2.69 2.69
_	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.69
5	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.68
	416207 420372	NM_014745 AW960049	Hs.79077	NM_014745:Horno sapiens KIAA0233 gene pro	2.68
	420542	NM_000505	Hs.293660 Hs.1321	Hs.293660:gene overexpressed in astrocyt NM_000505:Homo sapiens coagulation facto	2.68 2.67
10	425069	AA687465	Hs.298184	Hs.298184:potassium voltage-gated channe	2.67
10	418558	AW082266	Hs.88131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67
	426251 406701	M24283 AA780613	Hs.168383 Hs.62954	NM_000201:Homo sapiens intercellular adh	2.66
	431681	AK000378	Hs.267566	Hs.62954:ferritin, heavy polypeptide 1 Hs.267566:hypothetical protein FLJ20371	2.66 2.66
1.5	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
15	433101 414774	AW572317 X02419	Hs.12082	Hs.12082:TIGA1	2.66
	427868	A1360119	Hs.77274 Hs.181013	NM_002658:Homo saplens plasminogen activ NM_002629:Homo saplens phosphoglycerate	2.66 2.66
	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, sipha 2	2.66
20	424762	AL119442	Hs.183684	Hs.183684:eukaryotic translation initiat	2.66
20	422048 431350	NM_012445 Al192528	Hs.288126 Hs.164537	NM_012445:Homo saplens spondin 2, extrac Hs.164537:ESTs	2.65
	450184	W31096	Hs.237617	Hs.237617:dipeptidylpeptidase 9	2.65 2.65
	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein	2.65
25	414217 451253	Al309298	Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
23	435905	H48299 AW997484	Hs.26126 Hs.5003	NM_006984:Homo saplens claudin 10 (CLDN1 Hs.5003:SLIT-ROBO Rho GTPase-activating	2.64 2.64
	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	2.63
	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein 8C011406	2.63
30	430223 417526	NM_002514 AA568906	Hs.235935 Hs.82240	NM_002514:Horno saplens nephroblastoma ov NM_004177:Horno saplens syntexin 3A (STX3	2.63
-	409956	AW103364	Hs.727	NM_002192:Homo sapiens syntami sk (51x3	2.63 2.63
	449843	R85337	Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62
	417389	BE 260964	Hs.82045	NM_002391:Homo sapiens midkine (neurite	2.62
35	446312 435099	BE087853 AC004770	Hs.171802 Hs.4756	Hs.171802:Homo sapiens, clone IMAGE:3956 Hs.4756:flap structure-specific endonuci	2.62 2.62
	417920	\$47833	Hs.82927	NM_004037:Homo sapiens adenosine monopho	2.62
	435702	AI033647	Hs.121001	Hs.121001:Homo saplens, clone MGC:45521	2.62
	422959 419938	AV647015 AU076772	Hs.349256 Hs.1279	Hs.349256:paired immunoglobutin-like rec	2.62
40	450954	A1904740	Hs.25691	NM_001733:Homo sapiens complement compon NM_005856:Homo sapiens receptor (calcito	2.62 2.61
	421753	8E314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
	443577 453886	AI078033	Hs.177170	Hs.177170:ESTs, Weakly similar to ALU8_H	2.61
	421883	R66282 X55079	Hs.20247 Hs.1437	Hs.20247:ESTa NM_000152:Homo sapiens glucosidase, alph	2.61 2.60
45	440457	BE387593	Hs.21321	Hs.21321:granufe cell differentiation pr	2.60
	410295	AA741357	Hs.356624	Hs.356624:ESTs	2.59
	420679 451558	X57152 NM_001089	Hs.99853 Hs.26630	NM_001436:Homo sapiens fibrillarin (FBL) NM_001089:Homo sapiens ATP-binding casse	2.59
	444672	Z95636	Hs.11669	Hs.11669:taminin, alpha 5	2.59 2.59
50	408669	AJ493591	Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	426194 421814	T50872 L12350	Hs.2001 Hs.108623	Hs.2001:thromboxane A synthase 1 (platel	2.59
	456371	S76825	Hs.89695	NM_003247:Homo sapiens thrombospondin 2 Hs.89695:insulin receptor	2.59 2.59
	429098	AF030249	Hs.196176	NM_001398:Homo sapiens enoyl Coenzyme A	2.59
55	414443 428484	AU077268	Hs.76144	NM_002609:Homo sapiens platelet-derived	2.59
	453309	AF104032 AI791809	Hs.184601 Hs.32949	NM_003486:Homo sapiens solute carrier fa NM_005218:Homo sapiens defensin, beta 1	2.59 2.59
	412867	AU076861	Hs.74637	NM_003217:Homo sapiens testis enhanced g	2.58
60	432827	Z68128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
00	412669 412115	AW880841 AK001763	Hs.96908 Hs.73239	NM_006034:Homo sapiens p53-induced prote Hs.73239:hypothetical protein FLJ10901	2.58 2.58
	452866	R26969	Hs.268016	Hs.268016:Homo sapiens cD: FLJ21243 fis,	2.58
	435129	Al381659	Hs.267086	Hs.267086:ESTs	2.57
65	424482 410494	BE268621 M36564	Hs.149155	NM_003374:Homo sapiens voltage-dependent	2.57
05	433895	Al287912	Hs.64016 Hs.3628	NM_000313:Homo sapiens protein S (atpha) NM_004834:Homo sapiens mitogen-activated	2.56 2.56
	442566	R37337	Hs.12111	Hs.12111:ESTs	2.56
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
70	442622 430346	NM_000435 AK000331	Hs.8546 Hs.297641	NM_000435:Homo sapiens Notch homolog 3 ( Hs.297641:retinoblastoma-associated fact	2.56
	419344	U94905	Hs.277445	Hs.277445:diacytglycerol kise, zeta (104	2.55 2.55
	426500	NM_014638	Hs.170156	NM_014638:Homo sapiens KIAA0450 gene pro	2.55
	408048 450700	NM_007203 AW732799		NM_007203:Homo sapiens A kise (PRKA) and	2.55
75	417018	M16038	Hs.25348 Hs.80887	NM_005860:Homo sapiens folfistatin-like NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54 2.54
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.54
	422451	AA310753	Hs.42491	Hs.42491:ESTs, Moderately similar to hyp	2.53
	435906 400231	AI686379	Hs.110796	Hs.110796:SAR1 protein	253
80	417849	AW291587	Hs.82733	NM_007361:Homo sapiens nidogen 2 (NID2),	2.53 2.53
	427380	NM_005534	Hs.177559	NM_005534:Homo sapiens interferon garrima	2.52
	428385	AF112213 AJ825880	Hs.184062		2.52
	438000	V/053000	Hs.5985	Hs.5985:non-kise Cdc42 effector protein	2.52

	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteise i	252
	422396	W21872	Hs.7907	Hs.7907:L-fucose kise	2.52 2.52
	420787	AA564248	Hs.351292	Hs.351292:Homo sapiens cO FLJ32605 fis,	2.51
5	430590	AW383947	Hs.246381	NM_001251:Homo sapiens CD68 antigen (CD6	2.51
,	447026 439223	BE313144 AW238299	Hs.324844 Hs.250618	Hs.324844:hypothetical protein IMAGE3455 Hs.250618:UL16 binding protein 2	2.51
	435151	AA348482	Hs.4788	Hs.4788:nicastrin	2.50 2.50
	448202	AB002292	Hs.20695	NM_014629:Homo sapiens Rho guanine nucle	2.50
10	449943	AF104266	Hs.24212	Hs.24212datrophilin	2.50
10	425743 444681	BE396495 AJ243937	Hs.159428 Hs.288316	Hs.159428:BCL2-associated X protein	2.50
	421643	BE281170	Hs.106357	Hs.288315:chromosome 6 open reading fram NM_007126:Homo sapiens valosin-containin	2.50 2.50
	426865	D63476	Hs.172813	NM_003899:Homo sapiens Rho guanine nucle	2.50
16	432306	Y18207	Hs.303090	NM_005398:Homo sapiens protein phosphata	2.49
15	421846 421905	AA017707 Al660247	Hs.1432	NM_002743:Homo sapiens protein kise C su	2.49
	419493	AF001212	Hs.32699 Hs.90744	Hs.32699:Homo sapiens, Similar to RIKEN NM_002815:Homo sapiens proteasome (proso	2.49 2.49
	422530	AW972300	Hs.118110	NM_004335:Homo sepiens bone marrow strom	2.48
20	442821	BE391929	Hs.8752	NM_014255:Homo sapiens transmembrane pro	2.48
20	416919	T97839	Hs.80464	NM_006402-Homo sapiens hepatitis B virus	2.48
	.443105 430040	X96753 AW503115	Hs.9004 Hs.227823	NM_001897:Homo sapiens chondraitin suffa NM_014287:Homo sapiens pM5 protein (PM5)	2.48
	428028	U52112	Ha.182018	NM_001569:Homo sapiens interleukin-1 rec	2.48 2.47
25	424307	AW293399	Hs.356377	Hs.356377:Homo sapiens, clone IMAGE:3633	2.46
25	434511	R28982	Hs.18106	Hs.18106:ESTs, Wealdy similar to T06291	2.46
	454390 417785	AB020713 X59812	Hs.56966	Hs.56966:KIAA0906 protein	2.46
	424873	AA345051	Hs.82568 Hs.294092	NM_000784:Homo sapiens cytochrome P450, Hs.294092:Homo sapiens mR full length in	2.46 2.46
	422003	AA361760	Hs.296326	Hs.296326:ESTs, Weakly similar to A33533	2.46
30	432126	AA865239	Hs.37196	Hs.37196:putative G protein coupled rece	2.46
	445937	AJ452943	Hs.321231	NM_003779:Homo sapiens UDP-Gal:betaGlcc	2.46
	409354 401179	N68188	Hs.159472	Hs.159472:Homo sepiens cD; FLJ22224 fis,	2.46
	418151	AA864238	Hs.83583	NM_005731:Homo sapiens actin related pro	2.46 2.45
35	422648	D86983	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (prefo	2.45
	431222 411529	X56777	Hs.273790	NM_007155:Homo sepiens zo pellucida glyc	2.45
	411529	AA430348 AL133415	Hs.317596 Hs.297753	Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45
40	422242	AJ251760	Hs.273385	NM_003380:Homo sapiens vimentin (VIM), m NM_016592:Homo sapiens GS complex locus	2.45 2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44
	426410	BE298446	Hs.305890	Hs.305890:BCL2-like 1	2.44
	421064	AJ245432	Hs.101382	NM_006291:Homo sapiens tumor necrosis fa	2.44
45	428157 424398	AI738719 8E397787	Hs.198427 Hs.146393	NM_000189:Homo sapiens hexokise 2 (HK2), NM_014685:Homo sapiens homocysteine-indu	-244
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	2.44 2.44
	426031	AA295251	Hs.166056	Hs.166066:cisplatin resistance associate	2.43
	409817	BE295464	Hs.56607	Hs.56607:Williams-Beuren syndrome chromo	2.43
50	429359 426761	W00482 AJ015709	Hs.2399 Hs.172089	NM_004995:Homo sapiens matrix metallopro	2.43
-0	429332	AF030403	Hs.199263	Hs.172089:pro-encosis receptor inducing NM_013233:Homo sapiens serine threonine	2.43 2.43
	425923	NM_005028	Hs.162808	NM_005026:Homo sepiens phosphoinositide-	2.43
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.43
55	433339 420539	AF019226	Hs.8036	Hs.8036:RAB3D, member RAS oncogene famil	2.42
23	413243	AA282735 AA769266	Hs.44004 Hs.193657	Hs.44004:AD031 protein Hs.193657:ESTs	2.42 2.42
	435029	AF167706	Hs.19280	Hs. 19280:cysteine-rich motor neuron 1	2.42
	422374	AW732869	Hs.1519	Hs. 1519:protein kise, cAMP-dependent, re	2.42
60	444501	AW247624	Hs.11342	NM_004148:Homo sapiens ninjurin 1 (NINJ1	2.42
00	414919 419355	AW087337 AA428520	Hs.194461 Hs.90061	Hs.194461:ESTs NM_006667:Homo sapiens progesterone rece	2.42 2.42
	436042	AF284422	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
	418245	AA088767	Hs.83883	Hs.83883:transmembrane, prostate androge	2.42
65	444215	AB033075	Hs.10669	Hs.10569:development and differentiation	2.41
0.5	408683 423701	R58565 AA329856	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.41
	441783	BE313412	Hs.143022 Hs.7961	Hs.143022:ESTs Hs.7961:Homo sapiens clone 25012 mR sequ	2.41 2.41
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.41
70	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
70	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
	407894 453449	AJ278313 W16752	Hs.41143 Hs.32981	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	408688	A1634522	Hs.152925	Hs.32981:sema domain, immunoglobulin dom Hs.152925:KIAA1268 protein	2.40 2.40
	422448	AW372922	Hs.116774		2.39
75	416269	AA177138	Hs.161671	Hs.161671:ESTs	2.39
	452679	Z42387	Hs.83883	Hs.83883:transmembrane, prostate androge	2.38
	432981 419846	NM_002733 NM_015977		NM_002733:Homo sapiens protein kise, AMP Hs.285681:Williams Beuren syndrome chrom	2.38
	422110	Al376736	Hs.111779		2.38 2.38
80	413092	AA126856	Hs.118665		2.38
	433969	AW207279	Hs.271786		2.37
	451267 447526	AI033894 AI 048753	Hs.117865		2.37
	441320	AL048753	Hs.303649	NM_002982:Homo sapiens small inducible c	2.37

	444000				
	441623 420255	AA315805 NM_007289	Hs.348710 Hs.1298	Hs.348710:Homo sapiens, clone IMAGE:4242 NM_007289:Homo sapiens membrane metallo-	2.37
	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens are family associ	2.37 2.36
_	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.36
5	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) proteise i	2.36
	408212	AA297567	Hs.43728	NM_015696:Homo sepiens weakly similar to	2.36
	430478	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L,	2.36
	405102 423583	41 420055	1/- 120020	A	2.35
10	426125	AL122055 X87241	Hs.129836 Hs.166994	Hs.129836:KIAA1028 protein NM_005245:Homo sapiens FAT tumor suppres	2.35
10	425204	NM_002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35 2.35
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
	421079	AW404994	Hs.101695	Hs. 101695:NCK adaptor protein 2	2.35
16	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
15	412958	BE391579	Hs.75087	NM_006712Homo saplens FAST tise (FASTK)	2.34
	430363 425397	M28713 J04088	Hs.274464	NM_000398:Homo sepiens diaphorase (DH) (	2.34
	451035	AU076785	Hs.156346 Hs.430	NM_001067:Homo sapiens topoisomerase (D) NM_002670:Homo sapiens plastin 1 (I isof	2.34 2.34
	449027	AJ271216	Hs.22880	Hs.22880:dipeptidylpeptidase III	2.34
20	429457	BE243065	Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.34
25	430702 456804	U56979 AI421645	Hs.278568 Hs.139851	NM_000186:Homo septens H factor 1 (compt NM_001233:Homo septens caveolin 2 (CAV2)	2.33
20	453648	W21493	Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33 2.33
	450812	AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
	402575				2.33
20	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32
30	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine	2.32
	442968 410639	AK000606 BE269047	Hs.8868 Hs.65234	NM_004871:Homo sapiens golgi SP receptor Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32 2.32
	450160	BE048099	Hs.183738	Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32
35	407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	2.32
	426780	BE242284	Hs.172199	NM_001114:Homo sapiens adenylate cyclase	2.32
	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
	416354	NM_000633	Hs.79241	NM_000633:Homo sepiens B-cett CLL/lympho	2.31
40	453107 422963	NM_016113 M79141	Hs.279746 Hs.13234	NM_016113:Homo sapiens transient recepto Hs.13234:ESTs, Wealdy similar to hypothe	2.31 2.31
•••	433618	AA602539	Hs.345494	Hs.345494:ESTs, Moderately similar to ZN	2.31
	438584	AAB11347		AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	231
	446126	AW085909	Hs.356618	Hs.356618:ESTs, Wealty similar to PC4259	2.31
45	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
43	433230	AW136134	Hs.220277	Hs.220277:ESTs, Weakly similar to expres	2.30
	410168 446342	AW834050 BE298665	Hs.351432 Hs.14846	Hs.351432:tensin Hs.14846:Homo sapiens mR; cD 0KFZp564D01	2.30 2.30
	418452	BE379749	Hs.85201	NM_005127:Homo saplens C-type (calcium d	2.30
	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29
50	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848	A1417193	Hs.288912	Hs.288912:BBP-like protein 2	2.29
	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
	422562 432828	AI962060 AB042326	Hs.118397	NM_001129:Homo sapiens AE binding protei	2.28
55	412948	BE243313	Hs.287402 Hs.334851	Hs.287402:chondroitin 4-sulfotransferase NM_006148:Homo sapiens UM and SH3 prote	2.28 2.28
•••	426068	AF029778	Hs.166154	NM_002225:Homo saplens jagged 2 (JAG2),	2.28
	456919	NM_003900		NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.28
60	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
00	407736	N41744	Hs.349326		2.28
	413211 422051	AW967107 AW327546	Hs.109274 Hs.111024		2.28 2.27
	438438	AA257992	Hs.50651	Hs.50651:Janus kise 1 (a protein lyrosin	2.27
	436278	BE396290	Hs.5097	NM_004710:Homo sapiens syptogyrin 2 (SYN	2.27
65	454080	Ai199711	Hs.576	NM_000147:Homo sapiens fucosidase, alpha	2.27
	426542	AF190746	Hs.170310		2.27
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27
	402901 412898	AJ129903	Hs.74669	NM MCC74-Marco parismo vestalo conseinte	2.26
70	413020	R98736	FIS.14003	NM_005634:Homo sapiens vesicle-associate R98735;yr31h09.r1 Soares fetal liver sol	2.26 2.26
. •	413939	AL047051	Hs.199961		2.26
	408681	AW953853	Hs.281462		2.25
	412330	NM_005100		NM_005100:Homo sapiens A kise (PRKA) and	2.25
75	442083	R50192	Hs.165062		2.25
/3	418271 433376	NM_000919 AI249361		NM_000919:Homo sapiens peptidytglycine a	2.25
	438562	A1566826	Hs.74122 Hs.25890	NM_001225:Homo sapiens caspase 4, apopto Hs.25890:ESTs, Wealdy similar to transdu	2.25 2.25
	443883	AA114212	Hs.9930	NM_001235:Homo sapiens serine (or cystei	2.25 2.25
00	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.24
80	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24
	407904 429690	W44735 AW956329	Hs.107260 Hs.23721		2.24
	423030	V44320753	rts.23/21	Hs.23721:ESTs	2.24



	443813	AA876372	Un 02004	Un 02051: Unma assistant — D. a.D. DVF7a667000	224
	427458	BE208364	Hs.93961 Hs.29283	Hs.93961:Homo sapiens mR; cD DKFZp667D09 Hs.29283:ESTs, Wealdy similar to LKHU pr	2.24 2.24
	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
_	407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
5	425751	T19239	Hs.1940	NM_001885:Homo sapiens crystallin, alpha	2.23
	456437 413019	A1924228 BE281604	Hs.115165 Hs.75140	Hs.115185:ESTs NM_002337:Homo saplens low density Epop	2.23 2.23
	418862	BE550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23
• •	435284	AAB79470	Hs.96849	Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
10	429630	M85289	Hs.211573	NM_005529:Homo sapiens heparan sulfate p	2.23
	427609 421917	AK000436 AB028943	Hs.179791 Hs.109445	Hs.179791:RAB20, member RAS oncogene fam	2.23 2.23
	446616	R65964	Hs.334873	Hs.109445:hypermethylated in cancer 2 Hs.334873:carboxypep6dase M	2.23
	407232	X04526		X04526:Human liver mR for beta-subunit s	2.23
15	423798	AF047033	Hs.132904	Hs.132904:solute carrier family 4, sodiu	2.23
	446755 452865	AW451473 AI924046	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
	431393	AW971493	Hs.119567 Hs.134269	Hs.119567:ESTs, Wealdy similar to ALU1_H Hs.134269:ESTs, Wealdy similar to 200439	2.22 2.22
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, atpha 2	222
20	428782	X12830	Hs.193400	NM_000565:Homo sapiens interleukin 6 rec	2.22
	446006	NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
	435418 423869	AJ245874	Hs.4245	Hs.4245:chromosome 11 hypothetical prote	2.22
	437730	BE409301 AW071087	Hs.134012 Hs.239176	NM_006688:Homo septens C1q-related facto Hs.239176:insufin-filice growth factor 1 r	2.21 2.21
25	444020	R92962	Hs.35052	Hs.35052:EST8	221
	413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR; cD DKFZp66780	2.21
	412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
	448988 426841	Y09763 AI052358	Hs.22785 Hs.131741	NM_004961:Homo sapiens gamma-aminobutyri	2.21
30	408196	AL034548	Hs.43627	Hs.131741:ESTs NM_006943:Homo sapiens SRY (sex determin	2.21 2.21
	451711	AK000461	Hs.26890	Hs.26890:cat eye syndrome chromosome reg	2.20
	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
	424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20
35	448883 411296	8E614989 BE207307	Hs.7503 Hs.10114	Hs.7503:hypothetical protein FLJ14153 Hs.10114:growth suppressor 1	2.20 2.20
	452268	NM_003512	Hs.28777	NM_003512:Homo sepiens H2A histone famili	2.20
	416810	AF035606	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
	441415	H21497	Hs.7471	Hs.7471:BBP-like protein 1	2.20
40	444212 428044	AW503976 AAD93322	Hs.10649 Hs.301404	NM_004848:Homo sepiens basement membrane	2.19
40	430017	AA263172	Hs.35	NM_006743:Homo sapiens R binding motif p NM_002832:Homo sapiens protein tyrosine	2.19 2.19
	424490	AJ278016	Hs.55565	Hs.55565:ankyrin repeat domain 3	219
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.19
45	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19
43	448262 416065	AW880830 BE267931	Hs.186273 Hs.78996	Hs.186273:ESTs NM_002592:Homo sapiens proliferating cel	219
	442045	C05768	Hs.8078	Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19 2.19
	423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimul	2.19
50	428024	Z29067	Hs.2238	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
30	424503 437696	NM_002205 Z83844	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.19
	405204	203044	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18 2.18
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrob	2.18
55	417418	NM_002468	Hs.82116	NM_002468:Homo sapiens myeloid different	2.18
33	412773 409402	H15785 AF208234	Hs.74573	NM_012268:Homo saplens similar to vaccin	2.18
	443791	N64458	Hs.695 Hs.143345	NM_000100:Homo sapiens cystatin B (stefi Hs.143345:ESTs	2.18 2.18
	435049	AL122067	Hs.4746	Hs.4746: hypothetical protein FLJ21324	218
60	418389	AA830613	Hs.293849		2.18
φU	450712 422007	A1732130 A1739435	Hs.270496		2.18
	453676	AW853745	Hs.39168 Hs.286035	Hs.39168:ESTs, Weakly similar to T17340 Hs.286035:hypothetical protein FLJ22686	2.18 2.18
	415718	F30631	Hs.200237		2.18
66	452688	AA721140	Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18
65	415988	BE407713	Hs.78943	NM_000386:Homo saplens bleomycin hydrola	2,18
	409453 417512	AI885516 X76534	Hs.95812 Hs.82226	Hs.95612:ESTs NM_002510:Horno sapiens glycoprotein (tra	217
	427202	BE272922	Hs.173936		2.17 2.17
	440983	M20681	Hs.7594	NM_006931:Homo sepiens solute cerrier fa	2.17
70	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.17
	429642	X68264 AW007211	Hs.211579		2.17
	427213 437763	AA469389	Hs.348389 Hs.5831	Hs.348389:hypothetical protein FLJ12876 NM_003254:Homo sapiens tissue inhibitor	2.17 2.17
~-	454000	AA040620	Hs.5672	Hs.5672:golgi membrane protein S8140	2.17
75	424247	X14008	Hs.234734		2.16
	403857	44563304	M		2.16
	406648 400265	AA563730	Hs.277477	7 Hs.277477:major histocompatibility compl	215
	442379	NM_004613	Hs.8265	NM_004613:Homo sapiens transglutamise 2	2.16 2.16
80	441892	AB028981	Hs.8021	Hs.8021:KIAA1058 protein	2.16
	417446	AL118671	Hs.82163	NM_000898:Homo sepiens monoamine oxidase	2.16
	418386 414053	AA361739 BE391635	Hs.84549		2.16
	414033	96321032	Hs.75725	NM_003564:Homo sapiens transgelin 2 (TAG	2.16

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	440000	ANNICIEE	11. 0		
	440906 447660	AW161556 AW160386	Hs.240170 Hs.163667	Hs.240170:hypothetical protein MGC2731	2.16
	408279	AF216965	Hs.44095	Hs.163667:ESTs, Weakly similar to CA1H_H Hs.44095:cyclin M3	2.16 2.16
_	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	216
5	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier la	2.16
	415661	AF057307	Hs.78575	Hs.78575:prosaposin (variant Gaucher dis	2.15
	425302 425996	U79115 W67330	Hs.155566	NM_003805:Homo sapiens CASP2 and RIPK1 d	2.15
	413745	AW247252	Hs.374451 Hs.75514	Hs.374451:ESTs NM_000270:Homo sapiens nucleoside phosph	2.15 2.15
10	422070	AF149785	Hs.111126	Hs.111126:pituitary tumor-transforming 1	215
	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM_003463:Homo saplens protein tyrosine	2.15
	438407 435551	AI457122 AF212365	Hs.129673 Hs.5470	Hs.129673:eukaryotic translation initiat	2.15
15	437741	BE561610	Hs.5809	Hs.5470:Interleukin 17B receptor Hs.5809:putative transmembrane protein;	215 215
	441192	AA526626	Hs.7736	NM_016504;Homo sapiens mitochondrial rib	215
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	215
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	2.14
20	425252 427600	AW391162 AW630918	Hs.349306 Hs.179774	Hs.349306:hypothetical protein FLJ31951	214
LU	426818	AA554827	Hs.292996	NM_002818:Homo sapiens proteasome (proso Hs.292996:postmeiotic segregation increa	2.14 2.14
	442110	AF113008	Hs.8102	NM_001023:Homo saplens ribosomal protein	2.14
	407797	AK000524	Hs.39850	Hs.39850:uridine kise-like 1	2.14
25	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolite phospho	2.14
23	437103 442069	AW139408 AW664144	Hs.152940 Hs.297007	Hs.152940:ESTs Hs.297007:Homo sapiens cD FLJ32174 fis,	2.14 2.14
	424954	NM_000545	Hs.1846	NM_000546:Homo sapiens turnor protein p53	2.14
	458097	AW341135	Hs.58104	Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
20	411925	AW014588	Hs.72925	NM_003475:Homo sepiens chromosome 11 ope	2.14
30	449644 422675	AW960707 BE018517	Hs.148324	Hs.148324:ESTs	2.14
	428586	M36712	Hs.119140 Hs.2299	NM_001970:Horno sapiens eukaryotic transl Hs.2299:CD8 antigen, beta polypeptide 1	2.14 2.14
	429379	NM_014840	Hs.200598	NM_014840:Homo sapiens KIAA0537 gene pro	2.13
26	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	213
35	443895	AW979048	Hs.292566	Hs.292566:YEA4 protein	2.13
	428145 453518	BE243327 AW503205	Hs.182626 Hs.27268	NM_012264:Homo sapiens chromosome 22 ope	2.13
	456534	X91195	Hs.100623	Hs.27268:Homo sapiens cD: FLJ21933 fis, Hs.100623:protein phosphatase 1, regulat	213 213
	419972	AL041465	Hs.182982	Hs.182982:golgin-67	2.13
40	424950	AA602917	Hs.156974	Hs.156974:ESTs	2.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	213
	431449 418758	M55994 AW959311	Hs.256278 Hs.172012	NM_001066:Homo saplens tumor necrosis fa Hs.172012:hypothetical protein DKFZp434J	2.13 2.13
	434202	BE382411	Hs.3764	NM_000858:Homo sapiens guanylate kise 1	213
45	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.12
	452700	AI859390	Hs.288940	Hs.288940:transmembrane protein 6 (five	2.12
	438033 400847	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing fi	2.12
	447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12 2.12
50	417052	NM_000712	Hs.81029	NM_000712:Homo sepiens biliverdin reduct	2.12
	413284	AU077055	Hs.289107	NM_001166:Homo sapiens bacutoviral IAP r	2.11
	434558 404030	AW264102	Hs.39168	Hs.39168:ESTs, Wealdy similar to T17340	2.11
	410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	2.11 2.11
55	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kise	2.11
	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.11
	433026 426433	AW160616 L38969	Hs.279921	NM_016127:Homo sapiens hypothetical prot	2.11
	442439	U09759	Hs.169875 Hs.246857	NM_007112:Homo sapiens thrombospondin 3 NM_002752:Homo sapiens mitogen-activated	2.11 2.11
60	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	211
	400208			• •	2.11
	455705	AW161061	Hs.356580		2.11
	417599 416728	AA204688 AB024597	Hs.62954 Hs.79658	Hs.62954:fertiin, heavy polypeptide 1 NM_001894:Homo sapiens casein kise 1, ep	2.10 2.10
65	439920	H05430	Hs.288433	Hs.288433:neurotrimin	2.10
	422309	U79745	Hs.114924		2.10
	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517 421872	AA359753	Un 22024	No 2000 At DOD blades seek in 40400 4-	2.10
70	437712	X04588	Hs.22824 Hs.85844	Hs.22824:MY8 binding protein (P160) 1a Hs.85844:neurotrophic tyrosine klse, rec	2.10 2.10
	431214	AA294921	Hs.348024	NM_002881:Homo sapiens v-rat simian teuk	2.10
	412856	BE388745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442064	AJ422867	Hs.88594	Hs.88594:Homo sapiens, clone IMAGE:43329	2.10
75	434845 426728	BE267057 NM_007118	Hs.325321 Hs.367689		210
. –	419595	BE379320	Hs.91448	NM_007118:Homo sapiens triple functiol d NM_007026:Homo sapiens dual specificity	2.10 2.09
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.09
80	424658 432805	NM_002406			2.09
30	432805	X94630 AK000310	Hs.3107 Hs.17138	Hs.3107:C097 antigen Hs.17138:hypothetical protein FLJ20303	2.09 2.09
	447484	AA464839	Hs.292566	Hs.292568:YEAA protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09

	445584	AF217518	Hs.8360	Ne 935ADTD012 ambia	2.09
	402559			Hs.8360:PTD012 protein	2.09
	418043 448888	AW377752 AW196663	Hs.83341 Hs.200242	Hs.83341:AXL receptor tyrosine kise	2.09 2.09
5	436910	AA926944	Hs.261587	Hs.200242:caspase recruitment domain fem Hs.261587:GCN2 etF2alpha kise	2.09
-	422573	AW297985	Hs.295726	Hs.295726:integrin, atpha V (vitronectin	2.08
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.08
	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08
10	410301	AW502935	Hs.740	Hs.740:PTK2 protein tyrosine kise 2	2.08
10	449538	AJ559444	Hs.104679 Hs.102541	Hs.104679:Homo sepiens, clone MGC:18216	2.08
	421205 411779	AL137540 AA292811	Hs.72050	Hs.102541:netrin 4 NM_003551:Homo sapiens non-metastatic ce	2.08 2.08
	427704	AW971063	Hs.292882	Hs.292882:ESTs	2.07
	413518	BE149455	Hs.75415	NM_004048:Homo saplens beta-2-microglobu	2.07
15	447345	BE247767	Hs.18166	Hs.18166:KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431 412760	BE613081 AW379030	Hs.41324	Hs.337772:hypothetical protein BC009331 Hs.41324:ESTs	2.07 2.07
	446859	AJ494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
20	403966				2.07
	409115	AI223335	Hs.50651	NM_002227:Homo sapiens Janus kise 1 (a p	2.07
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	2.07
	414045 413980	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.06 2.06
25	439414	NM_002437 NM_001183	Hs.75659 Hs.6551	NM_002437:Homo sapiens MpV17 transgene, NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06
	429849	U33053	Hs.2499	NM_002741:Homo sepiens protein kise C-li	2.06
	402424				2.06
30	406626	X04526	Hs.215595	Hs.215595:guarrine nucleotide binding pro	2.06
20	458911 426086	AA373131 T94907	Hs.24322 Hs.188572	Hs.24322:ATPase, H+ transporting, lysoso Hs.188572:ESTs	2.05 2.05
	419726	U50330	Hs.1274	NM_006129:Homo saplens bone morphogeneti	2.05
	452344	AI264357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
25	442498	U54617	Hs.8364	NM_002612:Homo saplens pyruvate dehydrog	2.05
35	422114	AW194851	Hs.111801	NM_015908:Homo sapiens arsete resistance	2.05
	413420 409430	AW410235 R21945	Hs.75348 Hs.346735	NM_006263:Homo sapiens proteasome (proso Hs.346735:Homo sapiens, clone IMAGE:3881	2.05 2.05
	409932	AI376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
	434848	BE256304	Hs.32148	Hs.32148:AD-015 protein	2.04
40	453852	AW961818	Hs.374424	Hs.374424:ESTs	2.04
	427637	AK000816	Hs.179986	NM_005803:Homo sapiens flotillin 1 (FLOT	2.04
	400264 430016	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	. 2.04 2.04
	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
45	440975	AW499914	Hs.7579	Hs.7579:importin 9	2.04
	432280	BE440142	Hs.2943	NM_003135:Homo saplens sigl recognition	2.04
	409504	AA304961	Hs.699	NM_000942:Homo sapiens peptidylprolyl is	2.04
	412146 434203	M92444 BE262677	Hs.73722 Hs.283558	NM_001641:Homo sapians APEX nuclease (mu Hs.283558:hypothetical protein PRO1855	2.04 2.04
50	422754	AA316476	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
	413086	AA126841	Hs.183834	Hs.183834:ESTs	2.03
	424340 450440	AA339036	Hs.7033	Hs.7033:ESTs	2.03
55	424662	AB024334 NM_002870	Hs.25001 Hs.151536	NM_012479:Homo sapiens tyrosine 3-monoox NM_002870:Homo sapiens RAB13, member RAS	2.03 2.03
•	415740	N80486	Hs.39911	Hs.39911:Homo sapiens mR for FLJ00089 pr	2.03
	412749	AA378417	Hs.74564	NM_003145:Homo sapiens sigl sequence rec	2.03
	408393	AW015318	Hs.23165	Hs.23165:ESTs	2.03
60	421295 445417	AW081081 AK001058	Hs.103180 Hs.12680		2.03 2.03
Ų0	414883	AA926960	Hs.348669	Hs.12680:Homo sapiens cD FLJ10196 fls, c NM_001826:Homo sapiens CDC28 protein kis	2.03
	447298	BE617527	Hs.239818		2.02
	459580	AA022888	Hs.176065	Hs.176065:ESTs	2.02
65	422785	AI824114	Hs.289088		2.02
0.5	452696	AIB26645	Hs.211534		2.02
	452050 450690	AVV955U65 AA296698	Hs.333418		2.02
	423527	AI206965	Hs.105861		2.01
70	429545	AIB24164	Hs.356130		2.01
70	439180	A1393742	Hs.199067		2.01
	437193	BE259190	Hs.289721		2.01
	436014 453329	AF281134 T97205	Hs.283741 Hs.193400		2.01 2.01
	407347	AA829847		T23514:seq3329 1-NiB Homo sapiens cD do	201
75	435370	AI964074	Hs.225838	Hs.225838:ESTs	2.01
	430657	AA482910	Hs.370602		2.01
	427157 424833	U51166	Hs.173824		201
	424833 440086	NM_003894 NM_005402		i NM_003894:Homo sapiens period homotog 2 NM_005402:Homo sapiens v-rat simian leuk	2.01 2.01
80	438543	AA810141	Hs.192182		201
	417426	NM_002291	Hs.82124	NM_002291:Homo sapiens laminin, beta 1 (	2.01
	412790			NM_014767:Homo sapiens KIAA0275 gene pro	2.01
	445892	AV655500	Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667009	2.01

	TABLE 388		Fae archoest	idantifias symbos		
	Pikey: CAT number		ctuster number	identifier number		
5	Accession:		ank accession r	iumbers		
	Pkey 409745	CAT Number MH1944_5	Accession	771874 AW198972 GIACTOCC AIGATE ID AIGE14	52 AIDPO7E4 AINPO7401	AA077391 BG012775 BG997382 AA286833 AA150722 Bi007625
	403143	M2115-45_5				06266 BI006991 BI006990 BI007763 BI007762 BIG997377
10				33518 BI027818 BG015789 BI033807 AA3414		
	419671	253275_1		8866 AA248779 W02010		
	437495 418869	65231_1 12789_14	AL390180 AA AA229762 AA	359908 BE177778 BE177779 AW893733 BF75	6318	
	432648	129028_1		618150 AAS57952		·
15	421902	276321_1	BG171436 88	E079601 BE079534 AA299964 BE392717 BE85		
	414667	MH1944_5				AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
				09100 Bi006275 Bi006270 Bi031000 Bi029864 033518 Bi027818 BG015789 Bi033807 AA3414		06266 B1006991 B1006990 B1007763 B1007762 BG997377
	435185	127115_1		804346 AA669490		
20	411331	1076355_1		77002 F13038		
	451876	2328579_1		1021 BF370092 BF370127 BF370060 T62998	437 A1300773 AIAIE404 <i>4</i>	A 14 444FE A14/F0070 A1C70070 A12C0040 A1000477 A1440470
	400261	23110_1		165365 AW014799 AI767973 AW518041 AA909		) Al 144456 AW628070 Al629032 Al358810 Al880433 Al440472
	439195	21979_1		19360 H89546		
25	454694	1065666_1		W936544 AW813513		
	416913 459362	924456_1 12 <b>3</b> 8130_1	AW934714 A AW974073 T	W749864 AW749902 BE162498 BE161005 BE	162499 BE161006 AA19	0449 AW513465 BE182500 BE161007
	******	1230130_1	A1131 401 5 1	30307		
20	TABLE 38					
30	Pkéy: Ref;			esponding to an Eos probeset	Identifica (CI) aumber	Dunham, et al.* refers to the publication entitled "The DNA
	1461.			chromosome 22" Dunham, et al. (1999) Nature		Duttilant, et al. reses to the principles tribled the Orio
	Strand:	Indic	ates ONA stran	d from which exons were predicted.		
35	Nt_positio	n: Indic	cates nucleotide	positions of predicted exons.		
33	Pkey	Ref	Strand	Nt_position		
	403346	8569726	Plus	92752-93015		
	401621 403344	8570184	Minus Plus	193-608		
40	404240	8569726 5002624	Minus	70823-70990 116132-116407,116653-116922		
	401964	3126781	Minus	13510-13725,13847-14015		
	404277	1834458	Minus	91665-91946		
	405121 402493	8102330 9797670	Minus Minus	35816-36004,36587-36684 205146-205240,205428-205542		
45	402121	9188523	Plus	25692-25895		
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757		
	403887 403328	77 10553 8469086	Minus Minus	69533-69868 120428-120703		
	401241	4827300	Minus	30503-30844,31056-31248		
50	401736	3219338	Plus	1771-1894		
	405029 404171	7533975 9930793	Minus Plus	37929-38224 173667-173783,176876-177055		
	401797	6730720	Plus	6973-7118		
55	401234	9929642	Plus	120173-120337		
33	404170 406122	9930793 9144087	Plus Minus	168836-169248 30940-31386		
		3141007	uentha	303-10-31300		
	TABLE 3	9A: 856 GENES	B UP-REGULAT	ED IN RENAL CANCER COMPARED TO NOR	MAL ADULT TISSUES A	ND TO NON-MALIGNANT RENAL TISSUES THAT ARE LIKELY TO
60				ODULATION BY SMALL MOLECULES, PEPT		
00						nant renal fissues that are likely to encode proteins amenable to 0 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows:
	the ratio	of "average" rer	nal cancer to "a	erage" normal adult tissues was greater than or	equal to 2.0, the ratio of	"average" renal cancer to "everage" non-matignant renal tissues was
						s renal specimens, the "average" normal adult tissue level was sel to
65						was set to the 50th percentile value amongst various non-malignant ontained a structural domain that is indicative of having an oncogenic
•						lies (e.g. pkinase, death-domain, 7tm, phosphatase, or
	ion_trans	sporter).	·			
	Pkey: ExAccn:			set identifier number on number, Genbank accession number		
70	Unigene		igene number	Thermal, Company decouper names		
	Unigene		igene gene tite			
	R1:	Ra	dio of turnor to r	ormal adult tissues		
	Pkey	ExAcon	UnigeneID	Unigene Title		RI
75	435013	H91923	Hs.110024	_		15.71
	447768 445178	X86400 Al792241	Hs.19520 Hs.129614	Hs.19520:FXYD domain-containing ion tran		14.07
	432542			Hs.16098:claudin 2		12.56 12.41
90	443595	AF169312	Hs.9613	NM_016109:Homo sapiens angiopoietin-tike		11.77
80	413719 436878		Hs.75498 Hs.47448	NM_004591:Homo sapiens small inducible of Hs.47448:ESTs	:	10.39
	440304		Hs.125395			10.18 9.95
	407065	Y10141	_,	<del></del>		9.58

	413049	NM_002151	Hs.823	ANA 002151More analysis basely (transport	0.51
	425983	AK000226	Hs.165619	NM_002151:Homo saplens hepsin (transmemb Hs.165619:mucin and cadherin-like	9.51 8.88
	423161	AL049227	Hs.124776	Hs.124776:Homo sapiens mR; cD DKFZp564N1	8.77
_	430569	AF241254	Hs.178098	Hs.178098:angiotensin I converting enzym	8.45
5	416768	AA363733	Hs.1032	NM_002909:Homo saplens regenerating isle	7.94
	422357 420737	AF016272 L08096	Ks.115418 Hs.99899	NM_004062:Homo sapiens cadherin 16, KSP-	7.78
	409745	AA077391	ns.53655	NM_001252:Homo sapiens tumor necrosis fa AA077391:7814E12 Chromosome 7 Fetal Brai	7.78 7,74
	413938	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystel	7.32
10	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	7.20
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	7.03
	419508 428953	AW997938 AA306610	Hs.90786 Hs.348183	Hs.90786:ATP-binding cassette, sub-tamil	6.57
	436895	AF037335	Hs.5338	NM_003823:Homo saplens tumor necrosis fa NM_001218:Homo saplens carbonic anhydras	6.36 6.31
15	431842	NM_005764	Hs.271473	NM_005764:Homo sapiens epithelial protei	6.20
	430014	H59354	Hs.374303	Hs.374303:hypothetical protein MGC20576	6.20
	423803 434779	NM_005709 AF153815	Hs.132945	NM_005709:Homo sapiens PDZ-73 protein (P	6.19
	435767	H73505	Hs.50151 Hs.117874	Hs.50151:potassium inwardly-rectifying c Hs.117874:ESTs	6.11 6.08
20	422654	AA315933	Hs.120879	Hs.120879:Homo saplens, clone MGC:32871	6.02
	425280	U31519	Hs.1872	Hs.1872:phosphoenolpyruvate carboxykise	5.81
	426559	AB001914	Hs.170414	NM_002570:Homo sapiens paired basic emin	5.73
	451564 418526	AU076698 BE019020	Hs.132760 Hs.85838	NM_001487:Homo sapiens glucose-6-phospha NM_004207:Homo sapiens solute carrier ta	5.69
25	444151	AW972917	Hs.128749	Hs.128749;alpha-methylacyl-CoA racemase	5.68 5.66
	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
	432579	AF043244	Hs.278439	NM_003946:Homo sapiens nucleolar protein	5.45
	448733 446650	NM_005629 AB016625	Hs.187958	NM_005629:Homo sapiens solute carrier fa	5.42
30	417089	H52280	Hs.15813 Hs.18612	NM_003060:Homo sapiens sotute carrier fa Hs.18612:Homo sapiens cD: FLJ21909 fis,	5.36 5.35
• •	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamyltransferase 1	5.32
	423081	AF262992	Hs.123159	Hs. 123159:sperm associated antigen 4	5.30
	421893	NM_001078 BE265839	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
35	435886 410276	A1554545	Hs.12126 Hs.359201	Hs.12126:hepatocellular carcinoma-associ Hs.359201:ESTs	5.20
-	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygese (dec	5.20 5.14
	446404	AA019961	Hs.26216	Hs.26216:Homo sapiens cD: FLJ22811 fis,	5.13
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.09
40	449444 438106	AW818436 BE245551	Hs.351306 Hs.6079	NM_004696:Homo sapiens solute carrier fa	5.05
-10	400419	AF084545	FIS.0075	NM_014863:Horno sapiens B cell RAG associ AF084545:Horno sapiens versican Vint isof	5.02 5.01
	453920	AI133148	Hs.36602	NM_000204:Homo sapiens i factor (complem	4.99
	447881	BE620886	Hs.355279	Hs.355279:Homo sapiens cD FLJ23711 fis,	4.97
45	422253 439024	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
7,5	414799	R96696 AI752416	Hs.35598 Hs.77326	Hs.35598:ESTs NM_000598:Homo sapiens insulin-like grow	4.88 4.80
	426530	U24578	Hs.278625	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
50	404240 414617	A1220525	11- 000047	14- 0000 47 h	4.71
50	448249	AI339520 AW855331	Hs.288817 Hs.337124	Hs.288817:hypothetical protein FLJ22761 Hs.337124:ESTs	4.68 4.67
	447818	W79940	Hs.21906	Hs.21906:Homo sepiens clone 24670 mR seq	4.66
	449057	AB037784	Hs.22941	Hs. 22941:KIAA1363 protein	4.66
55	422424	Al186431	Hs.296638	NM_004864:Homo sapiens prostate differen	4.62
"	417336 425873	R70429 NM_013390	Hs.81988 Hs.160417	NM_001343:Homo sapiens disabled homolog NM_013390:Homo sapiens transmembrane pro	4.62 4.58
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.58
	414998	NM_002543	Hs.77729	NM_002543:Homo saplens oxidised low dens	4.56
60	414763	U97276	Hs.77266	NM_002826:Homo sapiens quiescin Q6 (QSCN	4.48
OO.	443358 440091	H65417 AJ767388	Hs.17757 Hs.37890	Hs.17757:pieckstrin homology domain-cont Hs.37890:Homo sapiens, clone IMAGE:48275	4.45 4.43
	447131	NM_004585		NM_004585:Homo sapiens retinoic acid rec	4.43
	406973	M34996	Hs.198253	Hs. 198253:major histocompatibility compl	4.42
65	427740	BE242604	Hs.180616		4.40
05	436258 452884	AWB67491 C05964	Hs.107125 Hs.31841	Hs.107125:plasmalemma vesicle associated Hs.31841:ESTs	4.38
	444006	8E395085	Hs.10086	NM_016639:Homo sapiens type I transmembr	4.37 4.38
	422627	8E336857	Hs.118787		4.35
70	418054	NM_002318		NM_002318:Homo sapiens tysyl oxidase-lik	4.34
70	419011 404277	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	4.34
	435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.33 4.30
	431779	AW971178	Hs.268571		4.29
75	406645	M57466	Hs.814	Hs.814:major histocompatibility complex,	4.28
75	421485 426812	AA243499 AF105365	Hs.104800		4.26
	407910	AA650274	Hs.172613 Hs.41296	NM_006598:Homo sepiens sotute carrier fa NM_013281:Homo sepiens fibronectin teuci	4.25 4.22
	438030	X98427	Hs.122634		4.22
90	430861	AC005551	Hs.130714	Hs. 130714:ESTs, Moderately similar to AF	4.21
80	444381	BE387335 BE540090	Hs.2B3713		4.20
	438203 411358	R47479	Hs.7345 Hs.94761	Hs.7345:MAD1 mitotic arrest deficient-li Hs.94761:KIAA1691 protein	4.16 4.15
	418323	NM_002118		NM_002118:Homo sapiens major histocompat	4.13 4.12

	449853	AF006823	Hs.24040	NM 002245:Nome serious selection shapped	411
	415198	AW009480	Hs.943	NM_002246:Homo sapiens potassium channel NM_004221:Homo sapiens tural killer cell	4.11 4.11
	418751	BE389014	Hs.372548	Hs.372548:phosphotnositide-3-kise, regul	4.09
	414166	AW888941	Hs.75789	NM_006096:Homo sapiens N-myc downstream	4.07
5	424125	M31669	Hs.1735	Hs.1735:inhibin, beta B (activin AB beta	4.00
	416926 419175	H03109 AW270037	Hs.263395 Hs.362995	Hs.263395:sema domain, transmembrane dom	3.92
	424218	AF031824	Hs.143212	Hs.362996:KIAA0779 protein NM_003650:Horno sapiens cystatin F (leuko	3.92 3.91
• •	412870	N22788	Hs.82407	Hs.82407:chemokine (C.X-C motif) ligand	3.88
10	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.67
	446872	X97058	Hs.16362	NM_004154:Homo sapiens pyrimidinergic re	3.87
	449961 424517	AW265634 Al539443	Hs.133100 Hs.137447	Hs.133100:ESTs Hs.137447:Homo sapiens cD FLJ12169 fis,	3.87 3.86
	425262	D87119	Hs.155418	Hs.155418:GS3955 protein	3.83
15	443639	BE269042	Hs.9661	NM_002801:Homo sapiens proteasome (proso	3.82
	448133	AA723157	Hs.73769	NM_000802:Homo sapiens folate receptor 1	3.81
	418030 412939	BE207573 AW411491	Hs.83321 Hs.75069	Hs.83321:neuromedin 8	3.81
	409162	H25530	Hs.50868	NM_005412:Homo saplens serine hydroxymet NM_002555:Homo saplens solute carrier ta	3.80 3.79
20	427715	BE245274	Hs.180428	Hs. 180428:KIAA1181 protein	3.78
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.77
	430413	AW842182	Hs.241392	NM_002985:Homo sapiens small inducible c	3.76
	422282 420747	AF019225 BE294407	Hs.114309 Hs.99910	Hs.114309:apolipoprotein L. 1 Hs.99910:phosphofructokise, platelet	3.76 3.76
25	414875	H42679	Hs.77522	NM_006120:Homo sapiens major histocompat	3.75
	418793	AW382987	Hs.88474	Hs.88474:prostaglandin-endoperoxide synt	3.74
	446291	BE397753	Hs.14623	NM_006332:Homo saplens interferon, gamma	3.71
	417289 422672	D86962 X12784	Hs.81875 Hs.119129	Hs.81875:growth factor receptor-bound pr	3.69
30	448569	BE382657	Hs.21486	NM_001845:Homo sapiens collegen, type IV NM_007315:Homo sapiens sigl transducer e	3.68 3.68
	437270	R18087	Hs.323769	Hs.323769:cisplatin resistance related p	3.67
	408452	AA054683	Hs.192455	Hs. 192455:ESTs, Moderately similar to hy	3.67
	443986 418869	AI381750 AW516565	Hs.283437	Hs.283437:HTGN29 protein	3.66
35	425998	AU076629	Hs.165950	AW516565:xq01d05.x1 Soares_NHCeC_cervica NM_002011:Homo sapiens fibroblast growth	3.65 3.62
	428699	AW578252	Hs.190161	NM_014020:Homo sapiens LR8 protein (LR8)	3.62
	418299	AA279530	Hs.83968	NM_000211:Homo sapiens integrin, beta 2	3.61
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
40	415765 445985	NM_005424 BE621800	Hs.78824 Hs.29444	NM_005424:Homo sapiens tyrosine kise wit Hs.29444:putative small membrane protein	3.58 3.57
	424893	AW295112	Hs.153648	Hs.153648:protein tyrosine phosphatase.	3.57
	426046	AA833655	Hs.206868	Hs.206868:Homo sapiens cD FLJ14056 fis,	3.57
	424415	NM_001975	Hs.146580	NM_001975:Homo sapiens enclase 2, (gamma	3.57
45	412612 443834	NM_000047 AI741510	Hs.74131 Hs.173548	NM_000047:Homo sapiens aryisulfatase E ( Hs.173548:ESTs	3.56 3.54
	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53
	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52
50	449378 411393	AW664026 AW797437	Hs.59892 Hs.69771	Hs.59892:ESTs, Wealdy similar to atpha 5 NM_001710:Homo sapiens B-factor, properd	3.52
-	414311	A1693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50 3.50
	415149	X12451	Hs.78056	NM_001912:Homo saplens cathepsin L (CTSL	3.50
	424321	W74048	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
55	414825 408194	X06370 AA601038	Hs.77432 Hs.191797	NM_005228:Homo sapiens epidermal growth Hs.191797:ESTs	3.48
•	410600	AW575742	Hs.351676	Hs.351676:ESTs, Westdy similar to T02670	3.48 3.47
	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47
	436856	AI469355	Hs.127310	Hs.127310:hypothetical protein BC014917	3.47
60	419660 413566	BE280337 AW604451	Hs.194693 Hs.285814	NM_003982:Homo sepiens solute carrier ta Hs.285814:growth factor receptor-bound p	3.47
•	412104	AW205197	Hs.240951	Hs.240951:ked cuticle homotog 2 (Orosoph	3.47 3.46
	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
65	412276 449338	8E262621 H73444	Hs.73798 Hs.394	NM_002415:Homo sapiens macrophage migrat	3.45 3.44
00	430304	AL122071	Hs.238927	NM_001124:Homo sapiens adrenomedullin (A Hs.238927:Homo sapiens mR; cD DKFZp434H1	3,43
	415388	AF018081	Hs.78409	(locuslink)NM_030582:Homo sapiens collag	3.43
	432210	AI567421	Hs.273330	Hs.273330:agrin	3.43
70	418177 414888	N44967 AL039185	Hs.351554 Hs.77558	Hs.351554:Homo sapiens cD FLJ32092 fis, Hs.77558:thyroid hormone receptor intera	3.42
	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.42 3.41
	414803	X03100	Hs.914	Hs.914:major histocompatibility comptex,	3.41
	419201	M22324	Hs.1239	NM_001150:Homo sapiens alanyl (membrane)	3.41
75	445139 435021	AB037848 AA922192	Hs.12365 Hs.73962	Hs.12365:syptotagmin XIII	3.41
	417259	AW903838	Hs.81800	Hs.73962:EphA7 Hs.81800:chondroitin suffate proteoglyca	3.41 3.40
	439737	A1751438	Hs.41271	Hs.41271:Homo sapiens mR full length ins	3.39
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.39
80	431590 415000	AB037789 AW025529	Hs.263395		3.38
50	416700	AW498958	Hs.239812 Hs.343475		3.36 3.36
	440516	S42303	Hs.161	NM_001792:Homo sapiens cadherin 2, type	3.35
	423720	AL044191	Hs.23388	Hs.23388:hypothetical protein DKFZp434F0	3.32
				44.	

	421902	BE392717		BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
_	421502 416729	AF111856 U46165	Hs.105039 Hs.1027	NM_006424:Homo sapiens solute carrier ta NM_004165:Homo sapiens Ras-related assoc	3.32 3.30
5	430302	AL137502	Hs.238679	Hs.238679:Rag D protein	3.30
	445084 406825	H38914	Hs.250848	Hs.250848:Homo sapiens cD FLJ14761 fis,	3.29
	446272	AI982529 BE268912	Hs.84298 Hs.14601	Hs.84298:CD74 antigen (invariant polypep NM_005335:Homo saplens hematopoletic cel	3.29 3.28
10	437145	AF007216	Hs.5462	NM_003759:Homo saplens solute carrier fa	3.27
10	444071 414662	AJ527808	Hs.110524	Hs. 110524:ESTs	3.27
	436576	AL036058 AJ458213	Hs.76807 Hs.77542	Hs.76807:major histocompatibility compte Hs.77542:ESTs, Wealtly similar to \$26650	3.27 3.26
	424675	NM_005512	Hs.151641	NM_005512:Homo sapiens glycoprotein A re	3.25
15	437897 449703	AA770561 H61001	Hs.146170 Hs.171802	Hs. 145170:hypothetical protein FLJ22969	3.25
10	414788	X78342	Hs.77313	Hs.171802:Homo sepiens, clone IMAGE:3956 NM_003674:Homo sepiens cyc@n-dependent	3.25 3.25
	414249	Al797994	Hs.279929	Hs.279929:gp25L2 protein	3.24
	430396 424456	D49742 AA341017	Hs.241363 Hs.25549	NM_004132:Homo sapiens hyaturon binding	3.23
20	452303	R27257	Hs.57734	Hs.25549:hypothetical protein Fi_J20898 Hs.57734:G protein-coupled receptor kise	3.23 3.22
	425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
	416033 450931	NM_012201 N25156	Hs.78979 Hs.25648	NM_012201:Homo sapiena golgi apparatus p	3.19
	428065	A1634046	Hs.157313	Hs.25648:tumor necrosis factor receptor Hs.157313:ESTs	3.19 3.18
25	422616	BE300330	Hs.118725	NM_012248:Homo saplens selenophosphate s	3.18
	439318 427640	AW837046 AF058293	Hs.6527 Hs.180015	Hs.6527:G protein-coupled receptor 56	3.17
	409936	AK001691	Hs.57655	NM_001355:Homo sapiens D-dopachrome taut Hs.57655:dudufin 2	3.17 3.18
30	436001	AW903849	Hs.173840	Hs.173840:similar to endothellal cell-se	3.16
20	451154 420256	AA015879 U84722	Hs.33536 Hs.76206	Hs.33536:ESTs NM_001795:Homo sapiens cadherin 5, type	3.16
	407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.16 3.15
	428593	AW207440	Hs.185973	NM_003676:Homo sapiens degenerative sper	3.15
35	410026 445333	AI912061 BE537641	Hs.55016 Hs.44278	Hs.55016:EPS8-related protein 2 Hs.44278:RAB17, member RAS oncogene fami	3.15 3.14
	448143	AF039704	Hs.20478	NM_000391:Homo saplens ceroid-lipoluscin	3.14
	423007	AA320134	Hs.196029	Hs.196029:Homo sepiens mR for KIAA1657 p	3.14
	416511 439237	NM_006762 AW408158	Hs.79356 Hs.318893	NM_006762:Homo sepiens Lysosomal-associa Hs.318893:ESTs, Weakly similar to Z195_H	3.14 3.13
40	446899	NM_005397	Hs.16426	NM_005397:Homo sapiens podocalyxin-like	3.13
	413916	N49813	Hs.75615	NM_000483:Homo saplens apolipoprotein C-	3.13
	434398 441283	AA121098 AA927670	Hs.3838 Hs.131704	NM_006622:Homo sapiens serum-inducible k Hs.131704:ESTs	3.12 3.12
45	418945	BE246762	Hs.89499	NM_000698:Homo sapiens arachidote 5-lipo	3.12
4)	418458 408989	AA332941 AW361666	Hs.85226 Hs.49500	NM_000235;Homo sepiens lipase A, lysosom Hs.49500;KIAA0746 protein	3.12
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11 3.11
	411089	AA456454	Hs.355702	Hs.355702:ESTs, Wealdy similar to AC0048	3.11
50	432990 425009	AL036071 X58288	Hs.279899 Hs.154151	NM_003820:Homo saplens tumor necrosis fa NM_002845:Homo saplens protein tyrosine	3.11 3.10
	443601	AI078554	Hs.42658	Hs.42658:Homo sapiens cD FLJ30167 ffs, c	3.10
	430603	AA148164	Hs.247280	Hs. 247280:chromosome 20 open reading fra	3.10
	413672 407786	BE156536 AA687538	Hs.353632 Hs.38972	Hs.353632:ESTs, Moderately similar to by NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09 3.09
55	414586	AA306160	Hs.16488	NM_002298:Homo sapiens lymphocyte cytoso	3.08
•	423712 438552	W46802 AJ245820	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08
	448364	T08958	Hs.6314 Hs.297214	NM_012410:Homo septens type I transmembr Hs.297214:HSPC141 protein	3.06 3.06
60	426437	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
60	437679 422262	NM_014214 AL022315	Hs.5753 Hs.113987	NM_014214:Homo sapiens inositot(myo)-1(o NM_006498:Homo sapiens tectin, gatactosi	3.06 3.06
	410480	R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
65	418883 453613	BE387036 F06838	Hs.1211 Hs.374476	NM_001611:Homo sapiens acid phosphatase Hs.374476:ESTs	3.05 3.05
	408051	AI623351	Hs.172148	Hs.172148:ESTs	3.05
	432278	AL137506	Hs.274258		3.04
	407949 418090	W21874 U57059	Hs.247057 Hs.83429	Hs.247057:ESTs, Wealdy similar to 210926 NM_003810:Homo sepiens tumor necrosis fe	3.04 3.04
70	433165	AA578904	Hs.292437	Hs.292437:ESTs	3.03
	425809 443884	AA370362 N20617	Hs.57958 Hs.194397	Hs.57958:EGF-TM7-latrophilin-related pro	3.03
	447831	AJ433293	Hs.184115		3.03 3.02
75	413278	BE563085	Hs.833	NM_005101:Homo sapiens interferon-stimul	3.01
13	418870 456376	AF147204 AA663904	Hs.89414 Hs.89862	Hs.89414:chemotine (C-X-C motif), recept Hs.89852:TNFRSF1A-associated via death d	3.00
	439738	BE246502	Hs.9598	Hs.9598:sema domain, immunoglobulin doma	3.00 3.00
	444416	AW288085	Hs.11156	NM_016494:Homo saplens hypothetical prot	3.00
80	406656 406826	M16714 AW516005	Hs.89643 Hs.84298	Hs.89643:transketolase (Wernicke-Korsako Hs.84298:CD74 antigen (invariant polypep	3.00 2.99
	418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
	421742 406824	AW970004 AW515961	Hs.107528	NM_016108:Homo sapiens androgen induced	2.99
	700024	ATT (1330)	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
				42	5

	435605	AF151815	Hs.4973	NM_015680:Homo sapiens hypothetical prot	2.98
	410491	AA465131	Hs.64001	Hs.64001:Homo sapiens clone 25218 mR seq	2.98 2.98
	427648	AJ376722	Hs.180062	NM_004159:Homo sapiens proteasome (proso	2.98
5	411125	AA151647	Hs.68877	NM_000101:Homo sapiens cytochrome b-245,	2.98
,	435550 429373	A1224456 NM_014694	Hs.324507 Hs.200594	Hs.324507:hypothetical protein FLJ20988	2.98
	445701	AF055581	Hs.13131	NM_014694:Homo sapiens KIAA0605 gene pro NM_005475:Homo sapiens lymphocyte adapto	2.98 2.97
	414649	AI672727	Hs.76753	NM_000118:Homo sapiens endoglin (Osler-R	2.97
10	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.97
10	423225 407792	AA852604 AI077715	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.97
	445707	AI248720	Hs.39384 Hs.114390	NM_014344:Homo sapiens four jointed box Hs.114390:ESTs	2.97 2.96
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
1.5	418478	U38945	Hs.1174	Hs.1174xyclin-dependent kise inhibitor	2.95
15	411441 443426	AL042355	Hs.70202	Hs.70202:WD repeat domain 10	2.95
	450876	AF098158 AF189062	Hs.9329 Hs.285976	Hs.9329:chromosome 20 open reading frame Hs.285976:LAG1 tongevity assurance homol	2.94 2.94
	426359	AA376409	Hs.10862	Hs. 10862:Homo sapiens cD: FLJ23313 fls.	2.94
20	425421	L11669	Hs.157145	NM_001120:Homo saplens tetracycline tran	2.93
20	449879 454075	H03573	Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93
	421595	R43826 AB014520	Hs.16313 Hs.301685	Hs.16313:Kruppel-like zinc finger protei Hs.301685:KIAA0620 protein	2.93
	457949	W69171	Hs.334814	Hs.334814;hypothetical protein FLJ14868	2.93 2.92
25	443987	AW163123	Hs.10071	NM_016551:Homo sepiens seven transmembra	2.92
25	430259	BE550182	Hs.375142	Hs.375142:RalGEF-like protein 3, mouse h	2.92
	415906 429762	A1751357 A1346255	Hs.288741 Hs.216354	Hs.288741:Homo sapiens cD: FLJ22256 fis, NM_006913:Homo sapiens ring finger prote	291
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91 2.91
	425356	BE244879	Hs.155939	NM_005541:Homo saplens inositol polyphos	2.91
30	427080	AW068287	Hs.301175	NM_002872:Homo sapiens ras-related C3 bo	2.91
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxose 2 (PON2	2.90
	431476 406659	BE612705 AA663985	Hs.256697 Hs.277477	Hs.256697:histidine triad nucleotide bin Hs.277477:major histocompatibility compl	2.89
	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cD FLJ31548 fis, c	2.89 2.89
35	456362	AW973003	Hs.179909	Hs.179909:nuclear receptor coactivator 6	2.88
	426440	8E382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	2.88
	456974 418174	M12529 L20688	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.68
	446055	AI815981	Hs.83656 Hs.12909	Hs. 83656:Rho GDP dissociation inhibitor Hs. 12909:mucolipin 1	2.88 2.88
40	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EF1),	2.87
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87
	410668	BE379794	Hs. 159651	NM_015629:Homo sapiens hypothetical prot	2.87
	444143 407151	AW747996 H25836	Hs.160999 Hs.301527	Hs.160999:ESTs, Wealdy similar to 178885 Hs.301527:ESTs, Moderately similar to un	2.87
45	449349	AI825386	Hs.352579	Hs.352579:Homo sapiens, chromosome 20 op	2.86 2.86
	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
	446143	BE245342	Hs.306079	NM_013338:Homo sapiens protein transport	2.86
	417355 431685	D13168 AW296135	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B NM_005113:Homo sapiens vav 3 oncogene (V	2.86
50	408877	AA479033	Hs.130315	Hs. 130315:ESTs	2.86 2.85
	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
	412014	AI620650	Hs.43761	Hs.43761:gap junction protein, alpha 7,	2.84
	438749 419825	AA584890 U91616	Hs.5302 Hs.182885	NM_006149:Homo saplens tectin, galactosi	2.84
55	439941	AI392640	Hs. 18272	NM_004556:Home sapiens nuclear factor of Hs.18272:solute carrier family 38, membe	2.84 2.84
	435496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84
	422100	A1096988	Hs.111554	NM_005737:Homo sapiens ADP-ribosylation	2.83
	439730	AF035292	Hs.6654 Hs.17778	Hs.6654:KIAA0657 protein	2.83
60	447217 428343	BE465754 AL043021	Hs.17778 Hs.12705	NM_003872:Homo sapiens neuropilin 2 (NRP Hs.12705:similar to HYPOTHETICAL 43.1 KD	2.83 2.82
	440524	R71264	Hs.16798	Hs.16798:Horno sepiens mR; cD DKFZp564O24	2.82
	415523	AL042003	Hs.296847	NM_003119:Homo saplens spastic paraplegi	2.81
	439668	AI091277	Hs.302634	Hs.302634:frizzled homolog 8 (Drosophila	2.81
65	414570 426535	Y00285 AU077012	Hs.76473 Hs.288582	NM_000876:Homo sapiens insufin-like grow NM_006287:Homo sapiens tissue factor pat	2.80
0,5	409649	AA159216	Hs.55505	Hs.55505:hypothetical protein FLJ20442	2.80 2.80
	406655	M21533	Hs.277477	Hs.277477:major histocompatibility compl	2.79
	415323	BE269352	Hs.949	NM_000433:Homo saplens neutrophil cytoso	2.79
70	443195	BE148235	Hs.193063		2.78
, 0	451356 450708	AA748418 AA376654	Hs.164577 Hs.350065		2.78 2.78
	433681	Al004377	Hs.200360		2.77
	442599	AFQ78037	Hs.324051		2.76
75	414509	AW161311	Hs.76294	NM_001780:Homo sapiens CD63 antigen (met	2.76
13	431394 417331	AK000692 AW411297	Hs.252351		2.76
	415995	NM_004573	Hs.81972 Hs.355888	Hs.81972:SHC (Src homology 2 domain cont NM_004573:Homo sepiens phospholipase C,	2.76 2.75
	414911	NM_000107		NM_000107:Homo sapiens damage-specific D	2.75 2.75
90	425976	C75094	Hs.334514	Hs.334514:chromosome 6 open reading fram	2.75
80	407893 407903	BE408359	Hs.43621	Hs.43621:hypothetical protein MBC3205	2.75
	416062	AI287341 AA724811	Hs.154029 Hs.334791		2.75 2.75
	428494	AA233439	Hs.184634		2.75 2.75
				·	~

	421506	BE302796	Hs.105097	NM_003258:Homo sapiens thymidine kise 1.	2.74
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.74
	424527 439578	AW138558 AW263124	Hs.334873 Hs.350547	Hs.334873:carboxypeptidase M Hs.350547:nuclear receptor co-repressor/	274
5	425188	AK002052	Hs.155071	Hs.155071:chromosome 20 open reading fra	2.74 2.74
-	428013	AF151020	Hs.181444	NM_016456:Homo sapiens hypothetical prot	2.73
	439333	AW384710	Hs.132986	Hs.132986:Homo sapiens cO FLJ31588 fis,	2.73
	450935	BE514743	Hs.355753	NM_005851:Homo sapiens tumor suppressor	2.73
10	421532	AW138207	Hs.146170	Hs.145170:hypothetical protein FLJ22969	2.73
10	440502 444981	AI824113	Hs.78281	Hs.78281:regulator of G-protein sigiling	2.73
	439219	AW855398 N33883	Hs.12210 Hs.41322	Hs.12210:turnor endothelial marker 6 Hs.41322:ESTs	2.72 2.72
	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
	433179	AW362945	Hs.162459	Hs.162459:ESTs	2.72
15	424528	AW073971	Hs.238954	Hs.238954:ESTs, Wealtly similar to putati	2.71
	411213	AA676939	Hs.69285	NM_003873:Homo sapiens neuropilin 1 (NRP	2.70
	433012 425345	NM_004045	Hs.279910	NM_004045:Horno sapiens ATX1 antioxidant	2.70
	428923	AU077297 BE047698	Hs.155894 Hs.188785	NM_002827:Homo sapiens protein tyrosine Hs.188785:ESTs	2.69
20	427923	AW274357	Hs.301406	Hs.301406:hypothetical protein PP3501	2.69 2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.69
	421743	T35958	Hs.107614	Hs.107614:DXFZP564I1171 protein	2.68
	416207	NM_014745	Hs.79077	NM_014745:Homo sepiens KIAA0233 gene pro	2.68
25	420372	AW960049	Hs.293660	Hs.293660:gene overexpressed in astrocyt	2.68
23	420542 425069	NM_000505 AA687465	Hs.1321 Hs.298184	NM_000505:Homo sapiens coagulation facto	2.67
	418558	AW082266	Hs.86131	Hs.298184:potassium voltage-gated channe NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67 2.67
	426251	M24283	Hs.168383	NM_000201:Horno sapiens intercetlutar adh	2.66
20	406701	AA780613	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.66
30	431681	AK000378	Hs.267566	Hs.267566:hypothetical protein FLJ20371	2.66
	412833	AW950547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
	433101 414774	AW572317 X02419	Hs.12082 Hs.77274	Hs.12082:TIGA1	2.66
	427868	Al360119.com		NM_002658:Homo saplens plasminogen activ NM_002629:Homo sapiens phosphoglycerate	2.66 2.66
35	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, alpha 2	2.66
	424762	AL119442	Hs.1B3684	Hs. 183684:eukaryotic translation initiat	2.66
	422048	NM_012445	Hs.288126	NM_012445:Homo sapiens spondin 2, extrac	2.65
	431350	AJ192528	Hs.164537	Hs.164537:ESTs	2.65
40	450184 419285	W31096 D31887	Hs.237617	Hs.237617:dipeptidytpeptidase 9 Hs.89868:KIAA0062 protein	2.65
-10	414217	AI309298	Hs.89868 Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.65 2.64
	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SUT-ROBO Rho GTPase-activating	2.64
45	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	263
45	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein BC011406	2.63
	430223 417526	NM_002514 AA568906	Hs.235935	NM_002514:Homo sapiens nephroblasioma ov	2.63
	409956	AW103364	Hs.82240 Hs.727	NM_004177:Horno sapiens syntæin 3A (STX3 NM_002192:Horno sapiens inhibin, beta A (	2.63 2.63
	449843	R85337	Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62
50	417389	BE260964	Hs.82045	NM_002391:Homo sapiens midkine (neurite	2.62
	446312	BE087853	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.62
	435099	AC004770	Hs.4756	Hs.4756:flap structure-specific endonucl	2.62
	417920 435702	S47833 A1033647	Hs.82927 Hs.121001	NM_004037:Homo sapiens adenosine monopho	2.62
55	422959	AV647015	Hs.349256	Hs.121001:Horno sapiens, clone MGC:4552 I Hs.349256:paired immunoglobulin-like rec	2.62 2.62
	419938	AU076772	Hs.1279	NM_001733:Homo sapiens complement compon	2.62
	450954	A1904740	Hs.25691	NM_005856:Homo sepiens receptor (calcito	2.61
	421753	8E314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
60	443577	AI078033	Hs.177170	Hs.177170:ESTs, Weakly similar to ALU8_H	2.61
00	453886 421883	R66282 X55079	Hs.20247 Hs.1437	Hs.20247:ESTs NM_000152:Homo sapiens glucosidase, alph	261
	440457	BE387593	Hs.21321	Hs.21321:granule cell differentiation pr	2.60 2.60
	410295	AA741357	Hs.356624		2.59
CE	420879	X57152	Hs.99853	NM_001435:Homo sapiens fibrillarin (FBL)	2.59
65	451558	NM_001089		NM_001089:Homo saciens ATP-binding casse	2.59
	444672	Z95636	Hs.11669	Hs.11669:laminin, alpha 5	2.59
	408669 426194	Al493591 T50872	Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	421814	L12350	Hs.2001 Hs.108623	Hs.2001:thromboxane A synthase 1 (platel NM_003247:Homo sapiens thrombospondin 2	2.59 2.59
70	456371	S76825	Hs.89695	Hs.89695:insutin receptor	2.59
	429098	AFQ30249	Hs.196176		2.59
	414443	AU077268	Hs.76144	NM_002609:Homo sapiens platetet-derived	2.59
	428484	AF104032	Hs.184601		2.59
75	453309 412867	A1791809 AU076861	Hs.32949	NM_005218:Homo sapiens defensin, beta 1	2.59
, ,	412867 432827	Z68128	Hs.74637 Hs.3109	NM_003217:Homo sapiens testis enhanced g Hs.3109:Rho GTPase activating protein 4	2.58 2.58
	412669	AW880841	Hs.96908	NM_006034:Homo saplens p53-induced prote	2.58 2.58
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.58
00	452866	R26969	Hs.268016	Hs.268016:Homo sapiens cD: FLJ21243 fis,	2.58
80	435129	AI381659	Hs.267086	Hs.267086:ESTs	2.57
	424482 410494	BE268621 M36564	Hs.149155		2.57
	433895	AI287912	Hs.64016 Hs.3628	NM_000313:Homo saplens protein S (alpha) NM_004834:Homo saplens mitogen-activated	2.56 2.56
	-50050		113.3020		4.90

	442566	R37337	Hs.12111	Hs.12111:ESTs	2.56
	417640 442622	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
	430345	NM_000435 AK000331	Hs.8546	NM_000435:Homo sapiens Notch homolog 3 (	2.56
5	419344	U94905	Hs.297641 Hs.277445	Hs. 297641:retinoblastoma-associated fact	2.55
•	426500	NM_014638	Hs.170156	Hs.277445:diacytglycerol kise, zeta (104 NM_014638:Homo sapiens KIAA0450 gene pro	2.55 2.55
	408048	NM_007203	Hs.42322	NM_007203:Homo sapiens A kise (PRKA) and	2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens foliistatin-Eke	2.54
	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaquchi	2.54
10	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.54
	422451	AA310753	Hs.42491	Hs.42491:ESTs, Moderately similar to hyp	2.53
	435906	AI586379	Hs.110796	Hs.110796:SAR1 protein	2.53
	400231				2.53
15	417849	AW291587	Hs.82733	NM_007361:Homo sepiens nidogen 2 (NID2),	2.53
13	427380 428385	NM_005534 AF112213	Hs.177559	NM_005534:Horno sapiens interferon gamma	2.52
	438000	AF112213 AI825880	Hs.184062 Hs.5985	Hs.184062:chromosome 20 open reading fra	2.52
	448719	AA033627	Hs.21858	Hs.5985:non-kise Cdc42 effector protein Hs.21858:serine (or cysteine) proteise i	2.52 2.52
	422396	W21872	Hs.7907	Hs.7907:L-fucose kise	2.52 2.52
20	420787	AA564248	Hs.351292	Hs.351292:Homo sapiens cD FLJ32605 fis,	2.51
-	430590	AW383947	Hs.246381	NM_001251:Homo sapiens CD68 antigen (CD6	2.51
	447026	BE313144	Hs.324844	Hs.324844:hypothetical protein IMAGE3455	2.51
	439223	AW238299	Hs.250618	Hs.250618:UL16 binding protein 2	2.50
26	435151	AA348482	Hs.4788	Hs.4788:nicestrin	2.50
25	448202	AB002292	Hs.20695	NM_014829:Homo sepiens Rho guanine nucle	2.50
	449943	AF104266	Hs.24212	Hs.24212:latrophilin	2.50
	425743	BE396495	Hs.159428	Hs.159428:BCL2-associated X protein	2.50
	444681 421643	AJ243937 BE281170	Hs.288316	Hs.288315:chromosome 6 open reading fram	2.50
30	426865	D63476	Hs.106357 Hs.172813	NM_007126:Homo sapiens valosin-containin	2.50
50	432306	Y18207	Hs.303090	NM_003899:Homo sapiens Rho guanine nucle NM_005398:Homo sapiens protein phosphata	2.50 2.49
	421846	AA017707	Hs.1432	NM_002743:Homo saplens protein kise C su	249
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	2.49
	419493	AF001212	Hs.90744	NM_002815:Homo sapiens proteasome (proso	2.49
35	422530	AW972300	Hs.118110	NM_004335:Homo sapiens bone marrow strom	2.48
	442821	BE391929	Hs.8752	NM_014255:Homo sapiens transmembrane pro	2.48
	416919	T97839	Hs.80464	NM_006402:Homo sapiens hepatitis B virus	2.48
	443105	X96753	Hs.9004	NM_001897:Homo sepiens chondroitin sulfa	2.48
40	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
70	428028 424307	U52112	Hs.182018	NM_001569:Homo septens interteukin-1 rec	2.47
	434511	AW293399 R28982	Hs.356377 Hs.18106	Hs.356377:Homo sapiens, clone IMAGE:3633	2.46
	454390	AB020713	Hs.56966	Hs.18105:ESTs, Wealdy similar to T06291 Hs.56966:K0AA0906 protein	2.46
	417785	X59812	Hs.82568	NM_000784:Homo saplens cytochrome P450,	2.46 2.46
45	424673	AA345051	Hs.294092	Hs.294092:Homo sapiens mR full tength in	2.46
	422003	AA361760	Hs.296326	Hs.296326:ESTs, Weakly similar to A33533	2.46
	432126	AA865239	Hs.37196	Hs.37196:putative G protein coupled rece	2.46
	445937	AI452943	Hs.321231	NM_003779:Homo sapiens UDP-Gal:betaGlcc	2.46
50	409354	N68188	Hs.159472	Hs.159472:Homo sapiens cD: FLJ22224 fis,	2.48
30	401179	A A OC 403D			2.46
	418151		mp Hs.83583		2.45
	422648 427759	D86983 BE245578	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	431222	X56777	Hs.2200 Hs.273790	NM_005041:Homo sapiens perforin 1 (prefo	2.45
55	411529	AA430348	Hs.317596	NM_007155:Homo sapiens zo pellucida glyc Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45 2.45
	426825	AL133415	Hs.297753	NM_003380:Homo sapiens vimentin (VIM), m	2.45
	422242	AJ251760	Hs.273385	NM_016592:Homo sapiens GS complex locus	2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44
60	426410	BE298446	Hs.305890	Hs.305890:BCL2-like 1	2.44
60	421064	AI245432	Hs.101382	NM_006291:Homo sapiens tumor necrosis fa	2.44
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokise 2 (HK2).	2.44
	424398	BE397787	Hs.146393	NM_014685:Homo saplens homocysteine-indu	244
	424825 426031	AF207069 AA295251	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	244
65	409817	BE295464	Hs.166068 Hs.56607	Hs.166066:cisplatin resistance associate Hs.56607;Williams-Beuren syndrome chromo	2.43
•••	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.43 2.43
	426761	AI015709	Hs.172089		243
	429332	AF030403	Hs.199263		2.43
70	425923	NM_005026			2.43
70	432211	BE274530	Hs.273333		2.43
	433339	AF019226	Hs.8036	Hs.8036:RAB3D, member RAS oncogene famili	2.42
	420539	AA282735	Hs.44004	Hs.44004:AD031 protein	2.42
	413243	AA769266	Hs.193657		2.42
75	435029 422374	AF187706	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
, ,	444501	AW732869 AW247624	Hs.1519 Hs.11342	Hs.1519:protein kise, cAMP-dependent, re	2.42
	414919	AW087337	Hs.194461	NM_004148:Homo sepiens ninjurin 1 (NINJ1 Hs.194461:ESTs	2.42
	419355	AA428520	Hs.90061	NM_005667:Horno sapiens progesterone rece	2.42 2.42
•	435042	AF284422	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
80	418245	AA088767	Hs.83883	Hs.83883:transmembrane, prostate androge	2.42
	444215	AB033075	Hs.10669	Hs.10669:development and differentiation	241
	408683	R58665	Hs.46847	NM_016614:Homo saplens TRAF and TNF rece	2.41
	423701	AA329856	Hs.143022	Hs.143022:EST8	2.41



	441783	8E313412	Un 70C1	11- 70C4-11	• • •
	428072	BE258602	Hs.7961 Hs.182366	Hs.7961:Homo sapiens clone 25012 mR sequ NM_016292:Homo sapiens heat shock protei	2.41 2.41
	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
_	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
5	407894	AJ278313	Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449	W16752	Hs.32981	Hs.32981:sema domain, immunoglobulin dom	2.40
	408688	AI634522	Hs.152925	Hs.152925:KIAA1268 protein	2.40
	422448 416269	AW372922 AA177138	Hs.116774 Hs.161671	Hs.116774:integrin, alpha 1	2.39
10	452679	Z42387	Hs.83883	Hs.161671:ESTs Hs.83883:transmembrane, prostate androge	2.39 2.38
- •	432981	NM_002733	Hs.3136	NM_002733:Homo sapiens protein kise, AMP	2.38
	419846	NM_015977	Hs.285681	Hs.285681:Williams Beuren syndrome chrom	2.38
	422110	AJ376736	Hs.111779	Hs.111779:secreted protein, acidic, cyst	2.38
16	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.38
15	433969	AW207279	Hs.271786	Hs.271786:ESTs, Wealthy similar to PC4395	2.37
	451267 447526	A1033894 AL048753	Hs.117865 Hs.303849	Hs.117865:solute carrier family 17 (anio	2.37
	441623	AA315805	Hs.348710	NM_002982:Homo sapiens small inducible c Hs.348710:Homo sapiens, clone IMAGE:4242	2.37
	420255	NM_007289	Hs.1298	NM_007289:Homo sapiens membrane metallo-	2.37 2.37
20	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens arc tamily associ	2.36
	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.35
	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) proteise i	2.36
	408212	AA297567	Hs.43728	NM_015696:Homo sapiens wealthy similar to	2.36
25	430478 405102	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L	2.36
23	423583	AL122055	Hs.129838	Hs.129836:KIAA1028 protein	2.35
	426125	X87241	Hs.166994	NM_005245:Homo sapiens FAT turnor suppres	2.35 2.35
	425204	NM 002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35
	420676	Al434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
30	421079	AW404994	Hs.101695	Hs.101695:NCK adaptor protein 2	2.35
	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
	412958	BE391579	Hs.75087	NM_006712:Homo sapiens FAST kise (FASTK)	2.34
	430363 425397	M28713 J04088	Hs.274464 Hs.156346	NM_000398:Homo sapiens diaphorase (DH) (	2.34
35	451035	AU076785	Hs.430	NM_001067:Homo sapiens topolsomerase (D) NM_002670:Homo sapiens plastin 1 (I isof	2.34
-	449027	AJ271216	Hs.22880	Hs.22880:dipeptidytpeptidase III	2.34 2.34
	429457	BE243065	Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
40	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
40	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.34
	430702 456804	U56979 Al421645	Hs.278568	NM_000186:Homo saplens H factor 1 (compl	2.33
	453648	W21493	Hs.139851 Hs.28329	NM_001233:Homo sapiens caveolin 2 (CAV2)	233
	450812	AB002360	Hs.25515	Hs.28329:protein phosphatase 1, regulato Hs.28515:MCF.2 cell line derived transfo	2.33 2.33
45	402575		1-0.25510	10.200 tollion is out this delited treation	2.33
	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32
	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine	2.32
	442968	AK000606	Hs.8868	NM_004871:Homo sapiens golgi SP receptor	2.32
50	410639 415169	BE269047 W42913	Hs.65234 Hs.78089	Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
50	450160	BE048099	Hs.183738	NM_004231:Homo sapiens ATPase, H+ transp Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32 2.32
	407223	H96850	1.0.1007.00	H96850:yw03b12.s1 Soares melanocyte 2NbH	2.32
	426780	BE242284	Hs.172199	NM_001114:Homo sapiens adenylate cyclase	2.32
66	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
55	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
	453107 422963	NM_016113	Hs.279746	NM_016113:Homo sapiens transient recepto	2.31
	433618	M79141 AA602539	Hs.13234 Hs.345494	Hs.13234:ESTs, Weakly similar to hypothe Hs.345494:ESTs, Moderately similar to ZN	231
	438584	AA811347	113.043434	AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	2.31 2.31
60	446126	AW085909	Hs.356618	Hs.356618:ESTs, Weakly similar to PC4259	2.31
	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
	433230	AW136134	Hs.220277	Hs.220277:ESTs, Wealdy similar to expres	2.30
	410168 446342	AW834050	Hs.351432	Hs.351432:tensin	2.30
65	418452	BE298665 BE379749	Hs.14846 Hs.85201	Hs.14846:Homo saplens mR; cD DKF2p564D01	2.30
0.5	453175	NM_006834	Hs.32217	NM_005127:Homo saptens C-type (calcium d NM_006834:Homo sapiens RAB32, member RAS	2.30 2.29
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848	AJ417193	Hs.288912		2.29
70	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
70	422562	Al962060	Hs.118397	NM_001129:Homo sapiens AE binding protei	2.28
	432828	AB042326	Hs.287402		2.28
	412948 426068	BE243313 AF029778	Hs.334851 Hs.166154	NM_006148:Homo sapiens LIM and SH3 prote	2.28
	456919	NM_003900			2.28 2.28
75	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.26 2.28
_	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
	407736	N41744	Hs.349326	Hs.349326:Homo seplens cD FLJ30677 fis,	2.28
	413211	AW967107	Hs.109274	Hs.109274:hypothetical protein MGC4365	2.28
80	422051	AW327548	Hs.111024		2.27
00	438438 436278	AA257992 BE396290	Hs.50651 Hs.5097	Hs.50651:Janus kise 1 (a protein tyrosin	2.27
	454080	AI199711	Hs.576	NM_004710:Homo sapiens syptogyrin 2 (SYN NM_000147:Homo sapiens fucosidase, alpha	2.27 2.27
	426542	AF190746	Hs.170310		2.27
	_				



	417115 402901	AW952792	Hs.334512	NM_003094:Homo sapiens small nuclear rib	2.27 2.26
	412898	Al129903	Hs.74669	NM_006634:Homo sapiens vesicle-associate	2.26
5	413020	R98736		R98736:yr31h09.r1 Soares fetal liver spl	2.26
3	413939 408681	AL047051 AW953853	Hs.199961 Hs.281462	Hs.199961:ESTs, Wealdy similar to hypoth Hs.281462:hypothetical protein FLJ14251	2.26 2.25
	412330	NM_005100	Hs.788	NM_005100:Homo sapiens A kise (PRKA) and	2.25
	442083	R50192	Hs.165062	Hs.165062:EST8	2.25
10	418271 433376	NM_000919 AI249361	Hs.83920 Hs.74122	NM_000919:Homo sapiens pepúdylglycine a NM_001225:Homo sapiens caspase 4, apopto	2.25
	438562	AI566826	Hs.25890	Hs.25890:ESTs, Wealdy similar to transdu	2.25 2.25
	443883	AA114212	Hs.9930	NM_001235:Homo sapiens serine (or cystei	2.25
	416976 416914	BE243985 AA344481	Hs.80680 Hs.80426	Hs.80680:major vautt protein Hs.80426:brain and reproductive organ-ex	2.24
15	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24 2.24
	407904	W44735	Hs.107260	Hs.107260:putative UDP-Gatc:polypeptide	2.24
	429690 443813	AW956329 AA876372	Hs.23721 Hs.93961	Hs.23721:ESTs	2.24
	427458	BE208364	Hs.29283	Hs.93961:Homo sapiens mR; cD DKFZp667D09 Hs.29283:ESTs, Weakly similar to UKHU pr	2.24 2.24
20	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
	407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
	425751 456437	T19239 AJ924228	Hs.1940 Hs.115185	NM_001885:Homo saplens crystallin, alpha Hs.115185:ESTs	2.23 2.23
0.5	413019	BE281604	Hs.75140	NM_002337: Homo sapiens low density lipop	2.23
25	418862	8E550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23
	435284 429630	AA879470 M85289	Hs.96849 Hs.211573	Hs.96849:Homo sapiens cD FLJ11492 fis, c NM_005529:Homo sapiens heparan sulfate p	2.23 2.23
	427609	AK000438	Hs.179791	Hs.179791:RAB20, member RAS oncogene (am	2.23
30	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.23
30	445616 407232	R65964 X04526	Hs.334873	Hs.334873:carboxypeptidase M X04526:Human liver mR for beta-subunit s	2.23 2.23
	423798	AF047033	Hs.132904	Hs. 132904:solute carrier family 4, sodiu	2.23
	446755	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
35	452865 431393	AI924046 AW971493	Hs.119567 Hs.134269	Hs.119567:ESTs, Weakly similar to ALU1_H	2.22
55	431890	X17033	Hs.271986	Hs.134269:ESTs, Weakly similar to 200439 NM_002203:Homo sapiens integrin, alpha 2	2.22 2.22
	428782	X12830	Hs.193400	NM_000565:Homo sapiens interleukin 6 rec	2.22
	446006 436418	NM_004403 AJ245874	Hs.13530 Hs.4245	NM_004403:Homo sapiens deafness, autosom	2.22
40	423869	BE409301	Hs.134012	Hs.4245:chromosome 11 hypothetical prote NM_006688:Homo sapiens C1g-related facto	2.22 2.21
	437730	AW071087	Hs.239176	Hs.239176:insulin-like growth factor 1 r	2.21
	444020 413882	R92962 AA132973	Hs.35052 Hs.184492	Hs.35052:ESTs	2.21
	412654	Al093480	Hs.374319	Hs.184492:Homo sapiens mR; cD DKFZp66780 Hs.374319:ESTs	2.21 2.21
45	448988	Y09763	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21
	426841 408196	AJ052358 AL034548	Hs.131741 Hs.43627	Hs.131741:ESTs	2.21
	451711	AK000461	Hs. 26890	NM_005943:Homo saplens SRY (sex determin Hs.26890:cat eye syndrome chromosome reg	2.21 2.20
50	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
50	424512 448883	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20
	411296	BE614989 BE207307	Hs.7503 Hs.10114	Hs.7503:hypothetical protein FLJ14153 Hs.10114:growth suppressor 1	2.20 2.20
	452268	NM_003512	Hs.28777	NM_003512:Homo sapiens H2A histone famil	2.20
55	416810 441415	AF035606 H21497	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
55	444212	AW503976	Hs.7471 Hs.10649	Hs.7471:88P-like protein 1 NM_004848:Homo sapiens basement membrane	2.20 2.19
	428044	AA093322	Hs.301404	NM_006743:Homo saplens R binding motif p	2.19
	430017 424490	AA263172 AJ278016	Hs.35 Hs.55565	NM_002832:Homo sapiens protein tyrosine	2.19
60	431193	AW749505	Hs.296770	Hs.55565;ankyrin repeat domain 3 Hs.296770;KIAA1719 protein	2.19 2.19
	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19
	448262 416065	AW880830 8E267931	Hs.186273 Hs.78996	Hs.186273:ESTs	2.19
	442045	C05768	Hs.8078	NM_002592:Homo sapiens profiferating cel Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19 2.19
65	423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimut	2.19
	428024 424503	Z29067 NM_002205	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
	437698	Z83844	Hs.149609 Hs.5790	NM_002205:Homo sapiens integrin, alpha 5 Hs.5790:hypothetical protein dJ37E16.5	2.19 2.18
70	405204			,	2.18
70	426158 417418	NM_001982 NM_002458			2.18
	412773	H15785	Hs.74573	NM_002468:Homo saplens myeloid different NM_012268:Homo saplens similar to vaccin	2.18 2.18
	409402	AF208234	Hs.695	NM_000100:Homo sapiens cystetin B (steff	218
75	443791 435049	N64458 AL122067	Hs.143345 Hs.4746		218
, ,	418389	AA830613	Hs.293849	Hs.4746:hypothetical protein FLJ21324 Hs.293849:ESTs	2.18 2.18
	450712	AI732130	Hs.270498	Hs.270496:ESTs, Wealthy similar to ALUB_H	2.18
	422007 453676	A1739435 AW853745	Hs.39168 Hs.286035	Hs.39168:ESTs, Weakly similar to T17340	218
80	415718	F30631	Hs.200237		2.18 2.18
	452688	AA721140	Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18
	415988 409453	BE407713 AI885516	Hs.78943 Hs.95612	NM_000386:Homo sapiens bleomycin hydrola	218
	<del>-10-100</del>	MO000010	119.33012	Hs.95612:ESTs	2.17



	417512	X76534	Hs.82226	NM_002510:Homo sapiens glycoprotein (tra	2.17
	427202 440983	BE272922 M20681	Hs.173936	NM_000628:Homo sapiens interleutin 10 re	2.17
_	416084	L16991	Hs.7594 Hs.79006	NM_006931:Homo sapiens solute carrier fa NM_012145:Homo sapiens deoxythymidytate	2.17 2.17
5	429642	X68264	Hs.211579	NM_006500:Homo sapiens melanoma adhesion	2.17
	427213 437763	AW007211	Hs.348389	Hs.348389:hypothetical protein FLJ12876	2.17
	454000	AA469369 AA040620	Hs.5831 Hs.5672	NM_003254:Homo sapiens tissue inhibitor Hs.5672:golgi membrane protein S8140	2.17 2.17
10	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (rel amy	2.16
10	403857	A A CC27700	II. 077477	All DODGE AND ALL ALL AND ALL	2.16
	406648 400265	AA563730	Hs.277477	Hs.277477:major histocompatibility compl	2.16 2.16
	442379	NM_004813	Hs.8265	NM_004613:Homo sapiens transglutamise 2	2.16
15	441892	AB028981	Hs.8021	Hs.8021:KIAA1058 protein	2.16
13	417446 418386	AL118671 AA361739	Hs.82163 Hs.84549	NM_000898:Homo sapiens monoamine oxidase NM_002494:Homo sapiens DH dehydropese (u	2.16 2.16
	414053	BE391635	Hs.75725	NM_003564:Homo sapiens transgelin 2 (TAG	216
	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
20	447660 408279	AW160386 AF216965	Hs.163667 Hs.44095	Hs.163667:ESTs, Weakly similar to CA1H_H Hs.44095:cyclin M3	2.16
	426152	8E299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.16 2.16
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.16
	415661 425302	AF057307 U79115	Hs.78575 Hs.155566	Hs.78575:prosaposin (variant Gaucher dis	2.15
25	425996	W67330	Hs.374451	NM_003805:Homo saplens CASP2 and RIPK1 d Hs.374451:ESTs	2.15 2.15
	413745	AW247252	Hs.75514	NM_000270:Homo seplens nucleoside phosph	2.15
	422070 448424	AF149785 AW009892	Hs.111126 Hs.31924	Hs.111126:pituitary tumor-transforming 1 Hs.31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15 2.15
30	438407	AJ457122	Hs.129673	Hs.129673:eukaryotic translation initiat	2.15
	435551 437741	AF212365 BE561610	Hs.5470	Hs.5470:interleukin 17B receptor	2.15
	441192	AA526626	Hs.5809 Hs.7736	Hs.5809:putative transmembrane protein; NM_016504:Homo sapiens mitochondrial rib	2.15 2.15
25	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.15
35	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	2.14
	425252 427600	AW391162 AW630918	Hs.349306 Hs.179774	Hs.349306:hypothetical protein FLJ31951 NM_002818:Homo sapiens proteasome (proso	2.14 2.14
	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
40	442110 407797	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.14
40	443044	AK000524 N28522	Hs.39850 THs.8935	Hs.39850:uridine kise-like 1 NM_014298:Homo sapiens quinofite phospho	2.14 2.14
	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cD FLJ32174 fis,	2.14
45	424954 458097	NM_000548 AW341135	Hs.1846 Hs.58104	NM_000548:Homo sapiens tumor protein p53 Hs.58104:Homo sapiens, clone IMAGE:47309	2.14 2.14
	411925	AW014588	Hs.72925	NM_003475:Homo sepiens chromosome 11 ope	2.14
	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
	422675 428586	BE018517 M36712	Hs.119140 Hs.2299	NM_001970:Homo sapiens eukaryotic transl Hs.2299:CD8 antigen, beta polypeptide 1	2.14 2.14
50	429379	NM_014840	Hs.200598	NM_014840:Homo sapiens KIAA0537 gene pro	2.13
	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	2.13
	443895 428145	AW979048 BE243327	Hs.292566 Hs.182626	Hs.292568:YEA4 protein NM_012264:Homo sapiens chromosome 22 ape	213 213
e e	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cD: FLJ21933 fis,	213
55	456534 419972	X91195	Hs.100623	Hs. 100623:protein phosphatase 1, regulat	2.13
	424950	AL041465 AA602917	Hs. 182982 Hs. 156974	Hs.182982:golgin-67 Hs.156974:ESTs	2.13 2.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	2.13
60	431449	M55994	Hs.256278	NM_001066:Homo sapiens tumor necrosis ta	2.13
00	418758 434202	AW959311 BE382411	Hs.172012 Hs.3764	Hs.172012:hypothetical protein DKFZp434J NM_000858:Homo sapiens guanylate kise 1	2.13 2.13
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.12
	452700 438033	AI859390	Hs.288940	Hs.288940:transmembrane protein 8 (five	2.12
65	400847	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing fi	2.12 2.12
	447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12
	417052 413284	NM_000712 AU077055	Hs.81029 Hs.289107	NM_000712:Homo sapians biliverdin reduct	2.12
	434558	AW264102	Hs.39168	NM_001166:Homo sapiens baculoviral IAP r Hs.39168:ESTs, Wealdy similar to T17340	2.11 2.11
70	404030			The state of the s	211
	410801 418613	BE275469 AA744529	Hs.66493	Hs.66493:Down syndrome critical region g	2.11
	447087	AW403870	Hs.86575 Hs.301872	Hs.86575:mitogen-activated protein kise Hs.301872:hypothetical protein MGC4840	2.11
75	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical grot	2.11 2.11
75	426433	L38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3	2.11
	4424 <b>3</b> 9 437379	U09759 AL359575	Hs.246857 Hs.23765	NM_002752:Homo sapiens mitogen-activated Hs.23765:membrane metallo-endopeptidase-	211
	400208		. 10.20103		211 211
80	455705	AW151051	Hs.356580		211
OU.	417599 416728	AA204688 AB024597	Hs.62954 Hs.79658	Hs.62954:ferrilin, heavy polypeptide 1 NM_001894:Homo sapiens casein kise 1, ep	2.10
	439920	H05430	Hs.288433	Hs.288433:neurotrimin	2.10 2.10
	422309	U79745	Hs.114924		2.10
				431	

	435114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517				2.10
	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
5	437712 431214	X04588 AA294921	Hs.85844 Hs.348024	Hs.85844:neurotrophic tyrosine kise, rec	2.10
,	412856	BE386745	Hs.74631	NM_002881:Homo sapiens v-ral simian teuk NM_001728:Homo sapiens basigin (BSG), mR	2.10 2.10
	442064	AJ422867	Hs.88594	Hs.88594:Homo sepiens, clone IMAGE:43329	2.10
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	210
10	426728	NM_007118	Hs.367689	NM_007118:Homo sapiens triple functiol d	2.10
10	419596	BE379320	Hs.91448	NM_007026:Homo sapiens dual specificity	2.09
	448913 414721	AA194422 X90392	Hs.22564 Hs.77091	NM_004999:Homo sapiens myosin VI (MYO6), NM_006730:Homo sapiens deoxyribonuclease	2.09 2.09
	424658	NM_002406	Hs.151513	NM_002406:Homo sapiens mannosyl (alpha-1	2.09
	432805	X94630	Hs.3107	Hs.3107:CD97 entigen	2.09
15	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188 445584	AK001812 AF217518	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09
	402559	AF217510	Hs.8360	Hs.8360:PTD012 protein	2.09 2.09
20	418043	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kise	2.09
	448888	AW196663	Hs.200242	Hs.200242:caspase recruitment domain fam	2.09
	436910	AA926944	Hs.261587	Hs.261587:GCN2 elF2alpha kise	2.09
	422573	AW297985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin	2.08
25	416448 428727	L13210 AF078847	Hs.79339 Hs.191356	NM_005567:Homo sapiens lectin, galactosi	2.08
23	410301	AW502935	Hs.740	NM_001515:Homo sapiens general transcrip Hs.740:PTK2 protein tyrosine kise 2	2.08 2.08
	449538	AI559444	Hs.104579	Hs.104579:Homo sapiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541:netrin 4	2.08
20	411779	AA292811	Hs.72050	NM_003551:Homo sapiens non-metastatic ce	2.08
30	427704 413518	AW971063	Hs.292882	Hs.292882:ESTs	2.07
	447345	BE149455 BE247767	Hs.75415 Hs.18166	NM_004048:Homo sapiens beta-2-microglobu Hs.18166:KIAA0870 protein	2.07 2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613061	Hs.337772	Hs.337772:hypothetical protein 8C009331	2.07
35	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.07
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
	403966 409115	AJ223335	Hs.50651	NIM 002227-House essions have bine 4 to a	2.07
	436823	AV749865	Hs.117077	NM_002227:Homo sapiens Janus kise 1 (a p Hs.117077:zinc finger protein 264	2.07 2.07
40	414045	NM_002951	Hs.75722	NM_002951:Homo saplens ribophorin II (RP	2.06
	413980	NM_002437	Hs.75659	NM_002437:Homo sapiens MpV17 transgene,	2.06
	439414	NM_001183	Hs.6551	NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572Homo sapiens interferon regula	2.06
45	429849 402424	U33053	Hs.2499	NM_002741:Homo sapiens protein kise C-B	2.06
	406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06 2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, tysoso	2.05
	426086	T94907	Hs.188572	Hs.188572:ESTs	2.05
50	419726	U50330	Hs.1274	NM_006129:Homo sapiens bone morphogeneti	2.05
50	452344 442498	AI264357 U54617	Hs.55405 Hs.8364	Hs.55405:hypothetical protein MGC16212	2.05
	422114	AW194851	Hs.111801	NM_002612:Homo sepiens pyruvate dehydrog NM_015908:Homo sepiens arsete resistance	2.05 2.05
	413420	AW410235	Hs.75348	NM_006263:Homo sapiens proteasome (proso	2.05
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	2.05
55	409932	A1376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
	434848 453852	BE256304 AW961818	Hs.32148 Hs.374424	Hs.32148:AD-015 protein	2.04
	427637	AK000816	Hs.179986	Hs.374424:ESTs NM_005803:Homo sapiens flotillin 1 (FLOT	2.04 2.04
	400264			ANGADARA ISIN BERMININ HAMILI I (I CO)	2.04
60	430016	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	2.04
	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
	440975 432280	AW499914 BE440142	Hs.7579 Hs.2943	Hs.7579:Importin 9	2.04
	409504	AA304961	Hs.699	NM_003135:Homo sepiens stgl recognition NM_000942:Homo sepiens peptidytprolyt is	2.04 2.04
65	412146	M92444	Hs.73722	NM_001641:Homo sapiens APEX nuclease (mu	2.04
	434203	BE262677	Hs.283558	Hs.283558:hypothetical protein PRO1855	2.04
	422754	AA316478	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
70	413086 424340	AA126841 AA339036	Hs.183834 Hs.7033	Hs.183834:ESTs Hs.7033:ESTs	2.03
, ,	450440	AB024334	Hs.25001	NM_012479:Homo sepiens tyrosine 3-monoox	2.03 2.03
	424662	NM_002870			2.03
	415740	N80486	Hs.39911	Hs.39911:Homo sapiens mR for FLJ00089 pr	2.03
75	412749	AA378417	Hs.74564	NM_003145:Homo sapiens sigl sequence rec	2.03
13	408393 421295	AW015318 AW081061	Hs.23165 Hs.103180	Hs.23165:ESTs	2.03
	445417	AK001058	Hs.12680	Hs.103160:DC2 protein Hs.12680:Homo sapiens cD FLJ10196 fis, c	2.03 2.03
	414883	AA926960	Hs.348669		2.03
00	447298	BE617527	Hs.239818	Hs.239818:phosphoinositide-3-kise, catal	2.02
80	459580	AA022888	Hs.176065	Hs.176065:EST8	2.02
	422785 452696	AJ824114 AJ826845	Hs.289088		2.02
	452056	AW955065	Hs.211534 Hs.101150		2.02 2.02
				· ····································	2.72

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	450690 423527	AA296696 AI206965	Hs.333418 Hs.105861	NM_014164:Homo sapiens FXYD domain-conta Hs.105861:engulfment and cell mofility 3	2.02 2.01
	429545	ALB24164	Hs.356130	Hs.356130:ESTs	2.01
_	439180	AI393742	Hs.199067	Hs. 199067:v-erb-b2 erythroblastic leukem	2.01
5	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.01
	436014	AF281134	Hs.283741		2.01
	453329 407347	T97205 AAB29847	Hs.193400	Hs.193400:interleukin 6 receptor T23514:seq3329 1-NIB Horno sapiens cD clo	201 201
	435370	AI964074	Hs.225838	Hs.225838:ESTs	201
10	430657	AA482910		Hs.370602:ESTs, Wealthy similar to hypoth	2.01
	427157	U51166	Hs.173824	NM_003211:Homo sapiens thymine-D glycosy	2.01
	424833	NM_00389		NM_003894:Homo sapiens period homolog 2	2.01
	440086 438543	NM_00540 AA810141		NM_005402:Homo saplens v-ral simian leuk Hs.192182:ESTs	201 201
15	417426	NM_00229		NM_002291:Homo sapiens laminin, beta 1 (	2.01
	412790	NM_01476	7 Hs.74583	NM_014767:Homo sapiens KIAA0275 gene pro	2.01
	445892	AV655500	Hs.93961	Hs.93961:Homo seplens mR; cD DKFZp667D09	201
	TABLE 398	<b>.</b>			
20	Pkey:		nique Eos probes	et identifier number	
	CAT numb	er: G	ene cluster numb		
	Accession:	G	enbank accessio	i numbers	
	Pkey	CAT Numi	per Accession		
25	409745	MH1944_		A921874 AW188822 BI027862 AI347618 AI361453	AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
					006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
	418869	12789_14		Bi033518 Bi027818 BG015789 Bi033807 AA341445	
	421902	276321_1		8E079601 BE079534 AA299964 BE392717 BE883	02 BE070532 BE018148 BE880427 WM1306
30	400231	MH494_5			01 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459
		_	BG926429	BG389312 BG477333 Al031799 Bl763443 Bl26043	2 AA989106 AV728576 BI091380 AA402499 AI200513 AI284734 AI223995 AI289749
					3E890952 AA401181 BG939668 F35525 BI088182 F34674 F33506 BM471326 F34677
					1076923 A1018505 BE879774 BM465637 A1753078 BG222159 AA595947 8F970917 71 BF339134 BE409272 BE266458 BE796770 BE745957 BG755835 BE266758
35					637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743
			BM459094	BM455306 BM472001 BM478247 BM478771 BM48	0379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359
	450004			BM455329 BM471815 BI862301 BG331736 H0490	3 AA374894 BE902964
	438584 413020	1241536_ 1485885_		AA811347 D79715 R98736 242904	
40	400265	1145_1			BE222576 Al191715 Al423108 BF064068 BG057819 Al208589 Al880535 Al262890
			A1246261	F939926 AI282848 AI802409 BE301053 AI884624	AI160385 AI335983 BF440017 BG231884 AI343699 AI280745 AI871338 AI123739
			AI871126	\W080375 Al350160 Al300855 Al818598 Al085263	AI306653 AW571658 BF 109839 AW273280 AI888380 AI571860 AI357126 AW194105
					674 BF509394 AI891077 BF221538 AI651874 F25731 AW881176 AI685962 D44936
45					1 A1908017 A1378261 AA975416 R16732 H47612 H45402 AA668719 AA722441 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806
					AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 Al292151
			H26003 R	2487 BG766512 BE815124 AW138122 H96767 R3	9407 BI044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180
			R92185 H	8680 R43192 AA401390 AA977841 AI091944 AA9	3369 AA617840 H14351 AI866242 AI915028 AA780787 AAS06995 AA827498 AA634305
50			AA846358	AA470463 AA618163 AA601963 W74212 AA02152	0 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793 42340 AA976636 AA360268 AA976223 T95788 AA527774 A1620298 AA180888
20					994 AA299572 Al092819 Al291438 AA459588 AA136373 R50213 BE622752 AA401414
				AA766800 W98432 81550308 H52236 AA491029 8	
	400208	16640_1			1 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391
55					25 BE455589 AW002786 AW591760 Al968816 AW006268 AW593787 BG236814
33			RIO14177	/ ANY-907000 ANY 073902 AV 240207 AV 102303 AV 111 121 AL 519136 RE675314 AWRD6520 RIR70778 RER704	70 A1249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 19 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893
				R09703 Bi013066	7 0C1 17313 G1 071 100 DG304101 A1033210 DG431029 BC1 33244 DC030033
	400264	1145_1			8E222576 Al191715 Al423108 BF064068 BG057819 Al208589 Al880535 Al262890
60	•		AJ246261	3F939926 Al282848 Al802409 BE301053 Al884624	A160385 A335983 BF440017 BG231884 A343699 A1280745 A1871338 A1123739
00			AI071120 AI131474	AVVOOGTO AIGGUTOO AIGUOGG AIGTGGGG AIGGGCGG AW318548 AW128942 AW571682 AIG82962 AW20	AI306653 AW571658 BF109839 AW273280 AI888380 AI571860 AI357126 AW194105 3674 BF509394 AI891077 BF221538 AI651874 F25731 AW881176 AI685962 D44938
					01 AI908017 AI378261 AA975416 R16732 H47612 H45402 AA668719 AA722441
					H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806
65					AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 Al292151
05			H26003 K	3248/ BG/66512 BE815124 AW136122 H96767 R:	9407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180 93369 AA617840 H14351 A1856242 A1915028 AA780787 AA506995 AA827496 AA634305
			AA846356	AA470463 AA618163 AA601963 W74212 AA0215	10 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793
			AA019060	AA814222 AA693469 N99931 N67840 R26834 BF	342340 AA976636 AA360268 AA976223 T95786 AA527774 AI620298 AA180888
70					1994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414
70	406729	0_0	AA180973 AA069711	AA766800 W96432 BI550308 H52236 AA491029 E	G420468 BG827522
	407347	810943_			
					1
75	TABLE 3	9C:	Halaua conti		
, ,	Pkey: Ref:			orresponding to an Eos probeset	tentifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA
			sequence of hum	ian chromosome 22" Dunham, et al. (1999) <u>Nature</u> 4	ленина (од нишена объемани, еток, тексто из окоришениот еписо тто отка. 02:489-495,
	Strand:		indicates DNA st	rand from which exons were predicted.	<del></del>
80	Nt_positi	on:	Indicates nucleot	ide positions of predicted exons.	
30	Pkey	Ref	Strand	Nt_position	
	404240	5002624	Minus	116132-116407,116653-116922	
	404277	1834458	Minus	91665-91946	

	401179	9438647	Plus	113477-113893
	405102	8076881	Minus	120922-121296
	402575	9884830	Minus	109742-109883
_	402901	8894222	Minus	175428-175667
5	405204	7230116	Plus	126569-126754
	403857	7708910	Minus	2524-3408
	400847	9188605	Plus	44643-44835
	404030	7671252	Plus	149362-151749
	405517	9454624	Plus	114757-114877
10	402559	9864273	Plus	33539-33715
	403966	6568881	Plus	158193-158277,160116-160290
	402424	9796344	Minus	64925-65073

15 TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER

Table 40A fixts about 977 Genes up-recoulded in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.0. The "average" stomach cancer to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-matignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-matignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. 20

Pkey: ExAccn:

EXACCN: UnigenelD: Unigene Titla: R1:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Ratio of tumor to normal adult tissues

25

	Pkey	ExAcen	UnigenelO	Unigene Title	R1
	411243	AB039886	Hs.69319	CA11	30.66
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	16.94
30	444325	AW152618	Hs.16757	ESTS	13.51
	445891	AW391342	Hs.199460	ESTs	11.92
	448811	AI590371	Hs.174759	ESTs	11.08
	431723	AW058350	Hs.16762	Homo seplens mRNA; cDNA DKFZp564B2062 (f	10.84
	409757	NM_001898	Hs.123114	cystatin SN	10.38
35	421110	AJ250717	Hs.1355	cathepsin E	9.11
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.66
	446998	N99013	Hs.16762	Homo sepiens mRNA; cDNA DKFZp564B2062 (f	8.50
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.11
	428651	AF198478	Hs.188401	annexin A10	6.86
40	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	6.51
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.49
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.39
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	6.31
	428664	AK001666	Hs.189095	similar to SALL1 (sat (Drosophila)-like	6.25
45	409041	AB033025	Hs.50081	KIAA1199 protein	5.72
	408380	AF123050	Hs.44532	distriguitin	5.72
	428953	AA306610	Hs.194676	DKFZP434C013 protein	5.46
	450685	L15533	Hs.423	pancreatitis-associated protein	5.40
	409187	AF154830	Hs.50966	carbamoyi-phosphate synthetase 1, mitoch	5.34
50	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	5.16
• •	421346	Z34277	Hs.103707	aportucio	5.14
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.06
	425679	X05997	Hs.159177	lipase, gastric	4.94
	421582	AI910275	Hs.1406	trefoil factor 1 (breast cancer, estroge	4.93
55	434414	AJ798376	113.1700	gb:tr34b07.x1 NCI_CGAP_Ov23 Homo saniens	4.92
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	4.89
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANS	4.84
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	4.72
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	4.72
60	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.68
••	448693	AW004854	Hs.228320	Homo saplens cDNA: FLJ23537 fis, clone L	4.53
	441377	BE218239	Hs.202656	ESTs	4.51
	419278	AU076799	Hs.1247	apolipoprotein A-IV	4.48
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP entagon	4.47
65	403422		113.10030	clarence next substituting it own supplies	4.38
	403776				4.32
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.32
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.30
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	4.30
70	451181	AI796330	Hs.207461	ESTs	4.26
	432168	AK000563	Hs.272805	hypothetical protein FLI20556	4.23
	454464	AW811606	Hs.271819	Homo sapiens cDNA: FLJ22751 fis, clone K	4.20
	448844	AI581519	Hs.177164	ESTs	4.20
	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	4.13
75	452461	N78223	Hs.108106	transcription factor	
	409420	Z15008	Hs.54451		4.08
	431611	U58766	Hs.264428	laminin, gamma 2 (nicein (100kD), kelini tissue specific transplantation antigen	4.04 4.04
	413719	BE439580	Hs.75498	small inducible cytokine subtamily A (Cy	
	430044	AA464510	Hs.152812	ESTs	4.03
80	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB 8	4.02
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superlami	4.01
	420159	AI572490	Hs.99785	Homo engine eDMA: El 121245 Se elec- O	4.00
	428227	AA321649	Hs.2248	Homo sepiens cDNA: FLJ21245 fis, clone C small inducible cytokine subfamily B (Cy	3.98
	12022		. 13.2470	the second of the companies and the second of the second o	3.91

	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	3.07
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.87 3.84
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.82
_	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.81
5	419833	AA251131	Hs.220697	ESTs	3.81
	446232	AJ281848	Hs.165547	ESTs	3.74
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.70
	451105 413281	AI761324 AA861271	U- 24300	gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	3.67
10	432867	AW016936	Hs.34396 Hs.233364	ESTs ESTs	3.66
• •	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	3.66 3.65
	457465	AW301344	Hs.195969	ESTs	3.65
	414918	AI219207	Hs.72222	Homo sapiens cONA FLJ13459 fis, clone PL	3.61
1.5	418738	AW388633	Hs.6682	ESTs	3.60
15	427778	AA412323	Hs. 105323	ESTs	3.60
	454293	H49739	Hs.134013	ESTs, Moderately similar to NK homeobox	3.59
	452194 442577	AI694413 AA292998	Hs.298262 Hs.163900	ESTs, Wealtly similar to dJ88J8.1 [H.sapi	3.57
	426174	AA547959	Hs.115838	ESTs ESTs	3.57 3.53
20	452862	AW378065	Hs.8687	ESTs	3.51
	418869	AW516565	Hs.258279	ESTs	3.48
	430178	AW449612	Hs.152475	ESTs	3.48
	430397	AJ924533	Hs.105607	ESTs	3.46
25	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	3.45
23	442295 425921	A1827248 NM_007231	Hs.224398 Hs.162211	Homo sapiens cDNA FLJ11469 fis, clone HE	3.44
	431764	AA515212	Hs.271819	solute carrier lamily 6 (neurotransmitte Homo sapiens cDNA: FLJ22751 fis, clone K	3.44 3.43
	421948	L42583	Hs.111758	keratin 6A	3.43
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	3.41
30	442896	R37725	Hs.261108	ESTs	3.41
	452281	T93500	Hs.28792	Homo saplens cDNA FLJ11041 fis, clone PL	3.39
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.39
	408832 406685	AW085690 M18728	Hs.63428	ESTs	3.39
35	437527	AJ241019	Hs.145644	gb:Human nonspecific crossreacting antig ESTs	3.37 3.37
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	3.37
	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro	3.36
	441318	AI078234	Hs.176130	ESTs	3.35
40	458897	U85642	Hs.138506	ESTs	3.33
70	413808 411274	J00287 NM_002776	Hs.182183 Hs.69423	caldesmon 1 kallikrein 10	3.33
	418406	X73501	Hs.84905	cytokeratin 20	3.32 3.32
	419559	Y07828	Hs.91096	ring finger protein	3.32
4.5	423217	NM_000094	Hs. 1640	collagen, type VII, alpha 1 (epidermolys	3.31
45	423271	W47225	Hs.126256	interleukin 1, beta	3.31
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.30
	427722 422310	AK000123 AA316622	Hs.180479 Hs.98370	hypothetical protein FLJ20116	3.30
	430704	AW813091	15.36370	cytochrome P540 family member predicted gb:RC3-ST0186-240400-111-d07 ST0186 Homo	3.30 3.29
50	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.29
	443211	AJ128388	Hs.143655	ESTs	3.29
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.28
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.28
55	452121 408633	NM_004081 AW963372	Hs.70936 Hs.46677	deleted in azoospermia	3.27
	447342	Al199268	Hs.19322	PRO2000 protein ESTs	3.27 3.25
	419229	AI827237	Hs.282884	ESTs	3.24
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	3.23
60	452699	AW295390	Hs.213062	ESTs	3.23
UU.	425188 400289	AK002052 X07820	Hs.155071	hypothetical protein FLJ11190	3.23
	408524	D87942	Hs.2258 Hs.46328	matrix metalloproteinase 10 (stromelysin	3.21
	437897	AA770561	Hs.146170	fucosyltransferase 2 (secretor status in hypothetical protein FLJ22969	3.20 3.20
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.19
65	453160	AI263307	Hs.146228	ESTs	3.19
	406690	M29540	Hs.220529	carcinoembryonic entigen-related cell ad	3.19
	430187 416209	A1799909	Hs.158989	ESTs	3.18
	447048	AA235776 AW393080	Hs.79078 Hs.228320	MAD2 (mitolic arrest deficient, yeast, h Homo sapiens cDNA: FLJ23537 fis, clone t	3.16
70	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.14
	425465	L18964	Hs.1904	protein kinase C, iota	3.14 3.13
	425826	U97698	Hs.159593	mucin 6, gastric	3.13
	431662	AA513406	Hs.152307	ESTs	3.13
75	419216	AU076718	Hs.164021	small inducible cytokine subfamily 8 (Cy	3.13
, ,	418203 417315	X54942 AI080042	Hs.83758 Hs.180450	CDC28 protein kinase 2 ribosomal protein S24	3.12
	433001	AF217513	Hs.279905	clone HQ0310 PRQ0310p1	3.11
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	3.11 3.11
00	450159	AI702416	Hs.200771	ESTs. Weakly similar to CAN2_HUMAN CALPA	3.11
80	434370	AF130988	Hs.58346	downless (mouse) homolog	3.10
	421190 421370	U95031 Y15221	Hs.102482		3.10
	421379 420380	AA640891	Hs.103982 Hs.102406		3.10
		1400-0071	F13.104400	LUID	3.10

	414774	X02419	Hs.77274	plasminogen activator, uroldnase	3,10
	415989	AJ267700	Hs.111128	ESTs	3.10
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.09
_	407289	AA135159	Hs 203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.09
5	420297	A1628272	Hs.88323	ESTs	3.08
	447519 448045	U46258 AJ297436	Hs.23448 Hs.20166	ESTs	3.08
	431956	AK002032	Hs.272245	prostate stem cell antigen Homo sapiens cDNA FLJ11170 fis, clone PL	3.07 3.06
• •	410286	AJ739159	Hs.61898	DXFZP586N2124 protein	3.05
10	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.05
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3	3.05
	436481 430573	AA379597 AA744550	Hs.5199 Hs.136345	HSPC150 protein similar to ubiquitin-con	3.05
	428987	NM_004751	Hs.194710	ESTs glucosaminyl (N-acetyl) transferase 3, m	3.05 3.04
15	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	3.04
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.03
	415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	3.03
	411789 417956	AF245505 AA210704	Hs.72157 Hs.190465	Homo sapiens adlican mRNA, complete cds ESTs	3.02 3.02
20	408908	BE296227	Hs.48915	serine/threonine kinase 15	3.02
	422330	O30783	Hs.115263	epiregulin	3.01
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.00
	425761	AW664214	Hs.196729	ESTs	2.99
25	432978 418546	AF126743 AA224827	Hs.279884	DNAJ domain-containing gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.99 2.99
	425371	D49441	Hs.155981	mesothelin	2.99
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member 811	2.98
	439453	BE 264974	Hs.6566	thyroid hormone receptor interactor 13	2.98
30	413278 428450	BE563085 NM_014791	Hs.833 Hs.184339	interferon-stimulated protein, 15 kDa	2.97
50	424345	AK001380	Hs.145479	KIAA0175 gene product Homo sapiens cDNA FLJ10518 fis, clone NT	2.95 2.95
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	2.94
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	2.94
35	432917	NM_014125	Hs.279812	PRO0327 protein	2.94
22	433384 432731	AI021992 R31178	Hs.124244 Hs.287820	ESTs fibronectin 1	2.93
	420552	AK000492	Hs.98806	hypothetical protein	2.93 2.92
	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.92
40	409687	T51125	Hs.8493	ESTs	2.91
40	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	2.89
	417791 457288	AW965339 AA521458	Hs.111471 Hs.192738	ESTs ESTs	2.89 2.89
	456181	L36463	Hs.1030	ras inhibitor	2.89
15	450190	T51387		gb:yb20e08.r1 Stratagene fetal spleen (9	2.88
45	411573 430204	AB029000	Hs.70823	KIAA1077 protein	2.68
	434808	AA618335 AF155108	Hs.146137 Hs.256150	ESTs, Wealdy similar to putative [C.eleg ESTs, Highly similar to NY-REN-41 antige	2.88 2.87
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.87
50	418670	AA601036	Hs.285083	ESTs	2.87
50	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	2.87
	409723 435099	AW885757 AC004770	Hs.257862 Hs.4756	ESTS	2.87
	408660	AA525775	Hs.292523	flap structure-specific endonuclease 1 ESTs	2.86 2.86
<i></i>	434032	AW009951	Hs.206892	ESTs	2.85
55	418216	AA66Z240	Hs.283099	AF15q14 protein	2.85
	453331 450221	AI240665 AA328102	Hs.8895 Hs.24641	ESTs	2.85
	402075	77-320102	TS.24041	cytosketeton associated protein 2	2.84 2.84
60	410145	AW885300		gb:RCS-OT0078-100400-023-C11 OT0078 Horno	2.83
60	410681	AW246890	Hs.65425	calbindin 1, (28kD)	2.83
	439867 443715	AA847510 AI583187	Hs.161292	ESTs	2.63
	420005	AW271106	Hs.9700 Hs.133294	cyclin E1 ESTs	2.83 2.83
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	2.83
65	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.82
	404567	1.40243	11. 44.0044		2.82
	422158 449224	L10343 AW995911	Hs.112341 Hs.299883	protease inhibitor 3, skin-derived (SKAL hypothetical protein FLJ23399	2.82 2.81
	407584	W25945	Hs.18745	ESTs	2.81
70	453884	AA355925	Hs.36232	KIAA0186 gene product	2.81
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	2.80
	422809 449722	AK001379 BE280074	Hs.121028 Hs.23960	hypothetical protein FLJ10549 cyclin 81	2.79
	445676	Al247763	Hs.15928	ESTs	2.79 2.79
75	424308	AW975531	Hs.154443		2.78
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.78
	421777 452571	BE562088 W31518	Hs.108196	The coor protons	2.78
_	420759	W31518 T11832	Hs.34665 Hs.127797	ESTs ESTs	2.77 2.77
80	422675	BE018517	Hs.119140		2.77
	412723	AA648459	Hs.179912	ESTS	2.76
	439670	AF088076	Hs.59507	ESTs, Wealthy similar to AC004858 3 U1 sm	2.76
	400298	AA032279	Hs.61635	six transmembrane epithetial antigen of	2.76

	414569 449378	AF109298	Hs.118258	prostate cancer associated protein 1	2.76
	423903	AW664026 M57765	Hs.59892 Hs.1721	ESTs Interleukin 11	2.75
	412059	AA317962	Hs.249721	ESTs	2.75
5	431104	AW970859	Hs.269109	ESTs	2.75 2.75
_	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	275
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.75
	452940	AA029722	Hs.20279	ESTs	2.74
10	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	274
10	407777	AA161071	Hs.71465	squalene epoxidase	2.73
	432201	AI538613	Hs.135557	ESTs .	2.73
	414416 414617	AW409985	Hs.76084	tamin 82	2.73
	432407	Al339520 AA221038	Hs.20524 Hs.285026	ESTs, Moderately similar to hexokinase I	273
15	444301	AK000136	Hs.10760	HERV-H LTR-associating 1 hypothetical protein FLI20129	273 272
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	272
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.72
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.72
^^	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	271
20	429432	AI678059	Hs.202676	synaptonemal complex protein 2	2.71
	450506	NM_004460	Hs.41B	fibroblast activation protein, alpha	2.71
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	271
	418801 440283	AA228366 A1732892	Hs.115122 Hs.190489	ESTs	2.71
25	429486	AF155827	Hs.203963	ESTs hypothetical protein FLJ10339	271
	408366	AW511255	Hs.258082	ESTs	2.71 2.70
	406399			2010	2.69
	434217	AW014795	Hs.23349	ESTs	2.68
20	449785	AJ225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	2.68
30	446269	AW263155	Hs.14559	hypothetical protein FLJ 10540	2.68
	443349	Al052572	Hs.269864	ESTs	2.68
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.67
	417079 444754	U65590 T83911	Hs.81134	Interleukin 1 receptor antagonist	2.67
35	424687	J05070	Hs.11881 Hs.151738	transmembrane 4 superfamily member 4	2.67
	439979	AW600291	Hs.6823	matrix metalloproteinase 9 (gelatinase 8 hypothetical protein FLJ10430	2.66 2.65
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.65
	430832	AJ073913	Hs.100686	ESTs. Wealdy similar to secreted cement	2.65
40	427217	AA399272	Hs.144341	ESTs	2.65
40	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	2.64
	450400	A1694722	Hs.279744	ESTs	2.64
	435380	AA679001	Hs.192221	ESTs	2.64
	432375 453700	8E536069 AB009426	Hs.2962	S100 calcium-binding protein P	2.63
45	422938	NM_001809	Hs.560 Hs.1594	apolipoprotein B mRNA editing enzyme, ca	2.63 2.63
	453134	AA032211	Hs.118493	centromere protein A (17kD) ESTs	2.63
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.62
	408868	AW292286	Hs.255058	ESTs	2.62
50	414972	BE263782	Hs.77695	KIAA0008 gene product	2.62
50	440255	A1932285	Hs.160569	ESTs	2.62
	403055				2.62
	443247	BE614387	Hs.47378	ESTs. Moderately similar to hypothetical	2.62
	447400 413753	AK000322 U17760	Hs.18457	hypothetical protein FLJ20315	2.61
55	445114	AW991959	Hs.301103 Hs.254664	Human DNA sequence from clone 272L16 on ESTs	2.61 2.61
	422397	AJ223366	Hs.116051	myeloma overexpressed gene(in a subset o	2.60
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.60
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	2.60
40	440249	A1246590	Hs.125325	ESTs	2.60
60	433220	AI076192	Hs.131933	EST:	2.60
	438533 436251	AI440266	Hs.170673	ESTs, Wealdy similar to AF126780 1 retin	2.60
	424717	BE515065 H03754	Hs.5092 Hs.152213	nucleolar protein (KKE/D repeat)	2.60
	448988	Y09763	Hs.22785	wingless-type MMTV integration site fami gamma-aminobutyric acid (GABA) A recepto	2.60 2.60
65	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	2.60
	435370	A1964074	Hs.225838	ESTs	2.59
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.59
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	2.59
70	443919	AI091284	Hs.135224	ESTs	2.58
70	413268	AL039079	Hs.75256	regulator of G-protein signatting 1	2.58
	404519 414998	NM 003543	No 77770	auldland law doneth, the second of the second	2.58
	429597	NM_002543 NM_003816	Hs.77729 Hs.2442	oxidised low density lipoprotein (lectin	2.57
	426841	AI052358	Hs. 193726	a disintegrin and metalloproteinase doma ESTs	2.57 2.57
75	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.57 2.57
	417933	X02308	Hs.82962	thymidylate synthetase	2.56
	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	2.56
	441384	AA447849	Hs.288660	protease, serine, 23	2.56
80	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	2.56
90	418867	031771	Hs.89404	msh (Orosophila) homeo box homolog 2	2.55
	449042 416065	AW294985 BE267931	Hs.301148 Hs.78996	potassium voltage-gated channel, isk-rel	2.55
	414132	AI801235	Hs.48480	proliferating cell nuclear antigen ESTs	2.55
				2010	2.55



	431890	X17033	Hs.271986	integrin, alpha 2 (CD498, alpha 2 subuni	2.55
	407830 434815	NM_001086 AF155582	Hs.587 Hs.46744	arylacetamide deacetylase (esterase) core1 UDP-galactose:N-acetylgalactosamin	2.55
	415250	F02614	Hs.27319	ESTs	2.54 2.54
5	435647	AI653240	Hs.49823	ESTs	2.54
	459306	AW578452	Hs.232988	ESTs, Wealdy similar to mucin (H.sapiens	2.54
	414381	A1086138	Hs.204044	ESTs	2.54
	425782 416984	U66468 H38765	Hs.159525	cell growth regulatory with EF-hand doma	2.53
10	431183	NM_006855	Hs.80706 Hs.250696	diaphorase (NADH/NADPH) (cytochrome b-5 KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.53 2.53
	436043	AW963838	Hs.168830	Homo sapiens cONA FLJ12136 fis, clone MA	2.53
	456743	AI630124	Hs.7434	ESTs	253
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.52
15	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	2.52
13	411734 432657	AW374954 AAB31815	Hs.71779 Hs.270940	Homo sapiens DNA from chromosome 19, cos	2.52
	434080	AI820719	Hs.154662	ESTs hypothetical protein PRO1472	2.51 2.51
	438190	AA780020	Hs.136798	ESTs	251
20	418969	W33191	Hs.28907	hypothetical protein FLJ20258	2.51
20	446405	AW451259	Hs.57851	ESTs	2.51
	450002 431808	A1879524 M30703	Hs.201629 Hs.270833	ESTs, Moderately similar to ALU8_HUMAN A	2.51
	429093	NM_000253	Hs.195799	amphiregulin (schwannoma-derived growth microsomal triglyceride transfer protein	2.51 2.50
	447634	AW967902	Hs.5152	Homo sapiens cONA: FLJ22618 fis, clone H	2.50
25	436393	AW022213	Hs.143617	ESTs	2.50
	453751	R35762	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	249
	445669 445865	A1570830 A1262584	Hs.174870	ESTs	2.49
	448437	AW470125	Hs.145575	ESTs gb:xw60c04.x1 NCI_CGAP_Pan1 Homo sapiens	2.49 2.49
30	414883	AA926960	Hs.77550	CDC28 protein kinase 1	2.49
	406747	Al925153	Hs.217493	annexin A2	2.49
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.49
	426322 412903	J05068 BE007967	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.48
35	422515	AW500470	Hs.155795 Hs.117950	ESTs multifunctional polypeptide similar to S	2.48
•-	447030	AW444659	Hs.232184	ESTs	2.48 2.48
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.48
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.48
40	406671 409640	AA129547 U78722	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.48
40	424639	AI917494	Hs.55481 Hs.131329	zinc finger protein 165 ESTs	2.48 2.48
	404171	72517454	113.131323	COTE	2.47
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	2.47
45	407839	AA045144	Hs.161566	ESTs	2.47
43	410406	AI969703	Hs.301842	EST8	2.47
	452220 427691	BE158006 AW194426	Hs.212296 Hs.20726	ESTs ESTs	2.46
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.45 2.46
	444838	AV651680	Hs.208558	EST8	2.46
50	413816	AW958181	Hs.189998	ESTs	2.46
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.46
	436513 445417	AA972691 AK001058	Hs.192974 Hs.12680	Homo sepiens cONA FLJ12735 fis, clone NT	2.45
	432874	W94322	Hs.279651	Homo sapiens cDNA FLJ10196 fis, clone HE melanoma inhibitory activity	2.45 2.45
55	425268	AI807883	Hs.156932	ESTs	2.45
	425397	J04088	Hs.156346	topolsomerase (DNA) II alpha (170kD)	2.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.45
	427961 422363	AW293165 T55979	Hs.143134 Hs.115474	ESTs replication factor C (activator 1) 3 (38	2.45
60	433083	AL042759	Hs.191762	ESTs	2.45 2.45
	439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	2.44
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 ffs, clone AD	2.44
	431457 443949	NM_012211 AW827419	Hs.256297	integrin, alpha 11	2.44
65	416498	U33632	Hs.235070 Hs.79351	ESTs potassium channel, subfamily K, member 1	2.44
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.44 2.43
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.43
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.43
70	407243 410044	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	243
, 0	424273	BE566742 W40450	Hs.58169 Hs.144442	highly expressed in cancer, rich in leuc	243
	409533	AW969543	Hs.21291	phospholipase A2, group X mitogen-activated protein kinase kinase	2.42 2.42
	453966	BE148734	Hs.252833	ESTs	2.42
75	427043	AA397679	Hs.298460	ESTs	2.42
75	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.42
	449987 433159	AW079749 AB035898	Hs.184719 Hs.150587	ESTs, Weakly similar to AF116721 112 PRO kinesin-like protein 2	2.42
	439396	BE562958	Hs.74346	ESTs. Wealty similar to /prediction	2.42 2.42
80	426427	M86699	Hs. 169840	TTK protein kinase	241
80	434725	AK000796	Hs.4104	hypothetical protein	241
	427719 433312	Al393122 Al241331	Hs.134726	ESTS	2.41
	433312	AI241331 AA557191	Hs.131765 Hs.55028	ESTs ESTs	2.41
					2.41

	407047	VEERCE		shall and see compa	
	407047 419220	X65965 AA811938	Hs.291759	gb:H.sapiens SOD-2 gene for manganese su ESTs	2.41 2.40
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.40
_	435219	AA676349	Hs.190331	ESTs	2.40
5	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	2.40
	416713	T70174		gb:yc18b03.s1 Strategene lung (937210) H	2.40
	418322 409902	AA284166 AI337658	Hs.84113 Hs.156351	cyclin-dependent kinase inhibitor 3 (CDK	2.40
	443597	AI078418	ns. 130331	ESTs gb:oz05e03.x1 Soares_fetal_liver_spleen_	2.40 2.40
10	404253	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		British and California and California	2.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	2.40
	443462	AI064690	Hs.171176	ESTS	2.39
	418693 451237	A1750878 AW600293	Hs.87409	firombospondin 1 gb:EST00049 pGEM-T fibrary Homo sapiens	2.39
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.39 2.39
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	2.39
	445625	8E246743	Hs.288529	Homo sapiens cONA: FLJ22635 fis, clone H	2.39
	435937 438993	AA830893 AA828995	Hs.119769	ESTS	2.39
20	422082	AA016188	Hs.111244	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens hypothetical protein	2.38 2.38
	435849	BE305242	Hs.112442	ESTs. Wealdy similar to CLDE_HUMAN CLAUD	2.38
	407242	M18728		gb:Human nonspecific crossreacting antig	2.38
	450396 430354	AU077002 AA954810	Hs.24950 Hs.239784	regulator of G-protein signalling 5	2.38
25	422578	AF239666	Hs.1545	human homolog of Drosophila Scribble caudal type homeo box transcription fact	2.38 2.38
	446342	BE298655	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	2.38
	450737	AW007152	Hs.203330	ESTs	2.38
	428070	T63918 AA033813	Hs.182313	retinol-binding protein 2, cellular	2.38
30	416111 433345	AI681545	Hs.79018 Hs.152982	chromatin assembly factor 1, subunit A ( Homo sapiens cDNA FLJ13117 fis, clone NT	2.37 2.37
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.37
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphata transamin	2.37
	453204 453876	R10799	Hs.191990	ESTs	2.37
35	425081	AW021748 X74794	Hs.110406 Hs.154443	ESTs minichromosome maintenance deficient (S.	2.36 2.36
-	434682	AA827165	Hs.191958	ESTs	2.36
	439737	AJ751438	Hs.41271	Homo sapiens mRNA full length insert cON	2.36
	414108 417900	AI267592 BE250127	Hs.75761 Hs.82906	SFRS protein kinase 1 CDC20 (cell division cycle 20, S. cerevi	2.36
40	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	2.36 2.36
	448826	AI580252	Hs.293245	ESTs, Wealdy similar to putative p150 [H	2.36
	441020 448019	W79283	Hs.35962	ESTs	2.36
	431753	AW947164 X76029	Hs.195641 Hs.2841	ESTs neuromedin U	2.36 2.36
45	441703	AW390054	Hs.192843	ESTs	2.36
	410361	8E391804	Hs.62661	guanylate binding protein 1, interferon-	2.36
	418526 444478	BE019020 W07318	Hs.85838 Hs.240	solute carrier family 16 (monocarboxylic M-phase phosphoprotein 1	2.36
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	2.36 2.35
50	428388	AA729827	Hs.101265	Homo sapiens cDNA: FLJ22593 fs, clone H	2.35
	436961	AW375974	Hs.156704	ESTs	2.35
	408194 438578	AA601038 AA811244	Hs.191797 Hs.164168	ESTs ESTs	2.35 2.35
	429183	AB014604	Hs.197955	KIAA0704 protein	2.35
55	435663	AI023707	Hs.134273	ESTs	2.35
	430290 423441	A1734110 R68649	Hs.136355 Hs.278359	ESTs absent in metanoma 1 like	2.34
	453900	AW003582	Hs.226414	ESTs, Wealdy similar to ALUB_HUMAN ALU S	2.34 2.33
<b>~</b>	450378	AW249181	Hs.19954	ESTs, Wealthy similar to cONA EST yk385e1	2.33
60	432877	AW974111	Hs.292477	ESTs	2.33
	451928 426227	AJ823801 U67058	Hs.30315 Hs.168102	ESTs Human proteinase activated receptor-2 mR	2.33 2.33
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.33
65	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fls, clone NT	2.33
65	435106 432193	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	2.33
	458531	AA372264 AA367718	Hs.273193 Hs.159083		2.33 2.33
	449532	W74653	Hs.271593		2.33
70	446354	AW449650	Hs.202249	ESTs	2.33
70	409703 419373	NM_006187	Hs.56009	2-5 oligoadenylate synthetase 3	2.33
	435607	NM_003244 W73428	Hs.90077 Hs.8750	TG-interacting factor (TALE family homeo uncharacterized bone marrow protein BM04	2.32 2.32
	405818			·	2.32
75	423132	AF070647	Hs.124126		2.32
75	444371 432675	BE540274 AI791855	Hs.239 Hs.105884	forkhead box M1 ESTs	2.32
	411773	NM_006799		protease, serine, 21 (testish)	2.32 2.31
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.31
80	434775	AA648983	Hs.212911		2.31
30	407378 442353	AA299264 BE379594	Hs.49138	gb:EST11752 Uterus Homo sepiens cONA 5 ESTs	2.31 2.31
	422611	AA158177	Hs.118722	! fucosyttransterase θ (alpha (1,6) fucosy	2.31
	409965	AA079229		gb:zm95f04,r1 Stratagene colon HT29 (937	2.31

	421677	H64092	Hs.38282	ESTs	2.31
	419493	AF001212	Hs.90744	proteasome (prosome, macropain) 26S subu	231
	424435	AB011167	Hs.146957	KIAA0595 protein	2.30
5	446880 452795	AI811807 AW392555	Hs.108646 Hs.18878	Homo sapiens cONA FLJ12534 fis, clone NT hypothetical protein FLJ21620	2.30 2.30
-	452834	AI638627	Hs.105685	ESTs	2.30
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.30
	428125 417655	AA393071 AA760791	Hs.182579 Hs.14014	teucine aminopeptidase ESTs, Weakly similar to KIAA0973 protein	2.30 2.29
10	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.29
	428923	BE047698	Hs.188785	ESTs	2.29
	452203 409402	X57522 AF208234	Hs.158164 Hs.695	ATP-binding cassette, sub-family 8 (MDR/ cystatin 8 (stefin 8)	2.29 2.29
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.29
15	451999	AW176401	Hs.27424	DEAD/H (Asp-Gh-Ala-Asp/His) box polypep	2.29
	400811 436396	AF219139 Al683487	Hs.87726 Hs.299112	KIAA0154 protein; ADP-ribosylation facto	2.29
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ11441 fis, clone HE Homo sapiens cDNA FLJ13495 fis, clone PL	2.28 2.28
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.28
20	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.28
	425247 438170	NM_005940 AI916685	Hs.155324 Hs.194601	matrix metalloproteinase 11 (stromelysin ESTs	2.28 2.28
	445378	AV653564	Hs.226946	ESTs	2.28
25	428048	AA705745	Hs.185070	ESTs	2.28
23	414696 444665	AF002020 BE613126	Hs.76918 Hs.47783	Niemann-Pick disease, type C1 ESTs, Wealdy similar to T12540 hypotheti	2.27 2.27
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.27
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	2.27
30	433535 415857	AF111106 AA866115	Hs.3382 Hs.301646	protein phosphatase 4, regulatory subuni	2.27 2.27
	421155	H87879	Hs.102267	Homo sapiens cDNA FLJ11381 fts, clone HE lysyl oxidase	2.27
	405545				2.27
	449467 445537	AW205006 AJ245671	Hs.197042	ESTs	2.27
35	450680	AF131784	Hs.12844 Hs.25318	EGF-like-domain, multiple 6 Homo sapiens clone 25194 mRNA sequence	2.27 2.26
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	2.26
	443868	W88483	Hs.293650	ESTs	2.26
	407742 428330	AF186252 L22524	Hs.38084 Hs.2256	sulfotransferase family, cytosolic, 1C, matrix metalloproteinase 7 (matrilysin,	2.26 2.26
40	432655	AA832195	Hs.292266	ESTs	2.26
	429731	AK001592	Hs.212172	beta,beta-carotene 15,15-dioxygenase ho	2.26
	400514 431846	BE019924	Hs.271580	uroplakin 1B	2.26 2.26
4.5	439521	AI808955	Hs.58248	ESTs	2.26
45	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	2.26
	437641 418982	AA811452 AI348838	Hs.291911 Hs.13073	ESTs ESTs	2.26 2.26
	411393	AW797437	Hs.69771	B-factor, properdin	2.26
50	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	2.25
50	419488 434540	AA316241 NM_016045	Hs.90691 Hs.5184	nucleophosmin/nucleoplasmin 3	2.25
	449962	AA004879	Hs.187820	TH1 drosophila homolog ESTs	2.25 2.25
	410196	A1936442	Hs.59838	hypothetical protein FLJ10808	2.25
55	456844 414368	AJ264155 W70171	Hs.152981 Hs.75939	COP-diacylglycerol synthase (phosphatida	2.25 2.25
55	408353	BE439838	Hs.44298	uridine monophosphate kinase hypothetical protein	2.25
	439223	AW238299	Hs.23945	ESTs	2.25
	448753 428479	AL048858 Y00272	Hs.224355	ESTs, Weakly similar to A39650 protein k	2.25
60	432403	AA550815	Hs.184572 Hs.124840	cell division cycle 2, G1 to S and G2 to ESTs	2.24 2.24
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid -	2.24
	432673 446887	AB028859 Al346656	Hs.278605 Hs.156652	ER-associated DNAJ; ER-associated Hsp40 Homo sapiens cDNA: FLJ22800 fls. clone K	2.24
	452833	BE559681	Hs.30736	KIAA0124 protein	2.24 2.24
65	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.24
	422039	BE567832	Hs.82148	hypothetical protein	2.24
	429925 445413	NM_000786 AA151342	Hs.226213 Hs.12677	cytochrome P450, 51 (lanosterol 14-alpha CGI-147 protein	2.24 2.23
~~	423645	AJ215632	Hs.147487	ESTs	2.23
70	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.23
	423515 444743	AA327017 AA045648	Hs.162204 Hs.11817		2.23
	434518	H56995	Hs.37372	nudix (nucleoside diphosphate linked mol Homo saplens DNA binding peptide mRNA, p	2.23 2.23
75	435602	AF217515	Hs.283532	uncharacterized bone marrow protein 8M03	2.23
, 5	449974 424927	AW970948 AW973566	Hs.269403 Hs.153850		2.23
	457982	AW856093	Hs.183617		2.23 2.23
	414420	AA043424	Hs.76095	immediate early response 3	2.23
80	449019 431840	AI949095 AA534908	Hs.67776 Hs.2860	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.23
-	452930	AW195285	Hs.194097	POU dornain, class 5, transcription facto ESTs	2.23 2.23
	438391	AJ227892	Hs.146274	ESTs	2.23
	439186	A1697274	Hs.6487	Xq28, 2000bp sequence contg. ORF	2.23
				440	)
				•••	-

	427254	AL121523	Hs.97774	ESTs .	2 22
	424517	AL121323 AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	2.22 2.22
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	222
_	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	2.22
5	427647	W19744	Hs.180059	Homo sapiens cONA FLJ20653 fis, clone KA	2.22
	438223	AA781171		gb:aj24d05.s1 Soares_testis_NHT Homo sap	2.22
	434504 450149	AJ887341	Hs.121590	Homo sepiens cDNA FLJ12827 ffs, clone NT	2.22
	439211	AW969781 AI890347	Hs.293440 Hs.271923	ESTs, Moderately similar to ZIC2 protein Homo sapiens cDNA: FLJ22785 fis, clone K	2.22 2.22
10	401519		14471320	Trusto Sapreis Collect PC222100 IIS, Collect	2.22
	441794	AW197794	Hs.253338	ESTs	2.22
	412108	AA100293	Hs.185043	ESTs	222
	431849	A1670823	Hs.85573	Homo sapiens mRNA; cDNA DKFZp566N034 (fr	2.22
15	444969 408901	AI203334	Hs.160628	ESTs	2.21
12	434423	AK001330 NM_006769	Hs.48855 Hs.3844	hypothetical protein FLJ10458 LIM domain only 4	2.21 2.21
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	2.21
	400021			AFFX control: STAT1	221
20	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.21
20	434170	AA626509	Hs.122329	ESTs	2.21
	423453	AW450737	Hs.128791	CGI-09 protein	2.21
	428438 433102	NM_001955 AI343966	Hs.2271 Hs.158528	endothelin 1 ESTs	2.21
	421470	R27496	Hs.1378	annexin A3	2.21 2.21
25	425499	T62489		gb:yc03f09.r1 Stratagene lung (937210) H	2.21
	438280	AW015534	Hs.217493	annexin A2	2.21
	440381	AA917808	Hs.190495	ESTs	2.20
	453779	N35187	Hs.43388	ESTs	2.20
30	433627 417944	AF078866 AU077196	Hs.284296 Hs.82985	Homo sapiens cDNA: FLJ22993 fis, clone K collagen, type V, alpha 2	2.20 2.20
50	452299	AW206330	Hs.73239	hypothetical protein FLJ10901	2.20
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Hamo	2.20
	448457	H65629	Hs.245997	ESTs	2.20
35	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.20
33	426125 430603	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	2.20
	425274	AA148164 BE281191	Hs.247280 Hs.155462	HBV associated factor minichromosome maintenance deficient (mi	2.20 2.20
	452679	Z42387	Hs.4299	Homo sapiens cDNA: FLJ20965 fis, clone A	2.20
40	410619	BE512730	Hs.65114	keratin 18	2.20
40	424332	AA338919	Hs.101615	ESTs	2.20
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.20
	418661 419341	NM_001949 N71463	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	2.20
	427920	Z11502	Hs.118888 Hs.181107	ESTs, Weakly similar to ALU1_HUMAN ALU S annexin A13	2.20 2.19
45	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fis, clone H	2.19
	419752	AA249573	Hs.152618	ESTs	2.19
	441436	AW137772	Hs.185980	ESTs	2.19
	413095	AA494359	Hs.30715	ESTs	2.19
50	403208 422596	AF063611	Hs.118633	2 Selicandendete austratea Ele	2.19
50	444261	AA298958	Hs.10724	2-5'oligoadenylate synthetase-like MDS023 protein	2.19 2.19
	419474	AW968619	Hs.155849	ESTs	2.19
	453883	AI638516	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamm	2.18
55	423401	NM_001992	Hs.128087	coagulation (actor il (thrombin) recepto	2.18
23	453450	AW797627 AA876179	Hs.89474	ADP-ribosylation factor 6	2.18
	440250 444334	BE296785	Hs.134650 Hs.10848	ESTs KIAA0187 gene product	2.18 2.18
	437616	AJ797163	Hs.207954	ESTs	218
	451807	W52854	Hs.27099	OKFZP564J0863 protein	2.18
60	430441	8E398091	Hs.6880	DKFZP434D156 protein	2.18
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (I	2.18
	411678 453735	Al907114 Al066629	Hs.71465 Hs.125073	squalene epoxidase ESTs	2.18
	450499	AA235207	Hs.250456	hypothetical protein DKFZp762F2011	2.18 2.18
65	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.18
	421532	AW138207	Hs.146170	hypothetical protein FLJ22969	2.18
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	2.18
	451099	R52795	Hs.25954	interteurun 13 receptor, alpha 2	218
70	444207 425873	AI565004 NM_013390	Hs.79572 Hs.160417	cathepsin D (lysosomal aspartyl protease	2.18
, ,	417404	NM_007350		transmembrane protein 2 pleckstrin homology-like domain, family	217
	449437	AJ702038	Hs.100057		2.17 2.17
	446995	AI355012		gb:qu16d10.x1 NCI_CGAP_Ov23 Homo sapiens	2.17
76	431548	AJ834273	Hs.9711	Homo saplens cDNA FLJ13018 fis, clone NT	2.17
75	411127	AA668995	Hs.218329		2.17
	439961	AA857451	Hs.269696		2.17
	429125 407103	AA446854 AA424881	Hs.271004 Hs.256301		2.17
• -	435990	AI015862	Hs.131793		2.17 2.17
80	415116	AA160363	Hs.269956		217
	440052	A1633744	Hs.195648	ESTs .	2.17
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.17
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.16

	443599	A1079559	Hs.134125	ESTs	2.16
	423623 427258	AB011117 AA400091	Hs.129943 Hs.39421	KIAA054S protein ESTs	2.16
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.16 2.16
5	450835	BE262773	Hs.25584	hypothetical protein FLJ 10767	2.16
	428698	AA852773	Hs.297939	ESTs, Wealdy similar to T17344 hypotheti	2.16
	421408	AI688223	Hs.104114	H.sapiens HCG I mRNA	216
	449057	AB037784	Hs.22941	KIAA1363 protein	2.16
10	408947 443552	AL080093 N65982	Hs.49117 Hs.109434	Homo sopiens mRNA; cDNA DKFZp564N1662 (f ESTs	2.16 2.16
••	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.16
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	2.16
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit.	2.16
15	452865	AI924048	Hs.119567	ESTS	2.16
13	432789 438580	D26361 AA811262	Hs.3104 Hs.299202	KIAA0042 gene product ESTs	2.16 2.16
	422192	AA305159	Hs.113019	fs485	215
	425607	<b>U09860</b>	Hs.158333	protease, serine, 7 (enterokinase)	2.15
20	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	2.15
20	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.15
	441021 442432	AW578716 BE093589	Hs.7644 Hs.38178	H1 histone family, member 2 Homo sepiens cDNA: FLJ23468 fis, clone H	2.15
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.15 2.15
~~	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	2.15
25	414761	AU077228	Hs.77256	enhancer of zesta (Drosophila) homolog 2	2.15
	447033	Al357412	Hs.157601	ESTS	2.15
	410407 446077	X66839 BE251048	Hs.63287 Hs.22579	carbonic anhydrase IX Homo sapiens clone CDABP0036 mRNA sequen	2.15 2.15
	420900	AL045633	Hs.44269	ESTs	2.15
30	411975	AJ916058	Hs.144583	ESTs, Wealdy similar to gag [H.sapiens]	215
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.15
	449571	AW016812	Hs.200266	ESTs .	2.15
	452721 410491	AJ269529 AA465131	Hs.30377 Hs.64001	Homo sapiens EST from clone 470080, full Homo sapiens clone 25218 mRNA sequence	2.15 2.14
35	410664	NM_006033	Hs.65370	lipase, endothelial	2.14
	435730	AB020635	Hs.4984	KIAA0828 protein	2.14
	452835	AK001269	Hs.30738	hypothetical protein FLJ10407	2.14
	452092 401708	BE245374	Hs.27842	hypothetical protein FL/11210	2.14
40	411400	AA311919	Hs.69851	GAR1 protein	2.14 2.14
. •	448526	AB028946	Hs.21361	KIAA1023 protein	2.14
	421175	AJ879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.14
	412338	AA151527	Hs.69485	Homo sapiens cDNA FLJ12436 ffs, clone NT	2.14
45	420894 409235	AA744597 AA188827	Hs.88854	ESTs	2.14
45	412870	N22788	Hs.7988 Hs.82407	ESTs, Weakly similar to endo-alpha-0-man Horrio sapiens HSPC296 mRNA, partial cds	214 214
	447760	AI431328	Hs.291179	ESTs, Weakly similar to topoisomerase I	2.14
	413511	AJ627178	Hs.75412	Arginine-rich protein	2.13
50	432945	AL043683	Hs.271357	ESTs, Wealdy similar to unnamed protein	213
50	418592 441790	X99226 AW294909	Hs.284153 Hs.132208	Fanconi anemia, complementation group A	2.13
	425298	AK000209	Hs.155556	ESTs hypothetical protein FLJ20202	2.13 2.13
	450956	AW193531	Hs.205647	ESTs. Moderately similar to ALU1_HUMAN A	2.13
55	419569	AJ971651	Hs.91143	jagged 1 (Alagille syndrome)	2.13
23	421508 453975	NM_004833 AW009808	Hs.105115	absent in melanoma 2	2.13
	413670	AB000115	Hs.270829 Hs.75470	ESTs hypothetical protein, expressed in osteo	2.13
	422783	AA598956	Hs.120439	ethanotamina kinase	2.13 2.13
60	444542	Al161293	Hs.146852	ESTs, Wealdy similar to KIAA0525 protein	2.13
60	410418	031382	Hs.63325	transmembrane protezse, serine 4	2.13
	419791 414860	A1579909 BE255593	Hs.105104	ESTs	2.13
	425860	129339	Hs.77502 Hs.1964	methionine adenosyttransferase II, alpha solute carrier family 5 (sodium/glucose	2.13 2.13
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyttransferase 1	2.13
65	437050	AA766420	Hs.291606	ESTS	2.13
	430217	N47863	Hs.180450	ribosomal protein S24	2.13
	420923 409012	AF097021 AL117435	Hs.273321 Hs.49725	differentially expressed in hernatopoieti OKFZP434I216 protein	2.12
	450645	AL117441	Hs.25264	DKFZP434N126 protein	2.12 2.12
70	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	212
	451356	AA748418	Hs.164577	ESTs	2.12
	429534	AW976987	Hs.163327	ESTs	2.12
	428365 441495	AA295331 AW294603	Hs.183861 Hs.127039	Homo sapiens cDNA FLJ20042 fis, clone CO	2.12
75	443564	A11234003 A192168\$	Hs.127039	ESTs ESTs	2.12 2.12
-	410839	NM_006849	Hs.66581	protein disuffide isomerase	2.12
	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	2.12
	442947	R40800	Hs.21303	ESTs	2.12
80	414987 450510	AA524394 AA010056	Hs.165544 Hs.242998		2.12
	427475	AA403151	Hs.191605		2.12 2.12
	444670	H58373	Hs.37494	ESTs	2.12
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.12

	422240	B1224		abud2at2at Casas forth acceler	0.10
	433748 415138	R12244 C18356	Hs.78045	gb:yf33c12x1 Scares fetal liver spleen tissue factor pathway inhibitor 2	2.12 2.11
	438138	R98299	Hs.177502	ESTs	2.11
_	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-like) 10	211
5	415474	NM_014252	Hs.78457	solute carrier family 25 (mitochondrial	2.11
	416472	AA180756	Hs.193094	ESTs, Moderately similar to ALU4_HUMAN A	211
	412490 410718	AW803564 AI920783	Hs.288850 Hs.191435	Homo sapiens cDNA: FLJ22528 fis, clone H ESTs	211
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	211 211
10	433344	AI741506	Hs.186753	ESTs, Wealdy similar to ALU1_HUMAN ALU S	211
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.11
	431621	AW292329	Hs.163481	ESTs	211
	418522 433849	AA505038 BE465884	Hs.7149 Hs.280728	Homo sapiens cONA: FLJ21950 fis, clone H ESTs	211 211
15	438038	AJ732629	Hs.194181	ESTs, Wealthy similar to TAZR HUMAN, BETA	211
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.11
	409717	AW452871	Hs.56043	CGI-115 protein	2.11
	410566 445837	AA373210 AI261700	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.11
20	414334	AA824298	Hs.145544 Hs.21331	ESTs hypothetical protein FLJ10036	2.11 2.11
	438326	8E085236	Hs.181244	major histocompatibility complex, class	2.10
	423880	BE278111	Hs.134200	DKFZP564C186 protein	2.10
	421574	AJ000152	Hs.105924	defensin, beta 2	2,10
25	437103 435550	AW139408 AJ224456	Hs.152940 Hs.4934	ESTs	210
2.5	450747	Al064821	Hs.48306	H.sapiens polyA site DNA ESTs, Highly similar to EWS_HUMAN RNA-BI	2.10 2.10
	437033	AW248364	Hs.5409	RNA polymerasa i subunit	210
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.10
30	431120	AA492588	044570	gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.10
30	430510 429669	AW162916 BE185499	Hs.241576 Hs.2471	hypothetical protein PRO2577 KIAA0020 gene product	2.10 2.10
	407881	AW072003	Hs.40968	heparan suffate (glucosamine) 3-0-suffot	2.10
	436124	AA705012	Hs.269584	ESTs	2.10
25	436415	BE265254	Hs.51B1	proliferation-associated 2G4, 38kD	2.10
35	451121	AW973795	Hs.128927	Homo saplens cDNA FLJ13903 fis, clone TH	2.10
	453968 437549	AA847843 AA759149	Hs.62711	ESTs gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.10 2.10
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.10
40	447720	AL038765	Hs.161304	ESTs	2.09
40	434769	AA648884	Hs.134278	Homo sepiens cDNA FLJ12676 fis, clone NT	2.09
	429743 447815	AA804398 AJ432199	Hs.288995 Hs.247084	hypothetical protein FLJ20813 ESTs	2.09
	441675	Al914329	Hs.5461	ESTs	2.09 2.09
	434274	AA828539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.09
45	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.09
	442525 423750	AF150282 AF165883	Hs.145945 Hs.132415	ESTs pretoldin 2	2.09 2.09
	449199	AI990122	Hs.196988		2.09
	415363	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas	2.09
50	432543	AA552690	Hs.152423		2.09
	418462 432093	BE001596 H28383	Hs.85266	integrin, bela 4	2.09
	407862	BE548267	Hs.50724	gb:yl52c03.r1 Soares breast 3NbHBst Homo Homo sapiens cDNA FLJ10934 fis, clone OV	2.09 2.09
	434442	AA737415	Hs.152826		2.09
55	442671	AI005668	Hs.134779		2.09
	428771 430335	AB028992	Hs.193143		2.09
	425087	D80007 R62424	Hs.239499 Hs.126059		2.08 2.08
	412530	AA768268	Hs.266273		2.08
60	443450	N66045	Hs.133529	ESTS	2.08
	418753	6E217818 Al916132	Hs.87016	Homo sapiens cDNA: FLJ22938 fis, clone K	2.08
	432204 439018	AW300887	Hs.121593 Hs.26638	Homo sapiens cDNA FLJ13123 fis, clone NT ESTs, Weakly similar to unnamed protein	2.08 2.08
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.08
65	431628	AF146277	Hs.265561	CD2-associated protein	2.08
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.08
	432284 411372	AA532807 AI147861	Hs.105822 Hs.213289		2.08 2.08
	459319	NM_000059		gb:Homo saplens breast cancer 2, early o	2.08
70	408730	AV660717	Hs.47144	OKFZPS86N0819 protein	2.08
	443607	AI452512	Hs. 134069		2.08
	422058 409220	AA862231 BE243323	Hs.51233	gb:oe13g03.s1 NCI_CGAP_Ov2 Homo sapiens	2.08
	429504	X99133	Hs.204238	tumor necrosis factor receptor superfami Epocalin 2 (oncogene 24p3)	2.08 2.08
75	409686	AK000002	Hs.55879	Homo sapiens mRNA for FLJ00036 protein,	2.08
	438394	BE379623	Hs.27693	CGI-124 protein	2.08
	413092 413715	AA126856 AW8\$1121	Hs.118665		2.08
	423020	AA383092	Hs.75497 Hs.1608	Homo sapiens cDNA: FLJ22139 fis, clone H replication protein A3 (14kD)	2.08 2.07
80	438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	2.07
	453379	AA035261	Hs.61753	ESTs	2.07
	432125 449370	AW972667 AK002114	Hs.287510		2.07
	443210	ANAU2114	Hs.23495	hypothetical protein FLJ11252	2.07

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	449318	AW236021	Hs. 108788	ESTs, Wealdy similar to seste (D.melanog	2.07
	450096 454011	A1682088 M31008	Hs.223368	ESTs	2.07
	427876	Al494291	Hs.37009 Hs.111977	alkatine phosphatase, intestinal ESTs	2.07
5	422901	R81936	Hs.121576	aspartate beta-hydroxytase	2.07 2.07
•	419235	AW470411	Hs.288433	heurotrimin	207
	449207	AL044222	Hs.23255	nucleoporin 15SkD	2.07
	408243	Y00787	Hs.624	interleukin 8	2.07
10	415652	T79213	Hs.272073	ESTs	2.07
10	446546	BE167687	Hs.156628	ESTs	2.07
	411765 423472	H43346 AF041260	U. 120057	gb:yp09a04.r1 Soares breast 3NbHBst Homo	2.07
	436211	AK001581	Hs.129057 Hs.80961	breast carcinoma amplified sequence 1 polymerase (DNA directed), gamma	2.07
	456157	AW979153	113.00301	gb:EST391263 MAGE resequences, MAGP Homo	2.07 2.06
15	407143	C14076	Hs.248968	EST	206
	454269	AI961060	Hs.296411	ESTs, Moderately similar to KF1A_HUMAN K	2.06
	432440	X63597	Hs.2996	sucrase-isomaltase	2.06
	410668	BE379794	Hs.65403	hypothetical protein	2.06
20	422765 450434	AW409701 AA166950	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.06
20	439832	T81829	Hs.18645 Hs.14870	ESTs, Weakly similar to partial CDS [C.e	2.06
	456264	AW974175	Hs.105251	ESTs ESTs	206
	431201	AA678405	Hs.8854	Human transcription unit PVT gene, exons	2.06 2.06
~~	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone PL	2.06
25	438714	AA814859	Hs.294112	ESTs	2.06
	445318	AW500652	Hs.200885	ESTs	2.06
	439951 433681	AI347067 AI004377	Hs.124636	ESTs	2.06
	428307	W27393	Hs.200360 Hs.183648	Homo sapiens cDNA FLJ13027 fis, clone NT	2.06
30	426874	N67325	Hs.247132	protein tyrosine phosphalase, receptor t ESTs	2.06 2.06
	451295	AI557212	Hs.17132	ESTs	2.06
	432584	AA928829	Hs.47099	Homo sapiens cDNA: FLJ21212 fls, clone C	2.06
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.06
35	433716	AA608808	Hs.225118	ESTs	2.06
33	429412 426235	NM_006235 AJ531964	Hs.2407 Hs.34447	POU domain, class 2, associating factor	2.06
	449026	BE500946	Hs.209105	ESTs .	2.06
	437016	AU076916	Hs.5398	guarrine monphosphate synthetase	2.06 2.06
40	400019			AFFX control: STAT1	2.06
40	408873	AL046017	Hs.23247	ÉSTs .	2.06
	442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	2.06
	455778 439975	BE088746 AW328081	No 6017	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.06
	433037	NM_014158	Hs.6817 Hs.279938	Homo saplens putative oncogene protein m HSPC067 protein	2.06
45	440086	NM_005402	Hs.288757	v-raf simian leukamia viral oncogene hom	2.06 2.06
	436414	BE264633	Hs.143638	WD repeat domain 4	2.05
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.05
	407293	AA602234	Hs.270551	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
50	409459 436238	D86407 AK002163	Hs.54481	low density lipoprotein receptor-related	2.05
50	400517	AF242388	Hs.301724 Hs.149585	ESTs, Highly similar to unnamed protein	2.05
	439943	AW083789	Hs.124620	lengsin ESTs	2.05 2.05
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	2.05
	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kO)	2.05
55	417491	AW376842	Hs.1085	guanylate cyclase 2C (heat stable entero	2.05
	453775 435525	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.05
	412627	AJ831297 BE391959	Hs.123310 Hs.74276	ESTs chloride intracellular channel 1	2.05
	439702	AW085525	Hs.134182	ESTs	2.05 2.05
60	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.05
	432979	AA573263	Hs.120860	ESTs	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	2.05
	432925	AA878324	Hs.192734	ESTs	2.05
65	446311 427871	AW007294 AW992405	Hs.149795 Hs.59622	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.05
••	453804	AA300204	Hs.35276	ESTs, Wealdy similar to unknown (H.sapie KIAA0852 protein	2.05 2.05
	449939	T86420	Hs.272139	ESTs	2.05
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo	2.05
70	417819	AJ253112	Hs.133540	ESTs	2.04
70	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.04
	415009 437829	C75253 AI358522	Hs.220950	ESTs	2.04
	435381	AU356322 AW136397	Hs.270188 Hs.247572	ESTs ESTs	2.04
	439778	AL109729	Hs.18948	ESTs, Highly similar to HPS1_HUMAN PROTE	2.04 2.04
75	428753	AW939252	Hs.192927	hypothetical protein FLJ 20251	2.04
	446475	AI908188	Hs.209245	ESTs .	2.04
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	2.04
	423701	AA329856	Hs.143022	ESTs	2.04
80	430680 422369	AW138724 AF005216	Hs.168974 Hs.115541	ESTs, Highly similar to ALU7_HUMAN ALU S	2.04
	432481	AW451645	Hs.151504	Janus kinase 2 (a protein tyrosine kinas Homo sapiens cONA FLJ11973 fis, clone HE	2.04 2.04
	443748	AW861379	Hs.160602	ESTs	2.04
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.04

	430000	Allemannes.			
	432393 430785	AW205863 Z30201	Hs.133988	ESTs, Wealdy similar to I52825 gene MAC2	2.04
	428343	AL043021	Hs.12705	gb:HHEA22G Atrium cDNA library Human hea ESTs, Weatry similar to ptakophilin 2b [	2.04 2.04
_	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	2.04
5	452488	N74921	Hs.184389	ESTs	2.04
	403485 413313	NM_002047	Hs.75260	about tOMA synthetone	2.04
	407634	AW016569	Hs.301280	glycyl-IRNA synthetase ESTs, Highly similar to AF241831 1 intra	2.04 2.04
10	433326	A1379486	Hs.159430	ESTs	2.03
10	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Horno	2.03
	429165 422963	AW009886 M79141	Hs.118258 Hs.13234	prostate cancer associated protein 1 ESTs	2.03
	418684	U82987	Hs.87246	Bcl-2 binding component 3	2.03 2.03
1.5	407824	AA147884	Hs.9812	ESTs	2.03
15	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN ONA-RE	2.03
	440246 444006	W52010 8E395085	Hs.191379 Hs.10086	ESTS	2.03
	431301	AA502384	Hs.151529	type I transmembrane protein Fn14 ESTs	2.03 2.03
20	452705	H49805	Hs.246005	ESTs	2.03
20	421724	AB037832	Hs.107287	KIAA1411 protein	203
	420637 450200	AW976153 AW975625	Hs.173088	gb:EST388262 MAGE resequences, MAGN Horno ESTs	2.03
	447474	AW614220	Hs.189402	ESTs	2.03 2.03
25	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	2.03
25	445019 435202	AI205540	Hs.281295	ESTs	2.03
	433202	AI971313 NM_005764	Hs.170204 Hs.271473	KIAAQSS1 protein epithelial protein up-regulated in carol	2.03 2.03
	435198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.03
20	440773	AA352702	Hs.37747	hypothetical protein FLJ12484	2.03
30	443425 454166	AI056776	Hs.133397	ESTs	2.03
	407975	AW993356 X89426	Hs.2055 Hs.41716	ubiquitin-activating enzyme E1 (A1S9T an endothelial cell-specific molecule 1 (NO	2.03 2.03
	428299	AL038004	Hs.29419	ESTs	2.03
25	418735	N48769	Hs.44609	ESTs	2.03
35	442053 415757	R35343 AA830854	Hs.24968	Human DNA sequence from clone RP1-233G16	2.03
	432559	AW452948	Hs.187810 Hs.257631	ESTs . ESTs	2.03 2.03
	425912	AL137629	Hs.162189	serine/threonine kinase with Obl- and pl	2.02
40	419395	BE268326	Hs.90280	5-aminolmidazote-4-carboxamide ribonucte	2.02
40	417576 418559	AA339449 AA225048	Hs.82285	phosphoribosylgtycinamide formyltransfer	2.02
	410855	X97795	Hs.104207 Hs.66718	ESTs RADS4 (S.cerevisiae)-like	2.02 2.02
	433906	AI167816	Hs.43355	ESTs	2.02
45	422072	AB018255	Hs.111138	KIAA0712 gene product	2.02
43	419546 446229	AA244199 AI744964	14 4440	gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	2.02
	450516	AA902656	Hs.14449 Hs.21943	KIAA1609 protein NIF3 (Ngg1 interacting factor 3, S.pombe	2.02 2.02
	431721	AB032996	Hs.268044	KIAA1170 protein	2.02
50	419807	R77402		gb:yi75f11.s1 Soares placenta NbZHP Homo	2.02
50	438192 401866	AI859065	Hs.16808	ESTs, Wealdy similar to paraplegin-like	2.02
	443129	R16075	Hs.21668	ESTs	2.02 2.02
	426991	AK001536	Hs.285803	Homo sapiens cDNA FLJ12852 fis, clone NT	2.01
55	414731	A1890434	Hs.77135	Homo sapiens mRNA; cDNA DKFZp586A191 (tr	2.01
33	424783 413293	AA913909 AL047483	Hs.153088 Hs.75270	TATA box binding protein (T8P)-associate	2.01
	435787	AW162767	Hs.100914	GTP-binding protein homologous to Saccha hypothetical protein FLJ10352	2.01 2.01
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.01
60	442660	AW138174	Hs.130651	ESTs	2.01
50	456553 431630	AA721325 NM_002204	Hs.189058 Hs.265829	ESTs, Weakly similar to cAMP-regulated g integrin, alpha 3 (antigen CD49C, alpha	2.01 2.01
	431300	AA502346	114.404023	gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.01
	443180	R15875	Hs.70945	ESTs	2.01
65	450914 448275	AJ743761 BE514434	Hs.142528	ESTs	2.01
00	405484	DE314434	Hs.20830	synaptic Ras GTPase activating protein 1	2.01 2.01
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	2.01
	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.01
70	439696 432378	W95298 AI493046	Hs.171882		201
. •	417975	AA641836	Hs.146133 Hs.30085	ESTs Homo sapiens cDNA: FLJ23186 fis, clone L	2.01 2.01
	453665	AA626250	Hs.181165		2.01
	419981	AA897581	Hs.128773	ESTs	2.01
75	445808 435767	AV655234 H73505	Hs.298083		201
	430466	AF052573	Hs.117874 Hs.241517		2.01 2.01
	452747	BE153855	Hs.61460	ESTs	2.01
	422790	AA809875	Hs.25933	ESTs	2.01
80	443303 433929	U67319 Al375499	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.01
- •	410008	AA079552	Hs.27379	ESTs gb:zm20h12.s1 Stratagene pancreas (93720	2.01 2.01
	448954	AB014564	Hs.22616	KIAA0664 protein	200
	440774	AJ420611	Hs.127832	ESTs	2.00

	451351	AW058261	Hs.168213	ESTe Wester in Days and an access at a S	2.00
	442961	BE614474	Hs.289074	ESTs. Weakly similar to ALU1_HUMAN ALU S Homo sapiens cONA FL113985 fis, clone Y7	2.00 2.00
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.00
~	407154	H79677		gb:yu76g10.s1 Soares fetal tiver spleen	2.00
5	410240	AL157424	Hs.61289	synaptojanin 2	2.00
	426830 435014	AA385751	Hs.160392	ESTs	200
	408520	BE560898 AI918693	Hs.10026 Hs.81848	ribosomal protein L17 isotog	2.00
	432829	W60377	Hs.57772	RAD21 (S. pombe) homolog ESTs	2.00 2.00
10	406752	AI285598	Hs.217493	annexin A2	2.00
	TABLE 40/	A:			
15	Pkey:		e Eos probes	et identifier number	
	CAT numb		cluster numb		
	Accession:	Genb	ank accession	unupers	
	Pkey	CAT number	Accession		
20	408690	107490_1		AA056567 AW882724	
	409955	116301_1		A079201 AA078874	
	410008 410145	116812_1 1178960_1		BE142525 BE142527	
	411765	125700_1	H43346 AA	AW887902 AW887893 AW886291 AW592641 248302 AA095182	
25	416713	1610889_1		244 T69850 H79151	
	418546	176677_1	AA224827 1	59708 T59843 BE 156903	
	419546 419807	185766_1		VA244272 H57440	
	420637	188252_1 195241_1		262462 AA250988 R06794 AA278945 AA747691	
30	422058	210815_1		VA659033 AA302799 AA302798	
	422128	211994_1	AWB81145	AA490718 M85637 AA304575 T06067 AA331991	
	422689	219896_1		AA315006 AW954733	
	425499 430704	252539_1 322217_1		1634 AA828581 AA358569 AW206655 AA484440	
35	430785	323486_1		486132 T72025	
	431120	328264_1		AA492498 AA492571	
	431300	331217_1	AA502346		
	431322 432009	331543_1 34025_1		AA503009 AA502998 AA502989 AA502805 T921 3E007148 T52277	88
40	432093	341283_1		/972670 H28359 AA525808	
	433748	37385_1		1290 Al110858 AF090916 AF075357 AA011531	
	434414	38585_1	A1798376 S	46400 AW811617 AW811616 W00557 BE142245	5 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
			AW857541	AW814172 H66214 AW814398 AF134164 AA243	3093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
45			AA149776	AADS9829 AW879188 AW813567 AW813538 AIZ AAD63634 AW840684 AW864666 COCC64 AW886	67168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			N66951 AA	527374 H66215 AA045564 AI694265 H60808 AA	2836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 A829309 AW991957 149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531	H59570	
	437549 438223	438403_1		AW751066 AW844938	
50	438223	452646_1 467651_1		A1202139 A1202098 AA834879 A1926361	
	439848	477806_1		D63277 AA846968	
	443597	574739_1	AI078418 V	V80626 AW387769	
	446995	702707_1	AI355012 /		
55	447197 448437	711623_1 763310_1		366546 R36167 - A1734872 A1740660 ANNISCENA ALCOZDAD ANATZI	0000 \$140042400 \$16044075 \$4500740 \$140047000
••	450190	827655_1	T51387 AV	/191595 T51271 Al686285	9036 AW843429 AW844876 AI520713 AW847236
	451105	859083_1		W880941 AW880937	
	451129	859870_1	8E072881	BE072946 AJ762181	
60	451237 455666	863269_1 1349545_1	AW600293 RE065813	A1767468 8E065788 BE065889 BE065832	
	455778	1364506_1		9E088802 8E088755 BE088876 BE088947 BE08	RRRA1 RE088952
	456157	158261_1	AW979153	AA176967 AA826015	
	TABLE 40	nc-			
65	Pkey:		ue number co	mesponding to an Eos probeset	
	Ref:	Seq	uence source.	The 7 digit numbers in this column are Genbank	Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
		pea	nence of num:	in chromosome 22" Dunham, et al. (1999) Nature	402:489-495.
	Strand: Nt_positio	India	cates DNA str	and from which exons were predicted.	
70	NCposiac	и: (Лусл	Cales nucleou	de positions of predicted exons.	
	Pkey	Ref	Strand	Nt_position	
	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,9375	50-93891
	401519	6649315	Plus	157315-157950	
75	401708 401866	2951946 8018106	Plus Plus	154511-155298 73126-73623	
	402075	8117407	Plus	121907-122035,122804-122921,124019-1241	61.124455-124610.125672-126076
	403055	8748904	Minus	109532-110225	with the control that the state of the state
	403208	7630829	Minus	147706-147903,148667-148804	
80	403422 403485	9665041 9986528	Minus Plus	151169-151561 2888-3001,3198-3532,3655-4117	
	403776	7770611	Minus	1414-1513,1624-1756	
	404171	9930793	Plus	173667-173783,176876-177055	
	404253	9367202	Minus	55675-56055	

5	404519	8152000	Plus	12817-13000
	404567	7249169	Minus	101320-101501
	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405818	4071056	Plus	29055-29196
	406399	9256288	Minus	63448-63554
	406399	9256268	Minus	63448-63554

TABLE 41A: ABOUT 634 SEQUENCES UP-REGULATED IN STOMACH CANCER
Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult issues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 40A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig. In3, egf, 7tm domains). Predicted protein domains are 10

15

tor Table 40A ai noted. Pkey: ExAcon: UnigeneID: Unigene Title: PSDomain: R1:

Unique Eos probeset Identifier number Exemptar Accession number, Genbank accession number Unigene number Unigene gene title Protein Structural Domain Ratio of turnor to normal adult tissues

20	Pkey	ExAcen	UnigenetD	Unigene Title	PS0omain .	RI
	411243	AB039886	Hs.69319	CA11	SS	30.66
	418007	M13509	Hs.83169	matrix metallop	hemopexin,Peptidase_M10,SS	16.94
	448811	AI590371	Hs.174759	ESTS	TM	11.08
	409757	NM_001898	Hs.123114	cystatin SN	cystatin,SS	10.38
25	421110	AJ250717	Hs.1355	catheosin E	asp.SS	9.11
	428368	BE440042	Hs.83326	matrix metallop	hemopexin,Peptidase_M10,SS	8.66
	406687	M31126	Hs.272620	pregnancy speci	hemopexin,TM,	7.11
	428651	AF196478	Hs.188401	annexin A10	annexin,TM,	6.86
20	425211	M18667	Hs.1867	progastricsin (	asp,TM,SS	6.51
30	423673	BE003054	Hs.1695	matrix metallop	hemopexin,Peptidase_M10,SS	6.49
	409683	U33317	Hs.711	defensin, atpha	defensins, Defensin_propep, SS	6.39
	428664	AK001666	Hs.189095	similar to SALL	z1-C2H2,TM,S\$	6.25
	408380	AF 123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,	5.72
35	428953	AA306610	Hs.194676	DKFZP434C013 pr	arf,TNFR_c6,DEAD,Stathmin,TM,SS	5.46
22	450685	L15533	Hs.423	pancreatitis-as	lectin_c,TM,SS	5.40
	409187	AF154830	Hs.50966	carbamoyl-phosp	GATase,CPSase_L_chain,CPSase_sm_chain,MGS,TM,	5.34
	434206	AW136973	Hs.288516	ESTs, Wealtly si	PH,TM,	5.16
	421346	Z34277	Hs.103707	apomucin	Cys_knot,vwd,	5.14
40	427585 425679	D31152 X05997	Hs.179729	collagen, type	C1q,Collagen,TM,SS	5.06
70	421582	AI910275	Hs.159177 Hs.1406	lipase, gastric	abhydrotase,SS	4.94
	422956	BE545072	Hs.122579	trefoil factor	trefoil,trypsin,TM,SS	4.93
	448105	AW591433	Hs.170675	hypothetical pr	TM	4.89
	413385	M34455	Hs.840	ESTs, Westly si	trypsin,TM,	4.84 4.72
45	417866	AW067903	Hs.82772	indoleamine-pyr collagen, type	IDO,TM,	
	419278	AU076799	Hs.1247	apolipoprotein	TSPN,Collagen,COLFI,SS Apolipoprotein,SS	4.68 4.48
	407811	AW190902	Hs.40098	cysteine knot s	SS	4.47
	403422	***********	110.4000	Cyclosic Mich	SS	4.38
	403776				IL8,TM,SS	4.32
50	418478	U38945	Hs.1174	cyclin-dependen	ank, TM, SS	4.32
	428242	H55709	Hs.2250	leukemia inhibi	UF_OSM,SS	4.30
	421341	AJ243212	Hs.279611	deleted in mali	SS	4.30
	428434	AW383590	Hs.65551	ESTs, Weakly si	SS	4.13
	409420	215008	Hs.54451	taminin, gamma	taminin_EGF,taminin_B,SS	4.04
55	431611	U58766	Hs.264428	tissue specific	Epimerase, TM, SS	4.04
	413719	BE439580	Hs.75498	small inducible	IL8,SS	4.03
	409956	AW103364	Hs.727	inhibin, beta A	TGF-beta,TGFb_propeptide,SS	4.01
	422420	U03398	Hs.1524	turnor necrosis	TNF,TM,	4.00
<b>~</b>	428227	AA321649	Hs.2248	small inducible	ILB,TM,SS	3.91
60	422168	AA586894	Hs.112408	S100 catcium-bi	efhand,TM,	3.87
	412140	AA219691	Hs.73625	RAB6 interaction	kinesin,TM,SS	3.82
	414812	X72755	Hs.77367	monokine induce	ILB,SS	3.81
	419833	AA251131	Hs.220697	ESTs	WHEP-TRS,TM,	3.81
65	446232	AI281848	Hs.165547	ESTs	7tm_3,TM,	3.74
05	432398	AA307808	Hs.2979	trefoil factor	trefoil,TM,SS	3.70
	432867 424046	AW016936	Hs.233364	ESTs	GSHPx_TM,SS	3.66
	414918	AF027856	Hs.138202	serine (or cyst	serpin,TM,	3.65
	454293	Al219207 H49739	Hs.72222	Homo sapiens cD	TM	3.61
70	442577		Hs.134013	ESTs, Moderatel	TM	3.59
, ,	426174	AA292998 AA547959	Hs.163900 Hs.115838	ESTs ESTs	TM	3.57
	418869	AW516565	Hs.258279	ESTs	\$S	3.53
	418054	NM_002318	Hs.83354	lysyl oxidase-l	Sema,TM,	3.48
	442295	AI827248	Hs.224398	Homo sapiens cD	Lysyl_oxidase.SRCR.SS	3.45
75	425921	NM_007231	Hs.162211	solute carrier	Collagen, COLFI, vwc, TM, SS	3.44
	421948	L42583	Hs.111758	keratin 6A	SNF,TM, filament,TM,	3.44 3.43
	444783	AK001468	Hs.62180	anillin (Drosop	mament, i M, PH, TM,	3.43
	437527	AJ241019	Hs.145644		PIPSKTM,SS	3.39 3.37
	433084	M18079	Hs.282265	fatty acid bind	lipocalin, SS	3.37
80	452401	NM_007115		tumor necrosis	Xink, CUB, TM, SS	3.36
-	458897	U85642	Hs.138506	ESTS	TM	3.33
	413808	J00287	Hs.182183	caldesmon 1	esp,TM,SS	3.33
	411274	NM_002776		kellikrein 10	trypsin, TM,	3.32
					-16	

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	418406	X73501	Hs.84905	cytokeratin 20	filament, TM,	3.32
	419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4,zf-B_box,TM,	3.32
	423217 411558	NM_000094 AA102670	Hs.1640 Hs.70725	collagen, type gamma-aminobuty	fn3,Collagen,Kunitz_BPTLvwa,SS neur_chan,TM,SS	3.31 3.30
5	427722	AK000123	Hs.180479	hypothetical pr	PHSS	3.30
	422310	AA316622	Hs.98370	cytochrome PS40	p450,SS	3.30
	41 1263 443426	BE297802	Hs.69360	kinesin-like 6	kinesin,TM,	3.29
	452121	AF098158 NM_004081	Hs.9329 Hs.70936	chromosome 20 o deleted in azoo	TM TM	3.28 3.27
10	447342	Al199268	Hs.19322	ESTs	TM,SS	3.25
	452699	AW295390	Hs.213062	ESTs	TM	3.23
	425188	AK002052	Hs.155071	hypothetical pr	TM	3.23
	400289 408524	X07820 D87942	Hs.2258 Hs.46328	matrix metallop fucosyltransfer	hemopexin,SS Glyco_transf_11,TM,SS	3.21 3.20
15	437897	AA770561	Hs.146170	hypothetical pr	TM	3.20
	453922	AF053306	Hs.36708	budding uninhib	TM	3.19
	406690 416209	M29540 AA236776	Hs.220529 Hs.79078	carcinoembryoni	ig.TM,SS	3.19
	408113	T82427	Hs.194101	MAD2 (mitotic a Homo sapiens cD	HORMA,SS 7tm_3,TM,	3.16 3.14
20	425465	L18964	Hs.1904	protein kinase	Ski_Sno,OAG_PE-bind,OPR.pkise.pkise_C,TM,SS	3.13
	419216	AU076718	Hs.164021	small inducible	ILB,TM,SS	3.13
	418203 417315	X54942 A1080042	Hs.83758 Hs.180450	CDC28 protein k ribosomal prote	CKS,TM,	3.12
	433001	AF217513	Hs.279905	ciona HQ0310 PR	TMSS TMSS	3.11 3.11
25	459587	AA031956		gb:zk15e04.s1 S	LIMITM	3.11
	421379	Y15221	Hs.103982	small inducible	ILB,TM,SS	3.10
	414774 407289	X02419 AA135159	Hs.77274 Hs.203349	plasminogen act	kringle, trypsin, SS	3.10
	447519	U46258	Hs.23448	Homo sapiens cD ESTs	TM histone,Ribosomal_L22e,TM,	3.09 3.08
30	448045	AJ297436	Hs.20166	prostate stem c	TM,SS	3.07
	431956	AK002032	Hs.272245	Homo sapiens cD	RA,SS	3.06
	409632 454034	W74001 NM_000691	Hs.55279 Hs.575	serine (or cyst	serpin,TM,	3.05
	436481	AA379597	Hs.5199	aldehyde dehydr HSPC150 protein	aldedh,TM, UQ_con,TM,	3.05 3.05
35	428987	NM_004751	Hs.194710	glucosaminyl (N	Branch, TM,SS	3.04
	424252	AK000520	Hs.143811	hypothetical pr	casein_kappa,SS	3.04
	436291 411789	BE568452 AF245505	Hs.5101 Hs.72157	protein regulat	TM	3.03
	417956	AA210704	Hs.190465	Homo sapiens ad ESTs	ig,LRRCT,SS sushi,SS	3.02 3.02
40	408908	BE296227	Hs.48915	serine/threonin	pkise,TM,SS	3.01
	422330	D30783	Hs.115263	epiregulin	EGF,TM,SS	3.01
	425071 425761	NM_013989 AW664214	Hs.154424 Hs.196729	deiodinase, iod	T4_deiodise.TM,SS	3.00
	432978	AF126743	Hs.279884	ESTs DNAJ domain-con	SH3,TM, DJ,TM,	2.99 2.99
45	418546	AA224827		gb:nc32g04.s1 N	wwa.integrin_A,FG-GAP,TM,SS	2.99
	425371	D49441	Hs.155981	mesothelin	TM,SS	2.99
	422440 439453	NM_004812 BE264974	Hs.116724 Hs.6566	aldo-keto reduc	aldo_ket_red,TM,	2.98
	413278	BE563085	Hs.833	thyroid hormone interferon-stim	AAA,TM, ubiquitin,TM,	2.98 2.97
50	428450	NM_014791	Hs.184339	KIAA0175 gene p	pkise,KA1,TM,	2.95
	424345	AK001380	Hs.145479	Homo sapiens cD	TM,SS	2.95
	433133 432269	AB027249 NM_002447	Hs.104741 Hs.2942	PDZ-binding kin macrophage stim	pkise,TM,	2.94
	432917	NM_014125	Hs.279812	PRO0327 protein	pkise,Sema,Plexin_repeat,TIG,TM,SS TM	2.94 2.94
55	432731	R31178	Hs.287820	fibronectin 1	SS	2.93
	420552	AK000492	Hs.98806	hypothetical pr	SS	2.92
	428303 409687	AW974476 TS1125	Hs.183601 Hs.8493	regulator of G- ESTs	RGS,TM,	2.92
	457288	AA521458	Hs.192738	ESTs	EB,SAM_PNT,TM, TM	2.91 2.89
60	456181	L36463	Hs.1030	ras inhibitor	RA,VPS9,TM,SS	2.89
	450190	T51387		gb:yb20e08.r1 S	SH3,TM,	2.68
	430204 434808	AA618335 AF155108	Hs.146137 Hs.256150	ESTs, Weakly si	TM	2.88
	450983	AA305384	Hs.25740	ESTs, Highly și ERO1 (S. cerevi	TM SS	2.87 2.87
65	418670	AA601036	Hs.285083	ESTs	тм	2.87
	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain, f M,	2.87
	435099 402075	AC004770	Hs.4756	flap structure-	XPG_I,XPG_N,TM,	2.86
	410681	AW246890	Hs.65425	calbindin 1, (2	serpin,TM, efhand,FHA,BRCT,adh_short,adh_short_C2,TM,	2.84 2.83
70	439867	AA847510	Hs. 161292		TM	283
	443715	AI583187	Hs.9700	cyclin E1	cyclin,TM,SS	2.83
	417366	BE185289	Hs.1076	smail proline-r	Cornifin, TM,	2.83
	422283 404567	AW411307	Hs.114311	CDC45 (cell div	CDC45,TM,SS HECT.zf-UBR1,TM,	2.82
75	422158	L10343	Hs.112341	protease inhibi	wap,SS	2.82 2.82
	449224	AW995911	Hs.299883	hypothetical pr	fn3,TM,	2.81
	407584	W25945	Hs.18745	ESTs	PKSS	2.81
	453884 449032	AA355925 AA045573	Hs.36232 Hs.22900	KIAA0186 gene p nuclear factor	TM h710 Change shadow TM SE	2.81
80	422809	AK001379	Hs.121028	hypothetical pr	bZIP,Chromo_shadow,TM,SS IQ,TM,	2.80 2.79
	449722	BE280074	Hs.23960	cyclin B1	cyclin,TM,	2.79
	453028	AB006532	Hs.31442	RecQ protein-ti	DEAD.helicase_C,TM,	2.78
	421777	BE562088	Hs.108196	HSPC037 protein	TM	2.78



	452571	W31518	Hs.34665	ESTs	TM	2.77
	422675	BE018517	Hs.119140	eukaryotic tran	elf-5a.TM.	2.17
	400298	AA032279	Hs.61635	six transmembra	TM	2.76
5	414569 449378	AF 109298 AW 664026	Hs.118258	prostate cancer	ŢM	2.76
•	423903	M57765	Hs.59892 Hs.1721	ESTs interleukin 11	TM TM,SS	2.75
	431104	AW970859	Hs.269109	ESTs	Sema,TM,SS	2.75 2.75
	452940	AA029722	Hs.20279	ESTs	7tm_1,TM,SS	2.74
	432201	AI538613	Hs.135657	ESTs	trypsin,TM,	2.73
10	414617	AI339520	Hs.20524	ESTs, Moderatel	hexokise,TM,	2.73
	444301	AK000136	Hs.10760	hypothetical pr	LRR,TM,	2.72
	426711	AA383471	Hs.180669	conserved gene	TM '	2.71
	429432	AI678059	Hs.202676	synaptonemai co	TM	2.71
15	450506	NM_004460	Hs.418	fibroblast acti	Pepildase_S9,DPPIV_N_term,SS	2.71
15	427528	AU077143	Hs.179565	minichromosoma	MCM,TM,SS	2.71
	418801	AA228366	Hs.115122	ESTs	integrin_A,FG-GAP,TM,SS	2.71
	429486 408366	AF155827 AW511255	Hs.203963	hypothetical pr	SNF2_N,helicase_C,TM,	2.71
	406399	AW311233	Hs.258082	EST\$	SS hand The CC	2.70
20	446269	AW263155	Hs.14559	hypothatiant ne	kazal,TM,SS	2.69
	426514	BE616633	Hs.301122	hypothetical pr bone morphogene	TM TGE both TGEb, amounted the 66	2.68
	417079	U65590	Hs.81134	interleukin 1 r	TGF-beta,TGFb_propeptide,TM,SS IL1.SS	2.67
	444754	T83911	Hs.11881	transmembrane 4	TM,SS	2.67 2.67
	424687	J05070	Hs.151738	matrix metallop	fn2,hemopexin,Peptidase_M10,SS	2.66
25	439979	AW600291	Hs.6823	hypothetical pr	TM	2.65
	430832	AI073913	Hs.100686	ESTs, Weakly si	TM,SS	2.65
	429170	NM_001394	Hs.2359	dual specificit	DSPc,Rhodanese,TM,	2.64
	450400	AI694722	Hs.279744	ESTs	TM	2.64
30	435380	AA679001	Hs.192221	ESTs	Occludin, TM, SS	2.64
30	432375	8E536069	Hs.2962	S100 calclum-bi	S_100,efhand,TM,SS	2.63
	453700 422938	AB009426	Hs.560	apolipoprotein	dCMP_cyt_deam.sugar_tr,TM,SS	263
	453134	NM_001809 AA032211	Hs.1594 Hs.118493	centromere prot	histone,TM,	263
	420727	H75701	Hs.99886	ESTs	adh_short,TM,SS	2.63
35	408868	AW292286	Hs.255058	complement comp ESTs	sushi, TM	2.62
	414972	BE263782	Hs.77695	KIAA0008 gene p	TM	2.62
	403055	56240.02	113.77033	varantoso Berra b	filament,TM,SS	2.62 2.62
	447400	AK000322	Hs.18457	hypothetical pr	zl-C3HC4.TM.	2.61
4.0	413753	U17760	Hs.301103	Human DNA seque	laminin_EGF,laminin_Nterm,SS	261
40	433220	AI076192	Hs.131933	ESTs	TM	2.60
	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.60
	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.60
	425463	AK000740	Hs.157986	hypothetical pr	TM	2.60
45	435370	A1964074	Hs.225838	ESTs	EGF,fn3,fibrinogen_C,TM,SS	2.59
4)	432215	AU076609	Hs.2934	ribonucleatide	ribonucleo_red,ribonuc_red_lg,TM,	2.59
	409142 443919	AL136877	Hs.50758	chromosome-asso	SMC_N,TM,SS	2.59
	413268	AI091284 AL039079	Hs.135224		adh_short,TM,SS	2.58
	404519	ME000019	Hs.75256	regulator of G-	RGS,TM,	2.58
50	414998	NM_002543	Hs.77729	oxidised low de	defensins,SS TM	2.58
	429597	NM_003816	Hs.2442	a disintegrin a	TM,SS	2.57 2.57
	426841	AI052358	Hs.193726	ESTs	asp,TM,SS	2.57
	416768	AA363733	Hs.1032	regenerating is	lectin_c,SS	2.57
	417933	X02308	Hs.82962	thymidylate syn	thymidylat_synt.SS	2.56
55	441384	AA447849	Hs.288660	protease, serin	TM	2.56
	451939	U80456	Hs.27311	single-minded (	PAC,PAS,BPL,BPL_C,TM,	2.56
	418867	D31771	Hs.89404	msh (Drosophila	homeobox,TM,	2.55
	416065	BE267931	Hs.78996	proliferating c	TM	2.55
60	431890	X17033	Hs.271986	integrin, alpha	www.integrin_A.F.G.GAP,TM,SS	2.55
UU	407830 434815	NM_001086 AF155582	Hs.587	arytacetamide d	COesterase,7tm_1,TM,SS	2.55
	435647		Hs.46744	core1 UDP-galac	SS	2.54
	459306	AI653240 AW578452	Hs.49823 Hs.232988	ESTS	TM	2.54
	414361	AI086138	Hs.204044	ESTs, Weakly si ESTs	TM,SS TM	2.54
65	425782	U66468	Hs.159525	cell growth reg	SS	2.54
	416984	H38765	Hs.80706	diaphorase (NAD	TM	2.53 2.53
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-G	ER_lumen_recept,IRK,DEAD,helicase_C,TM,SS	2.53 2.53
	456743	AI630124	Hs.7434	ESTs	TM	2.53
=0	410268	AA316181	Hs.61635	six transmembra	TM	2.52
70	424905	NM_002497	Hs.153704	NIMA (never in	pkise,TM,	2.52
	432657	AA831815	Hs.270940	ESTs	TM	2.51
	434080	AJ820719	Hs. 154662	hypothetical pr	DJ_CXXCXGXG,TM,SS	2.51
	418969	W33191	Hs.28907	hypothetical pr	SH3.TM,	2.51
75	431808	M30703	Hs.270833		EGF,TM,SS	2.51
13	429093	NM_000253		microsomal trig	Vitellogenin_N,TM,S\$	2.50
	447634	AW967902	Hs.5152	Homo sapiens cD	TM	2.50
	436393 453751	AW022213	Hs.143617	ESTs	Galactosyl_T_2,TM,SS	2.50
	445865	R36762 AI262584	Hs.101282		TM ee	2.49
80	414883	AA926960	Hs.145575 Hs.77550	ESTs CDC28 protein k	SS CKS TM	2.49
- •	406747	AI925153	Hs.217493		CKS,TM, TM	2.49
	446921	AB012113	Hs.16530	small inducible	ILB.SS	2.49
	426322	J05068	Hs.2012	transcobalamin	Cobalamin_bind,TM,SS	2.49 2.48
						4.40

	422515	AW500470	Hs.117950	multifunctional	AIRC.SAICAR_synt,TM,	2.48
	447030 448454	AW444659 NM_005879	Hs.232184	ESTs	TM	2.48
	419092	J05581	Hs.21254 Hs.89603	TRAF interactin mucin 1, transm	zi-C3HCA,TM,	2.48
5	409640	U78722	Hs.55481	zinc finger pro	SEA,TM,SS zi-c2H2,SCAN,TM,	2.48 2.48
	404171			ga- p-0	sodie,TM,	247
	414747	U30872	Hs.77204	centromere prot	SS	247
	410406	AI969703	Hs.301842	ESTs	FGGY.TM,	2.47
10	452220 421493	BE158006 BE300341	Hs.212296 Hs.104925	ESTS	FG-GAP,TM,SS	2.46
10	444838	AV651680	Hs.208558	ectodermat-neur ESTs	BTB,Ketch,TM, integrin_A,FG-GAP,TM,SS	246
	413816	AW958181	Hs.189998	ESTs	AMP-binding.G_glu_transpept,TM,	2.46 2.46
	436613	AA972691	Hs. 192974	Homo sapiens cD	TM,SS	245
15	432874	W94322	Hs.279651	melanoma Inhibi	SH3,SS	2.45
1.5	425397 422353	J04088 T55979	Hs.156346 Hs.115474	topolsomerase (	HATPase_c,SS	2.45
	431924	AK000850	Hs.272203	replication fac Homo sapiens cD	TM SH3.TM.	2.45
	431457	NM_012211	Hs.256297	integrin, atpha	FG-GAP,vwa,TM,SS	2.44 2.44
20	416498	U33632	Hs.79351	potassium chann	TM	244
20	428484	AF104032	Hs.184601	solute carrier	aa_permeases,TM,	2.43
	431958 413833	X63629 Z15005	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM,SS	2.43
	407243	AA058357	Hs.75573 Hs.74466	centromere prot cercinoembryoni	kinesin,TM, TM,SS	243
	410044	BE566742	Hs.58169	highly expresse	TMSS	2.43 2.43
25	424273	W40460	Hs.144442	phospholipase A	phosfip,TM,SS	2.42
	409533	AW969543	Hs.21291	mitogen-activat	TM,SS	2.42
	419741 449987	NM_007019	Hs.93002	ubiquitin carri	UQ_con,efhand,TM,SS	2.42
	433159	AW079749 A8035898	Hs.184719 Hs.150587	ESTs, Weakly si kinesin-like pr	ABC_tran_ABC_membrane,TM,	2.42
30	439396	8E562958	Hs.74346	ESTs, Wealdy si	kinesin,Myosin_tail,TM,SS SS	2.42 2.42
	426427	M86699	Hs.169840	TTK protein kin	pkise,TM,	2.42
	434725	AK000796	Hs.4104	hypothetical pr	TM	2.41
	433312	AI241331	Hs.131765	ESTs	z1-C2H2,SS	241
35	407047 419220	X65965 AA811938	Hs.291759	gb:H.sapiens \$0	sodfe,TM,	2.41
-	416530	U62801	Hs.79361	ESTs kallikrein 6 (n	TM,SS trypsin,pro_isomerase,TM,SS	2.40 2.40
	435219	AA676349	Hs. 190331	ESTs	TM	2.40
	418322	AA284166	Hs.84113	cyclin-dependen	SS	2.40
40	404253	0500000			histone,TM,SS	2.40
70	428970 418693	BE276891 Al750878	Hs.194691 Hs.87409	retinoic acid i	7tm_3,TM,	2.40
	451237	AW600293	NS.07409	thrombospondin gb:EST00049 pGE	EGF.TSPN.tsp_1.tsp_3,vwc,SS TM	2.39
	407756	AA116021	Hs.38260	ubiquitin speci	UCH-1,UCH-2,SS	2.39 2.39
45	437935	AW939591	Hs.5940 .	hypothetical pr	TMSS	2.39
45	445625	BE246743	Hs.288529	Homo sapiens cD	TM	2.39
	435937 438993	AA830893 AA828995	Hs.119769	ESTs	TM	2.39
	422082	AA016188	Hs.111244	gb:od77b08.s1 N hypothetical pr	integrin_8,TM,SS TM	2.38
	450396	AU077002	Hs.24950	regulator of G-	RGS,TM.	2.38 2.38
50	422578	AF239666	Hs.1545	caudal type hom	homeobox,SS	2.38
	428070	T63918	Hs.182313	retinal-binding	lipocalin,TM,	2.38
	416111 433345	AA033813 AI681545	Hs.79018 Hs.152982	chromatin assem	TM,SS	2.37
	427557	NM_002659	Hs.179657	Homo sapiens cD plasminogen act	TM UPAR_LY6,SS	2.37
55	423554	M90516	Hs.1674	glutamine-fruct	GATase_2,SIS,TM,SS	2.37 2.37
	453204	R10799	Hs.191990	ESTs	TM	2.37
	425081	X74794	Hs.154443	minichromosome	MCM,TM,	2.36
	434682 414108	AA827165 AI267592	Hs.191958 Hs.75761	ESTs	TM	2.36
60	417900	BE250127	Hs.82906	SFRS protein ki CDC20 (cell div	pkise,TM, WD40,TM,	2.36
	428046	AW812795	Hs.155381	ESTs, Moderatel	ank,SS	2.36 2.36
	448019	AW947164	Hs.195641	ESTs	TM	2.36
	431753	X76029	Hs.2841	neuromedin U	NMU,TM,SS	2.36
65	410361 418526	BE391804 BE019020	Hs.62661 Hs.85838	guanylate bindi	GBP,TM,SS	2.36
	444478	W07318	Hs.240	solute carrier M-phase phospho	MCT,TM,SS	2.36
	436961	AW375974	Hs.156704	ESTs	rinesin,55 TM	2.35 2.35
	408194	AA601038	Hs.191797	ESTs .	TM	2.35
70	438578	AA811244	Hs.164168		formyl_transf,AIRS,GARS,TM,	2.35
70	429183 453900	AB014604 AW003582	Hs.197955		TM	2.35
	432877	AW974111	Hs.226414 Hs.292477		TM EIs,SAM_PNT,TM,	2.33
	451928	AI823801	Hs.30315	ESTS	EB,SAM_PNI,IM, TM	2.33 2.33
75	418245	AA088767	Hs.83883	transmembrane,	kg_recept_e,TM,SS	2.33
75	435106	AA100847	Hs.193380	ESTs, Highly si	TM	2.33
	432193 449532	AA372264	Hs.273193		TM,SS	2.33
	409703	W74653 NM_006187	Hs.271593 Hs.56009	ESTs 2-5oligoadeny	TM NTD boost 2 TM CC	2.33
	419373	NM_003244		TG-interacting	NTP_transf_2,TM,SS homeobox,SS	2.33 2.32
80	435607	W73428	Hs.8750	uncharacterized	SS S	2.32
	405818	DEC 1000 ·			TM,SS	2.32
	444371 432675	BE540274	Hs.239	forkhead box M1	Fork_head,SS	2.32
	-32013	A1791855	Hs.105884	ESTs	PDEase,TM,	2.32

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	411773	NM_006799	Hs.72026	protease, serin	trypsin, SS	2.31
	434775	AA648983	Hs.212911	EST\$	TM,SS	2.31
	422611	AA158177	Hs.118722	fucesyltransfer	SS	231
•	419493	AF001212	Hs,90744	proteasome (pro	SS	2.31
5	424435	AB011167	Hs.146957	KIAA0595 protei	TM	2.30
	409262	AK000631	Hs.52256	hypothetical pr	WD40,TM,SS	2.30
	428125	AA393071	Hs.182579	leucine aminope	Peptidase_M17,TM,SS	2.30
	417655	AA780791	Hs.14014	ESTs, Wealdy si	TM	2.29
10	407287	AI678812	Hs.201658	ESTs. Wealdy si	ras,TM,SS	2.29
10	428923	BE047698	Hs.188785	ESTS	TM,SS	2.29
	452203	X57522	Hs.158164	ATP-binding cas	ABC_tran,ABC_membrane,TM,	2.29
	409402		· Hs.695	cystatin 8 (ste	cystatin,SS	2.29
	419359	AL043202	Hs.90073	chromosome segr	TMLSS	2.29
1.5	4519 <del>99</del>	AW176401	Hs.27424	DÉAD/H (Asp-Glu	TM,SS	2.29
15	400811	AF219139	Hs.87726	KIAA0154 protei	Cobalamin_bind,SS	2.29
	420931	AF044197	Hs.100431	smali inducible	ilb,tm,ss	2.28
	425247	NM_005940	Hs.155324	matrix metallop	hemopexin,Peptidase_M10,TM,SS	2.28
	438170	AI916685	Hs.194601	ESTs .	2-Hacid_DH,TM,	2.28
20	445378	AV653564	Hs.226946	ESTs	TM	2.28
20	428048	AA705745	Hs.185070	ESTs .	AMP-binding,TM,	2.28
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS	2.27
	433535	AF111106	Hs.3382	protein phospha	TM	2.27
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,SS	2.27
25	405545				ABC_tran,ABC_membrane,TM,SS	2.27
23	445537	AJ245671	Hs.12844	EGF-lilke-domain	EGF,SS	2.27
	423634	AW959908	Hs.1690	heparin-binding	TM,SS	2.26
	407742	AF185252	Hs.38084	sulfotransferas	Suttotranster, SS	2.26
	428330	L22524	Hs.2256	matrix metallop	Peptidase_M10,SS	2.26
30	429731	AK001592	Hs.212172	beta,beta-carot	TM	2.26
30	400514				p450,TM,SS	2.26
	431846	BE019924	Hs.271580	uroplakin 18	transmembrane4,TM,SS	2.26
	425010	AA136563	Hs.1975	Homo sapiens cD	TM	2.26
	437641	AA811452	Hs.291911	ESTs	TM	2.26
35	411393	AW797437	Hs.69771	8-factor, prope	sushi,trypsin,vwa,DEAD,rrm,EGF,fn3,fibrinogen_C,SS	2.26
22	414809	AI434599	Hs.77356	transferrin rec	PA,Ribosomat_S2,TM,	2.25
	419488	AA316241	Hs.90691	nucleophosmin/n	SS	2.25
	434540	NM_016045	Hs.5184	TH1 drosophila	TM	2.25
	410196	AJ936442	Hs.59838	hypothetical pr	UBACT_repeat.TM,	2.25
40	456844	AI264155	Hs.152981	CDP-diacylglyce	Cytidylyltrans,TM,	2.25
40	408353	BE439838	Hs.44298	hypothetical pr	Ribosomal_S17,TM,	2.25
	448753	AL048858	Hs.224355	ESTs, Weakly si	TM	2.25
	428479	Y00272	Hs. 184572	cell division c	pkise,TM,SS	2.24
	424971	AA479005	Hs.154036	tumor suppressi	ion_trans,PH,TM,	2.24
45	432673	AB028859	Hs.278605	ER-associated D	DJ,DJ_C,TM,SS	2.24
43	409432	D49372	Hs.54460	small inducible	IL8,TM,SS	2.24
	429925	NM_000786	Hs.226213	cytochrome P450	p450,TM,SS	2.24
	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099,TM,SS	2.23
	447532	AK000614	Hs.18791	hypothetical pr	TM	2.23
50	423515	AA327017	Hs.162204		SS	2.23
50	444743	AA045648	Hs.11817	nudix (nucleosi	mut,TM,	2.23
	434518	H56995	Hs.37372	Homo sapiens DN	TM	2.23
	435602	AF217515	Hs.283532		TM,SS	2.23
	449974	AW970948	Hs.269403		TM.SS	2.23
55	424927 414420	AW973666	Hs.153850		TM .	2.23
33	431840	AA043424 AA534908	Hs.76095	immediate early	TM	2.23
	452930	AW195285	Hs.2860	POU domain, cla	homeobox,pou,TM,SS	2.23
	436391	AJ227892	Hs.194097		SS	2.23
	439186	AJ697274	Hs.146274 Hs.6487		SS COLUMN	2.23
60	414732	AW410976	Hs.77152	Xq28, 2000op se	Epimerase, SS	2.23
00	411835	U29343	Hs.72550	minichromosome	MCM,TM,	2.22
	438223	AA781171	rg./2330	hyaturonan-medi	TM	2.22
	450149	AW969781	Hs.293440	gb:aj24d05.s1 S	myosin_head,TM,	2.22
	401519	MAASOSIEI	N3.233440	ESTs, Moderatel	TM	2.22
65	441794	AW197794	Hs.253338	CCT-	filament, TM,	2.22
05	408901	AK001330	Hs.48855		ank,TM,	2.22
	434423	NM_006769		hypothetical pr LIM domain only	TM	2.21
	432140	AK000404	Hs.272688		LIM, TM,	2.21
	423453	AW450737	Hs.128791		SS Carrie COO OU D 447M	2.21
70	428438	NM_001955		endothelin 1	Granin,CDP-OH_P_transf,TM,	2.21
. •	421470	R27496	Hs.1378	annexin A3	endothelin, TM, SS	2.21
	440381	AA917808	Hs.190495		annexin,TM,SS	2.21
	453779	N35187	Hs.43388	ESTS	TM,SS TM,SS	2.20
	433627	AF078866	Hs.284296			2.20
75	417944	AU077196	Hs.82985		SURF4,TM,	2.20
, ,	422689	AW856665	110.02303	coflagen, type gb:RC3-CT0297-2	COLFI, Collagen, vwc, TM, SS	2.20
	448457	H65629	Hs.245997		SNF2_N,TM,	2.20
	426125	X87241	Hs.166994		TMSS ECE codhada Israinia, C TAA CC	2.20
	430603	AA148164	Hs.247280	HBV associated	EGF,cadherin,taminin_G,TM,SS	2.20
80	425274	8E281191	Hs.155462		zi-C3HC4,TM,	2.20
	452679	Z42387	Hs.4299	Homo sapiens cD	MCM,TM, TM	2.20
	410619	BE512730	Hs.65114	keratin 18	filament,TM,	2.20
	424332	AA338919	Hs.101615		SS	2.20 2.20
					~~	LA

	418661	NM_001949	Hs.1189	Human mRNA for	E2F_TOP,TM,S\$	2.20
	419341	N71463	Hs.118888	ESTs, Weakly si	UPF0016,TM,SS	2.20
	427920 403208	Z11502	Hs.181107	annexin A13	annexin, TM,	2.19
5	422596	AF063611	Hs.118633	2-Soligoadeny	lectin_c,TM,SS	2.19
•	444251	AA298958	Hs.10724	MOSO23 protein	ubiquitin,SS TM	2.19 2.19
	423401	NM_001992	Hs.128087	coagulation (ac	7tm_1,TM,SS	2.18
	453450	AW797627	Hs.89474	ADP-ribosytatio	SS	2.18
• •	444334	BE296785	Hs.10848	KIAA0187 gene p	SS	218
10	437616	AI797163	Hs.207954	ESTs	SMC_N,TM,SS	2.18
	451807	W52854	Hs.27099	DKFZP564J0863 p	TM	2.18
	430441	BE398091	Hs.6880	DKFZP434D156 pr	TM	2.18
	411678	AI907114	Hs.71465	squalene epoxid	Monogxygese,TM,	2.18
15	452291	AF015592	Hs.28853	CDC7 (cell divi	pkise,TM,	2.18
13	444342	NM_014398	Hs.10887	similar to tyso	Lamp,TM,SS	2.18
	451099 425873	R52795 NM_013390	Hs.25954 Hs.160417	Interleukin 13	tn3,TM,SS TM	2.18
	417404	NM_007350	Hs.82101	transmembrane p pleckstrin homo	TM	2.17 2.17
	446995	AI355012	13.02101	gb:qu16d10.x1 N	TM	217
20	439961	AA857451	Hs.269696	ESTs	TM	217
	429125	AA446854	Hs.271004	ESTs	TM	217
	407103	AA424881	Hs.256301	ESTs	TM	2.17
	415116	AA160363	Hs.269956	ESTs	ER_lumen_recept,TM,SS	2.17
25	440052	AI633744	Hs.195648	ESTs	PAC,TM,SS	2.17
23	423961	D13666	Hs.136348	osteoblast spec	Fascidin,TM,SS	2.17
	431070 443599	AW408164	Hs.249184	transcription f	FHASS	2.16
	427258	AI079559 AA400091	Hs.134125 Hs.39421	ESTs ESTs	TM The	2.16
	418113	AJ272141	Hs.83484	SRY (sex determ	TM HMG_box,TM,	216
30	450835	BE262773	Hs.25584	hypothetical or	ArfGap,SS	2.16 2.18
	449057	AB037784	Hs.22941	KIAA1363 protei	TM	2.16
	448153	Y10805	Hs.20521	HMT1 (hnRNP met	TMSS	2.16
	424653	AW977534	Hs.151469	calcium/calmodu	Guanylate_kin,PDZ.pkise,SH3,TM,	2.16
25	431341	AA307211	Hs.251531	proteasome (pro	proteasome,TM,	216
35	452865	A1924046	Hs.119567	ESTs	PMP22_Claudin,TM,SS	2.16
	432789	D26361	Hs.3104	KIAA0042 gene p	TM	2.16
	438580 422192	AA811262 AA305159	Hs.299202	ESTs	pkise,TM,	216
	425607	U09860	Hs.113019 Hs.158333	fis485	SS	2.15
40	447289	AW247017	Hs.36978	protease, serin metanoma antige	ldl_recept_a,trypsin,CUB,SRCR,MAM,SEA,TM,SS 3Beta_HSD,Epimerase,MAGE,TM,	2.15 2.15
. •	447674	BE270640	Hs.19192	cyclin-dependen	pkise,TM,	2.15
	441021	AW578716	Hs.7644	H1 histone fami	linker_histone,TM,	2.15
	426471	M22440	Hs.170009	transforming gr	EGF.TM,SS	2.15
45	431941	AK000106	Hs.272227	Homo sapiens cD	pkise,Furin-like,TM,SS	2.15
45	414761	AU077228	Hs.77256	enhancer of zes	SET,TM,	2.15
	410407	X66839	Hs.63287	carbonic anhydr	carb_anhydrase,TM,SS	2.15
	420900 419239	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C.FAD_binding_5,TM,	2.15
	452721	AA468183 AJ269529	Hs.184598 Hs.30377	Homo sapiens cD	TM	215
50	410664	NM_006033	Hs.65370	Horno sapiens ES lipase, endothe	TM Ribosomal_L22,lipase,PLAT,TM,SS	2.15 2.14
	452835	AK001269	Hs.30738	hypothetical pr	TM	2.14
	452092	BE245374	Hs.27842	hypothetical pr	Acyltransferase, TM, SS	2.14
	401708				SS	214
<i>E E</i>	411400	AA311919	Hs.69851	GAR1 protein	TM	2.14
55	448526	AB028946	Hs.21361	KIAA 1023 protei	TM	2.14
	421175	A1879099	Hs.102397	GIOT-3 for gona	z1-C2H2,KRAB,TM,SS	214
	413511	AI627178	Hs.75412	Arginine-rich p	TM	2.13
•	432945 418592	AL043683 X99226	Hs.271357 Hs.284153	ESTs, Wealdy si	PKSS	2.13
60	425298	AK000209	Hs.155556	Fanconi anemia, hypothetical pr	TM TM	2.13
•	450956	AW193531	Hs.205647	ESTs, Moderated	pkise,TM,SS	2.13 2.13
	419569	AI971651	Hs.91143	jagged 1 (Alagi	EGF,DSL,TM,SS	2.13
	421508	NM_004833	Hs.105115	absent in melan	TM	2.13
	413670	AB000115	Hs.75470	hypothetical pr	TM	213
65	422783	AA598956	Hs.120439	ethanolamine ki	Choline_kise,TM,	2.13
	410418	D31382	Hs.63325	transmembrane p	trypsin.ld1_recept_a.TM.SS	2.13
	414860	BE255593	Hs.77502	methionine aden	S-AdoMet_synt,SS	2.13
	425860 414839	L29339 X63692	Hs.1964	solute carrier	SSF,Ribosomal_S17e,TM,	2.13
70	437050	AA766420	Hs.77462 Hs.291606	DNA (cytosine-5	zi-CXXC.BAH.TM.SS	2.13
. •	430217	N47863	Hs.180450	ESTs ribosomal prote	TM TM,SS	2.13
	409012	AL117435	Hs.49725	DKFZP434I216 pr	PhoGEF,TM,	2.13
	428365	AA295331	Hs.183861		TM	2.12 2.12
~-	410839	NM_006849		protein disulfi	thiored, TM,	2.12
75	450510	AA010056	Hs.242998	EST ₅	TM,SS	2.12
	427475	AA403151	Hs.191605	EST8	SS	2.12
	433748	R12244		gb:yf33c12.r1 S	AMP-binding, TM,	2.12
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma,TM,SS	2.11
80	414788 415474	X78342 NM_014252	Hs.77313	cyclin-dependen	pkise,TM,SS	2.11
	416472	AA180756	Hs.78457 Hs.193094	solute carrier ESTs, Moderatel	mito_carr,TM,	2.11
	410718	AI920783	Hs.191435		TM SOS PSY THES	211
	425811	AL039104	Hs.159557		SQS_PSY,TM,SS Armadiilo_seq.iBB,TM,SS	2.11 2.11
					CE'lm + 'Achiffor and a	

	447197	R36075		gb:yh88b01.s1 S	SDF.TM.	2.11
	431621	AW292329	Hs.163481	ESTs	PH,Band_41,TM,SS	2.11
	433849 438038	BE465884 AI732629	Hs.280728 Hs.194161	ESTs ESTs, Weakly si	SS	2.11
5	422032	AA476966	Hs.110857	polymerase (RNA	Cytidyhytrans,TM, TFIIS,TM,SS	2.11 2.11
_	409717	AW452871	Hs.56043	CGI-115 protein	TM	211
	445837	AI261700	Hs.145544	EST8	TM	2.11
	423880 421574	BE278111 AJ000152	Hs.134200	DKFZP564C186 pr	TM	2.10
10	437103	AW139408	Hs.105924 Hs.152940	defensin, beta ESTs	Detensin_beta,TM,SS Choline_kise,TM,	2.10 2.10
	450747	AI064821	Hs.48306	ESTs, Highly si	rm,TM,	2.10
	437033	AW248364	Hs.5409	RNA polymerase	TM	2.10
	417640 431120	D30857 AA492588	Hs.82353	protein C recep gb:ng99c08.s1 N	TM,SS TM,SS	2.10
15	430510	AW162916	Hs.241576	hypothetical pr	TM	2.10 2.10
	429669	BE185499	Hs.2471	KIAA0020 gene p	TM	2.10
	407881	AW072003	Hs.40968	heparan sulfate	SS	2.10
	436415 407887	BE265254 AA579668	Hs.5181 Hs.41072	proliferation-a serine (or cyst	Peptidase_M24,TM,SS serpin,TM.	2.10 2.10
20	447815	Al432199	Hs.247084	ESTs	LIM,TM,	2.09
	434274	AA628539	Hs.116252	ESTs, Moderatel	mm,TM,SS	2.09
	411571	AA122393	Hs.70811	hypothetical pr	SS	2.09
	442525 423750	AF150282 AF165883	Hs.145945 Hs.132415	ESTs prefoldin 2	pkise,TM, TM	2.09 2.09
25	449199	AI990122	Hs.196988	ESTS	ras,TM,	2.09
	415363	AI670947	Hs.78406	phosphatidylino	PtP5K,pkise,TM,SS	2.09
	418462 430335	8E001596 D80007	Hs.85266	integrin, beta	integrin_8,fn3,TM,SS	2.09
	443450	N56045	Hs.239499 Hs.133529	KIAA0185 protei ESTs	S1,TM. TM	2.08 2.08
30	418753	BE217818	Hs.87016	Homo sapiens cD	TM	2.08
	439018	AW300887	Hs.26638	ESTs, Wealdy si	TM,SS	2.08
	431628 446528	AF148277	Hs.265561	CD2-associated	SH3.SS	2.08
	411372	AU076640 Ai147861	Hs.15243 Hs.213289	nucleotar prote low density lip	Nol1_Nop2_Sun,TM, EGF,Id1_recept_a,Id1_recept_b,TM,SS	2.08 2.08
35	459319	NM_000059		gb:Homo sapiens	BRCA2_repeat_TM,	2.08
	408730	AV660717	Hs.47144	DKFZP586N0819 p	TM,SS	2.08
	409220 429504	BE243323 X99133	Hs.51233 Hs.204238	furnor necrosis	TNFR_c6,death,TM,	2.08
	409686	AK000002	Hs.55879	fipocalin 2 (on Homo sapiens mR	fipocatin,SS ABC_tran,ABC_membrane,TM,	2.08 2.08
40	413092	AA126856	Hs.118665	ESTs	EGF,TM,SS	2.08
	413715	AW851121	Hs.75497	Homo sapiens cD	cyclin,TM,	2.08
	423020 438378	AA383092 AW970529	Hs.1608 Hs.86434	replication pro Homo sapiens cD	TM TM,SS	2.07
	432125	AW972667	Hs.287510	Homo sapiens cO	Band_41,TM,SS	2.07 2.07
45	449370	AK002114	Hs.23495	hypothetical pr	TM,SS	2.07
	454011 427876	M31008	Hs.37009	alkaline phosph	alk_phosphatase,TM,SS	2.07
	422901	AI494291 R81936	Hs.111977 Hs.121576	ESTs aspartate beta-	TM SS	207 207
	449207	AL044222	Hs.23255	nucleoporin 155	TM,SS	2.07
50	408243	Y00787	Hs.624	interleukin 8	IL8,TM,SS	2.07
	446548 423472	BE 167687 AF041260	Hs.156628 Hs.129057		Sulfotransfer,TM,SS TM	2.07
	436211	AK001581	Hs.80961	polymerase (DNA	TM	2.07 2.07
	456157	AW979153		gb:EST391263 MA	transmembrane4,TM,	2.06
55	407143	C14076	Hs.248968		TM	2.06
	432440 410668	X63597 BE379794	Hs.2996 Hs.65403	sucrase-isomati hypothetical pr	Glyco_hydro_31,trefoil,TM,SS TM	2.06 2.06
	422765	AW409701	Hs.1578	bacutoviral IAP	BIRTM	2.06
60	439832	T81829	Hs.14870	ESTs	SS	2.06
60	445318 439951	AW500652	Hs.200885		TM	2.06
	428307	AJ347067 W27393	Hs.124636 Hs.183648		TM,SS TM	2.06 2.06
	432584	AA928829	Hs.47099	Homo sapiens cD	SS	2.06
65	433027	AF191018	Hs.279923		MMR_HSR1,TM,	2.06
05	433716 429412	AA608808 NM_006235	Hs.225118 Hs.2407	ESTs POU domain, da	TM TM	2.06
	449026	BE500946	Hs.209105		TM	2.06 2.06
	437016	AU076916	Hs.5398	guanine monphos	GATase,GMP_synt_C,TM,	2.06
70	442547	AA306997	Hs.268362		SS	2.06
70	455778 439975	BE088746 AW328081	Hs.6817	gb:CM2-8T0693-2 Homo sapiens pu	TM TM,SS	2.06
	433037	NM_014158			TM,33	2.06 2.08
	440086	NM_005402	Hs.288757	v-ral simian te	ras,TM,	2.06
75	436414 411770	BE264633	Hs.143838		WD40,TM,	2.05
,,	409459	NM_014278 D86407	Hs.71992 Hs.54481	heat shock prot low density lip	HSP70,TM, EGF,kdl_recept_a,kdl_recept_b,TM,SS	2.05 2.05
	436238	AK002163	Hs.301724		MMR_HSR1,TM	2.05
	400517	AF242388	Hs.149585	tengsin	TM	2.05
80	421904 417850	BE143533 AA215724	Hs.109309		SS SS	2.05
-	417491	AW376842	Hs.82741 Hs.1085	primase, polype guanylate cycla	pkise.guanytete_cyc,ANF_receptor.TM,SS	2.05 2.05
	453775	NM_002916	Hs.35120	replication fac	AAA.TM,SS	2.05
	435525	AI831297	Hs.123310	) ESTs	TM	2.05

	412627	BE391959	Hs.74276	chloride intrac	G-patch.ig.MutS_C,TM,	2.05
	439702 440006	AW085525 AK000517	Hs.134182 Hs.6844	ESTs	A2M,SS	2.05
	417308	H60720	Hs.81892	hypothetical pr KIAA0101 gene p	TM TM	2.05
5	446311	AW007294	Hs.149795	ESTs, Wealthy si	pkise,TM,	2.05 2.05
	427871	AW992405	Hs.59622	ESTs, Weakly si	SS	2.05
	453804	AA300204	Hs.35276	KIAA0852 protei	TM.SS	2.05
	449939	T86420	Hs.272139	ESTs	Ott.,myosin_head,TM,SS	2.05
10	417819	AI253112	Hs.133540	ESTs	TM	2.04
10	427747	AW411425	Hs.180655	serine/threonin	pkise,TM,	2.04
	415009 437829	C75253 AI358522	Hs.220950 Hs.270188	ESTs	TM	204
	428753	AW939252	Hs.192927	ESTs hypothetical pr	TM TM	2.04
	446475	AI908188	Hs.209245	ESTs	OPR,TM,	2.04 2.04
15	431394	AK000692	Hs.252351	HERV-H LTR-asso	ig,TM,SS	2.04
	423701	AA329856	Hs.143022	ESTs	TM	2.04
	422369	AF005216	Hs.115541	Janus kinase 2	SH2,pkise,TM,	2.04
	432481	AW451645	Hs.151504	Homo sapiens cD	TSPN,Collagen,TM,SS	2.04
20	443746	AW861379	Hs.160602	ESTs .	TM	2.04
20	400792 428343	AA635062 AL043021	Hs.50094 Hs.12705	Homo saplens mR	z-C3HC4,CARD,BIR,TM,	2.04
	419329	AY007220	Hs.288998	ESTs, Wealdy si S100-type calci	TM TM	2.04
	403485	***************************************	14.200330	O TOO Type Casts	filament,TM,	2.04 2.04
25	413313	NM_002047	Hs.75280	glycyl-tRNA syn	WHEP-TRS,7tm_2,TM,SS	2.04
25	433326	AJ379486	Hs.159430	ESTs	TM	2.03
	440246	W52010	Hs.191379	ESTs	serpin,TM,	2.03
	444006	BE395085	Hs.10086	type I transmem	TM,SS	2.03
	452705 421724	H49805 AB037832	Hs.246005	EST\$	TM	2.03
30	447474	AW614220	Hs.107287 Hs.189402	KIAA1411 protei ESTs	TM SS	2.03
-	418852	BE537037	Hs.273294	hypothetical pr	TM	2.03
	431842	NM_005764		epithelial prot	TM.SS	2.03 2.03
	440773	AA352702	Hs.37747	hypothetical pr	TM	2.03
25	443425	AI056776	Hs.133397	ESTs	TM,SS	2.03
35	407975	X89426	Hs.41716	endothelial cet	IGFBP.SS	2.03
	428299 415757	AL038004 AA830854	Hs.29419	ESTs	TM,SS	2.03
	432559	AW452948	Hs.187810 Hs.257631	ESTs ESTs	TM	2.03
	425912	AL137629	Hs.162189	serine/threonin	PAC,TM,SS fn3,ig,PH,RhoGEF,TM,SS	2.03
40	419395	BE268326	Hs.90280	5-aminoimidazol	AICARFT_IMPCHas,MGS,TM,	2.02 2.02
	417576	AA339449	Hs.82285	phosphoribosytg	AIRS,formyl_transi,GARS,TM,	2.02
	418559	AA225048	Hs.104207	ESTs	TM	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevi	SNF2_N,helicase_C,TM,	2.02
45	422072	AB018255	Hs.111138	KIAA0712 gene p	TM	2.02
45	419546 450516	AA244199	11- 21012	gb:nc06c05.s1 N	Y_phosphatase,TM,	2.02
	419807	AA902656 R77402	Hs.21943	NIF3 (Ngg1 into	DUF34,TM,	2.02
	438192	AI859065	Hs.16808	gb:yi75f11.s1 S ESTs, Wealdy si	TM TM,SS	2.02
	401866		14.1000	CO13, 11030y 31	filament,TM,SS	2.02 2.02
50	443129	R16075	Hs.21668	ESTs	TM,SS	2.02
	424783	AA913909	Hs.153088	TATA box bindin	TM	2.01
	413293	AL047483	Hs.75270	GTP-binding pro	ras,TM,SS	2.01
	435787 422599	AW162767	Hs. 100914	hypothetical pr	SS	2.01
55	431630	BE387202 NM_002204	Hs.118638 Hs.265829	non-metastatic integrin, aipha	NDK,SS	2.01
	448275	BE514434	Hs.20830	synaptic Ras GT	FG-GAP,integrin_A,TM,SS kinesin,PHD,abhydrolase_2,TM,SS	2.01
	405484			o)opoo 1 aas Q 1	filament,SS	2.01 2.01
	436469	AK001455	Hs.5198	Down syndrome c	TM	2.01
60	451273	NM_014811		KIAA0649 gene p	TM	2.01
60	432378	A1493046	Hs.146133	ESTs	TM	2.01
	419981 445808	AA897581 AV655234	Hs.128773 Hs.298083	ESTs ESTs	Ski_Sno.SS	201
	435767	H73505	Hs.117874	ESTs	sushLTMSS	2.01
	430466	AF052573	Hs.241517	polymerase (DNA	Peptidase_S8,P,TM, TM	2.01
65	422790	AA809875	Hs.25933	ESTS	TM	2.01 2.01
	443303	U67319	Hs.9216	caspase 7, apop	ICE_p10.ICE_p20,TM,	2.01
	410008	AA079552		gb:zm20h12.s1 S	FG-GAP.TM,SS	2.01
	440774	AI420611	Hs.127832	ESTs	zi-mynd,tm,ss	2.00
70	442961 424420	BE614474	Hs.289074		TM	2.00
	410240	BE614743 AL157424	Hs.146688 Hs.61289	prostaglandin E synaptolanin 2	MAPEG,TM,SS	2.00
	435014	BE560898	Hs.10026	ribosomal prote	TM Ribosomal_L17,TM,	2.00
	406752	AI285598	Hs.217493		TM	2.00 2.00
76						2.00
75	TABLE 4		_			
	Pkay:			set identifier number		
	CAT num		ne cluster numi			
	Accession	ı. Ge	nbank accessio	n numbers		
80	Pkey	CAT numbe	r Accession			
	410008	116812_1		BE142525 BE142527		
	418546	176677_1	AA224827	T59708 T59843 BE15690	3	
	419546	185768_1	AA244199	AA244272 H57440		
					464	

	419807	188252_1	977402 A A20	2462 AA250988 R06794				
	422689	219896_1		A315006 AW954733				
	431120	328264_1	AA492588 AA	492498 AA492571				
5	433748	37385_1		90 Al110858 AF090916 AF075357 AA011531				
,	438223 438993	452646_1 467651_1		202139 AJ202098 1834870 AJ026361				
	446995	702707_1	AA828995 AA834879 AI926361 AI355012 AW812856					
	447197	711623_1	R36075 Al366	5546 R36167				
10	450190	827655_1		91595 T51271 AI686285				
10	451237 455778	863269_1 1364506_1	AW600293 A	1767458 E088802 BE088755 BE088876 BE088947 BE088881	DE000053			
	456157	158261_1		A176967 AA826015	9 95000335			
15	TABLE 410 Pkey:			esponding to an Eos probeset				
	Ref:				titler (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA			
		seque	Suce of primar	chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:4	189-495			
	Strand: Nt_position	Indica	ites DNA stran	from which exons were predicted.				
20	МДООНИИ		nucieudus	positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position				
	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93	891			
	401519 401708	6649315 2951946	Plus Plus	157315-157950 154511-155298				
25	401868	8018106	Plus	73126-73823				
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,12	24455-124610,125672-126076			
	403055 403208	8748904 7630829	Minus Minus	109532-110225				
	403422	9665041	Minus	147706-147903,148667-148804 151169-151561	•			
30	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	•			
	403776 404171	7770611	Minus	1414-1513,1624-1756				
	404253	9930793 9367202	Plus Minus	173667-173783,176876-177055 55675-56055	•			
26	404519	8152000	Plus	12817-13000	•			
35	404567	7249169	Minus	101320-101501				
	405484 405545	5922025 1054740	Plus Plus	199214-199579,199672-199920,200262-200495 118677-118807,119091-119296,121626-121823				
	405818	4071056	Plus	29055-29196				
40	406399	9256288	Minus	63448-63554				
40								
	TABLE 42	A: ABOUT 561	GENES UP-RE	GULATED IN STOMACH CANCER				
	Table 42A	lists about 561	genes up-regul	ated in stomach cancer compared to normal stomaci	h. These were selected as for Table 40A except using various non-malignant stomach			
46	specimens							
45		n oetermaning	vie denominau	or varue.				
45	Pkey: ExAcon:	un determanung Uniq	vie denominau ve Eos probesi	or varue. et identifier number	•			
43	Pkey: ExAcon; UnigenelC	Uniq Exen Exen	<i>the denominau</i> ue Eos probese optar Accession ene number	or varue.	•			
43	Pkey: ExAcon: UnigenetC Unigene T	Uniq Uniq Exen It Unig Itle: Unig	une denominau une Eos probesio nplar Accessior enn number enne gene title	or varue. et identifier number n number, Genbank accession number				
50	Pkey: ExAcon; UnigenelC	Uniq Uniq Exen It Unig Itle: Unig	<i>the denominau</i> ue Eos probese optar Accession ene number	or varue. et identifier number n number, Genbank accession number				
	Pkey: ExAccn: UnigenelC Unigene T R1: Pkey	Uniq Exen t: Unig itle: Unig Ratio	une demorrinate une Eos probesso reptar Accession ene number ene gene title of turnor to no  UnigeneID	or value.  It identifier number In number, Genbank accession number Irmal tissue  Unigene Title	Ri			
	Pkey: ExAccn: UnigenelC Unigene T R1: Pkey 42836B	Uniq. Exen  Uniq. Exen  Uniq. Exen  Execon  Execon  Execon  BE440042	une conominate une Eos probesso unptar Accession ene number ene gene title of turnor to no  UnigeneID Hs.83326	or value.  It klentifier number In number, Genbank accession number  Irmal tissue  Unigene Title Inath's metalloproteinase 3 (stromelysin	R1 60.4			
50	Pkey: ExAccn: Unigene IC Unigene T R1: Pkey 42836B 448693	Unique Exercition Unique Exercities Unique Ration ExAccin BE440042 AW004854	use conforminate use Eos probest optar Accession ene number ene gene title of turnor to no  UnigenelD Hs.83326 Hs.228320	or value.  It identifier number  In number, Genbank accession number  Irmal tissue  Unigene Title  matrix metalloproteinase 3 (stromelysin  Homo sapiens CDNA: FLJ23537 fls., clone L	R1 60.4 28.6			
	Pkey: ExAccn: Unigene!C Unigene T R1: Pkey 428368 448693 428664 422330	Execution of the control of the cont	une conominate une Eos probesso unptar Accession ene number ene gene title of turnor to no  UnigeneID Hs.83326	or value.  It klentifier number In number, Genbank accession number  Irmal tissue  Unigene Title Inath's metalloproteinase 3 (stromelysin	R1 60.4			
50	Pkey: ExAccn: Unigenet C Unigene T R1: Pkey 42836B 448664 422330 415989	Uniq Exen Exen Itle: Unig Ratio ExAcon BE440042 AW004854 AK001666 D30783 AI267700	use canominate use Eos probests probest	or value.  It identifier number In number, Genbank accession number  I imal tissue  Unigene Title I matrix metalloproteinase 3 (stromelysin I Homo sapiens cDNA: FLJ23537 fis, clone L  similar to SALL1 (sal (Orosophila)-like eptregulin ESTs	R1 60.4 28.6 26.8 22.0 21.2			
50	Pkey: ExAccn: Unigene T R1: Pkey 428368 448693 428693 42834 422330 415989 439979	Execution   Execut	use conformation use conformation under the conformation of tumor to no UnigenellD Hs.83326 Hs.228320 Hs.189095 Hs.115263 Hs.111128 Hs.6823	or value.  It identifier number In number, Genbank accession number  Imal tissue  Unigene Title Imaritx metalloproteinase 3 (stromelysin  Homo sapiers cDNA; FLJ23537 fis, clone L  similar to SALL1 (sal (Drosophila)-like  epiregulin  ESTe  hypothetical protein FLJ10430	R1 60.4 28.6 26.8 22.0 21.2 19.0			
50	Pkey: ExAccn: Unigenet T R1: Pkey 428368 448693 428664 422330 415989 439979 451099 403776	Uniq Exen Exen Itle: Unig Ratio ExAcon BE440042 AW004854 AK001666 D30783 AI267700	use canominate use Eos probests probest	or value.  It identifier number In number, Genbank accession number  I imal tissue  Unigene Title I matrix metalloproteinase 3 (stromelysin I Homo sapiens cDNA: FLJ23537 fis, clone L  similar to SALL1 (sal (Orosophila)-like eptregulin ESTs	R1 60.4 28.6 26.8 22.0 21.2 19.0 17.1			
50	Pkey: ExAccn: Unigenel C Unigene T R1: Pkey 42836B 448693 428664 422330 415989 43979 451099 403776 424905	Exacca BE440042 AW004854 AK001666 D30783 A1267700 AW600291 R52795 NM_002497	use demoranamente use comprehension unimber en number en gene title of tumor to no UnigenelD Hs. 83326 Hs. 228320 Hs. 115263 Hs. 11128 Hs. 6823 Hs. 153704	or value.  It identifier number in number, Genbank accession in Sale in Genbank accession in Genbank accession in Italia in Itali	R1 60.4 28.6 26.8 22.0 21.2 19.0			
50	Pkey: ExAcon: Unigene!C Unigene T R1: Pkey 428368 448693 428364 422330 415989 439979 451099 403776 424905 414132	ExAccn BE440042 AW004854 AW01666 D30783 AI267700 AW600291 R52795 NM_002497 AI801235	use canominate use control was control with the control was con	or value.  It identifier number in number, Genbank accession number in number, Genbank accession number in number, Genbank accession number in number.  Unigene Title in a strong title in a str	R1 60.4 28.5 26.8 22.0 21.2 19.0 17.1 14.9 14.8			
50	Pkey: ExAccn: Unigenel C Unigene T R1: Pkey 42836B 448693 428664 422330 415989 43979 451099 403776 424905	Exacca BE440042 AW004854 AK001666 D30783 A1267700 AW600291 R52795 NM_002497	use demoranamente use comprehension unimber en number en gene title of tumor to no UnigenelD Hs. 83326 Hs. 228320 Hs. 115263 Hs. 11128 Hs. 6823 Hs. 153704	or value.  In umber, Genbank accession number an umber, Genbank accession number an umber, Genbank accession number armal tissue  Unigene Title matrix metalloproteinase 3 (stromelysin Homo sapiers cDNA: FLJ23537 ffs, clone L similar to SALL1 (sal (Drosophila)-like epiregulin ESTs hypothetical protein FLJ10430 interteutkin 13 receptor, alpha 2  NIMA (never in milosis gene a)-related k ESTs a disintegrin and metalloproteinase doma	R1 50.4 28.6 26.8 22.0 21.2 19.0 17.1 14.9 14.8 14.8			
50 55 60	Pkey: ExAcon: Unigene T R1: Pkey 428368 448693 428368 448694 422330 415989 439776 434776 444132 450375 45375 453032	ExAcca BE440042 AW004854 AW004854 AW004866 D30783 AI267700 AW600291 R52795 NM_002497 AI801235 AA005647 AF053306 AA150797	use canoramasus use canoramasus canoramasus use Eos probess on ene gene title of tumor to no UnigenelD Hs.83326 Hs.228320 Hs.115263 Hs.11128 Hs.6823 Hs.25954 Hs.153704 Hs.8850 Hs.86708 Hs.109276	or value.  In umber, Genbank accession number  In number, Genbank accession number  In umber, Genbank accession number  In unigene Title  matrix metalloproteinase 3 (stromelysin  Homo sapiens cDNA: FLJ23537 fls, clone L  similar to SALL1 (sal (Drosophila)-like  epiregulin  ESTs  hypothetical protein FLJ10430  intertaukin 13 receptor, alpha 2  NIMA (never in milosis gene a)-related k  ESTs  a disintegrin and metalloproteinase doma  budding uninhibited by benzimidazoles 1  latexin protein	R1 60.4 28.5 26.8 22.0 21.2 19.0 17.1 14.9 14.8			
50	Pkey: ExAccn: Unigenei T Unigene T R1: Pkey 428368 438693 428369 439979 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 451099 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109 45109	Exacca BE440042 AW004854 AK001666 D30783 AL267700 AW600291 R52795 NM_002497 AJ801235 AA009647 AF053306 AA150797 D31152	use conformation use conformation of the conformation uniformation uni	A value.  A value.  A value.  A number, Genbank accession number  A number, Genbank accession number  A number, Genbank accession number  A value  Unigene Title  matrix metalloproteinase 3 (stromelysin  Homo sapiens cDNA: FLJ23537 ffs, clone L  similar to SALL1 (sal (Drosophila)-like  epiregulin  ESTs  hypothetical protein FLJ10430  interteutin 13 receptor, alpha 2  NIMA (never in milosis gene a)-related k  ESTs  a disintegrin and metalloproteinase doma  budding unlihibited by benzimidazoles 1  latexin protein	R1 60.4 28.6 26.8 22.0 21.2 19.0 17.1 14.9 14.8 14.2 14.0 13.8 13.1 12.5			
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50 55 60 65 70	Pkey: ExAcon: Unigene T R1: Pkey 428368 448693 428368 448693 422330 415989 439776 424905 439776 424905 439776 444132 450375 453922 47585 416861 414972 445900 446619 441377 419423 415138 416439 412472 445900 44639 412472 445900 44639 41379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 418379 423008 423008 423008 423008 423008 423008 423008 423008 423008 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42308 42	Exacen BE440042 AW004854 AK001666 D30783 A1267700 AW600291 R52795 NM_002497 AI801235 AA009647 AF053306 AA150797 D31152 AA634543 BE218239 D26483 BE218239 D26483 BE318239 D26483 AU377694 AW9775398 AW393080 AA218940 AA383092 BE296227 AB041035 BE5622388 AB041035 BE5622388 AW3448047	ue cenorimate use control of the con	an variue.  It identifier number in number. Genbank accession number  Unigene Title matrix metalloproteinase 3 (stromelysin Horno sapiers cDNA: FLJ23537 fls, clone L similar to SALL1 (sal (Drosophila)-like epiregulin ESTs hypothetical protein FLJ10430 interteukin 13 receptor, atpha 2  NIMA (never in milosis gene a)-retated k ESTs a disintegrin and metalloproteinase doma budding uninhibited by benzimidazoles 1 latexin protein collagen, type X, atpha 1 (Schmid metaph 1GF-II mRNA-binding protein 3 KIAA0008 gene product Homo sapiens cbnoe 24787 mRNA sequence secreted phosphoprotein 1 (osteopontin, ESTs KIAA0007 protein tissue factor pathway inhibitor 2 ESTs Homo sapiens cbnA: FLJ23537 fis, clone L fdgetin-rike 1 replication protein A3 (14kD) serfne/fhreonine kinase 15 NADPH oxidase 4 KIAA0112 protein; homotog of yeast ribos gbill3-C10214-291299-052-A12 C10214 Homo	R1 50.4 28.6 26.8 22.0 21.2 19.0 17.1 14.9 14.8 14.2 14.0 13.8 13.1 12.5 12.2 10.6 10.5 10.5 10.5 10.5 9.6 9.4 9.2 8.9 8.8 8.6 8.5 8.3 8.1			

	409041	AB033025	Hs.50081	KIAA1199 protein	8.0
	450480	X82125	Hs.25040	zinc finger protein 239	7.6
	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	7.6
5	453878	AW964440	Hs. 19025	ESTs	7.6
,	430403 427961	AF039390 AW293165	Hs.241382 Hs.143134	tumor necrosis factor (ligand) superfami ESTs	7.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matriysin,	7.4 7.3
	426235	AI631964	Hs.34447	ESTs	7.1
10	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	7.0
10	418205 409757	L21715 NM_001898	Hs.83760 Hs.123114	troponin I, skeletal, fast	7.0
	430044	AA464510	Hs.152812	cystatin SN ESTs	6.9 6.6
	444783	AK001468	Hs.62180	anillin (Drosophile Scraps homolog), act	6.5
15	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.5
13	449020 431958	AI621170 X63629	Hs.192699 Hs.2877	ESTs	6.3
	434699	AA643687	Hs.149425	cadherin 3, type 1, P-cadherin (placenta Homo sapiens cDNA FL/11980 fs. clone HE	5.8 5.7
	424345	AK001380	Hs.145479	Homo sapiens cONA FLJ 10518 fis, clone NT	5.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily 8 (Cy	5.4
20	434551	BE387162 AJ741320	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	5.3
	427660 424960	BE245380	Hs.114121 Hs.153952	Homo sapiens cDNA: FLJ23228 fis, clone C 5 nucleotidase (CD73)	5.0
	400268	022.000	113,133332	3 Hacesocase (CO73)	4.9 4.8
25	408427	AW194270	Hs.177236	ESTs	4.7
25	453785	AJ368236	Hs.283732	ESTs	4.7
•	411274 424717	NM_002776 H03754	Hs.69423 Hs.152213	katlikrein 10 wingless-type MMTV integration site fami	4.7
	415752	BE314524	Hs.78776	putative transmembrane protein	4.7 4.6
20	434370	AF130988	Hs.58346	downless (mouse) homolog	4.6
30	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	4.6
	400205 422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.6
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.5 4.4
26	453160	AJ263307	Hs.146228	ESTs	4.4
35	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.4
	431211 446638	M86849 AL133063	Hs.5566 Hs.15783	gap junction protein, beta 2, 26kD (conn	4.4
	406741	AA058357	Hs.74466	Homo sapiens mRNA; cDNA DKFZp434P1115 (f carcinoembryonic antigen-related cell ad	4.3 4.3
40	411560	AW851186		gb:#L3-CT0220-150200-071-H05 CT0220 Homo	4.1
40	433159	AB035898	Hs.150587	kinesin-like protein 2	4.1
	446142	AJ754693 BE466904	Hs.145968	ESTs	4.1
	414727 422285	AI803103		gb:hz28f03.x1 NCI_CGAP_GC6 Homo sepiens	4.1
	451807	W52854	Hs.27099	gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi DXFZP564J0863 protein	4,1 4,1
45	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.0
	415701	NM_003878	Hs.78619	gamma-glutarnyl hydrolase (conjugase, fol	4.0
	409420 452909	Z15008 NM_015368	Hs.54451 Hs.30985	laminin, gamma 2 (nicein (100kD), kalini pannexin 1	3.9
	443211	Al128388	Hs.143655	ESTs	3.9 3.9
50	442896	R37725	Hs.261108	ESTs	3.8
	407788	8E514982	Hs.38991	S100 calcium-binding protein A2	3.8
	406671 421155	AA129547 H87879	Hs.285754 Hs.102267	met proto-oncogene (hepatocyte growth fa	3.8
	420552	AK000492	Hs.98806	lysyl oxidase hypothetical protein	3.8 3.8
55	420727	H75701	Hs.99886	complement component 4-binding protein,	3.7
	422665	AJ011812	Hs.119018	transcription factor NRF	3.7
	447425 417715	AI963747 AW969587	Hs.18573 Hs.86366	acytphosphatase 1, erythrocyte (common)	3.7
	406076	AL390179	Hs.137011	ESTs Homo saplens mRNA; cDNA DKFZp547P134 (fr	3.7 3.6
60	452281	T93500	Hs.28792	Homo sapiens cONA FLJ11041 fis, clone PL	3.6
	412723	AA648459	Hs.179912	ESTs	3.6
	452461 453331	N78223 A1240665	Hs.108106 Hs.8895	transcription factor	3.6
	406434	A0240003	rs.0095	ESTs	3.6 3.6
65	417956	AA210704	Hs.190465	ESTs	3.6
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.6
	426471 425782	M22440	Hs.170009	transforming growth factor, alpha	3.5
	442558	U66468 AL137761	Hs.159525 Hs.8379	cell growth regulatory with EF-hand doma Homo sepiens mRNA; cDNA DKFZpS86L2424 (f	3.5
70	426957	AA393676	Hs.97459	ESTs, Weakly similar to KIAA0819 protein	3.5 3.5
	448105	AW591433	Hs.170675	ESTs. Weakly similar to TMS2_HUMAN TRANS	3.5
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.5
	442942 416391	AW167087 AI878927	Hs.131562 Hs.79284		3.4
75	420230	AL034344	Hs.298020	mesoderm specific transcript (mouse) hom Homo sapiens cDNA FLJ11796 fts, clone HE	3.4
	408243	Y00787	Hs.624	Interleukin 8	3.4 3.4
	412978	AI431708	Hs.820	homeo bax C6	34
	412851	AI826502	Hs.106149		3.4
80	417720 414812	AA205625 X72755	Hs.208067		3.4
- •	453884	AA355925	Hs.77367 Hs.36232	monokine induced by gamma interferon KIAA0186 gene product	3.4
	436396	AI683487	Hs.299112		3.4 3.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	3.4

	400000				
	420092 423441	AA814043 R68649	Hs.88045 Hs.278359	ESTs absent in melanoma 1 Eke	3.3 3.3
	421787	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m	3.3
_	447342	Al199268	Hs.19322	ESTs	3.3
5	430178	AW449612	Hs.152475	ESTs	3.3
	452826	BE245286	Hs.301636	ESTs. Moderately similar to PEX6_HUMAN P	3.3
	414821 413339	M53835 Al818080	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.3
	448756	A1739241	Hs.194290 Hs.171480	ESTs ESTs	3.3 3.3
10	421948	L42583	Hs.111758	keratin 6A	3.3
	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	3.3
	438538	AA832203	Hs.291955	ESTs	3.3
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	3.3
15	431721 436391	AB032996 AJ227892	Hs.268044 Hs.146274	KIAA1170 protein ESTs	3.3 3.3
	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans	3.3
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.2
	411678	AI907114	Hs.71465	squalene epoxidase	3.2
20	422958 450400	BE545072	Hs.122579	hypothetical protein FLJ10461	3.2
20	453857	A1694722 AL080235	Hs.279744 Hs.35861	ESTs DKFZP586E1621 protein	3.2 3.2
	423528	AB011137	Hs.129740	KIAA0565 gene product	3.2
	440659	AF134160	Hs.7327	claudin 1	3.2
25	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 ffs, clone NT	3.2
23	412022 418203	A1005043 X54942	Hs.24143	ESTs	3.2
	416111	AA033813	Hs.83758 Hs.79018	CDC28 protein kinase 2 chromatin assembly factor 1, subunit A (	3.1 3.1
	408633	AW963372	Hs.46677	PRO2000 protein	3.1
20	445808	AV655234	Hs.298083	ESTs	3.1
30	414618	AI204600	Hs.96978	ESTs	3.1
	421340 422689	F07783 AW856665	Hs.1369	decay accelerating factor for complement	3.1
	456508	AA502764	Hs.123469	gb:RC3-CT0297-290100-013-d03 CT0297 Homo ESTs, Weakly similar to AF208855 1 8M-01	3.1 3.1
~ ~	420759	T11832	Hs.127797	ESTs	3.1
35	452637	AW971231	Hs.291020	ESTs	3.1
	415857	AA866115	Hs.301645	Homo sapiens cDNA FLJ11381 fis, clone HE	3.1
	439451 424051	AF086270 AL110203	Hs.278554 Hs.138411	heterochromatin-like protein 1	3.1
	440138	AB033023	Hs.6982	Homo sapiens mRNA; cDNA DKFZp586J1922 (f hypothetical protein FLJ10201	3.1 3.1
40	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	3.0
	429125	AA446854	Hs.271004	ESTs .	3.0
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 ffs, clone NT	3.0
	438394 409361	BE379623 NM_005982	Hs.27693 Hs.54416	OGI-124 protein	3.0
45	439453	BE264974	Hs.6566	sine oculis horneobox (Drosophila) hornelo thyroid hormone receptor interactor 13	3.0 3.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.0
	422746	NM_004484	Hs.119651	glypican 3	3.0
	424947 453775	R77952 NM_002916	Hs.239625	integral membrane protein 2B	3.0
50	449386	AA001308	Hs.35120 Hs.193213	replication factor C (activator 1) 4 (37 ESTs	3.0 3.0
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	2.9
	401747	AUL 000000	11- 044600	04044	2.9
55	429682 444735	NM_006306 BE019923	Hs.211602 Hs.243122	SMC1 (structural maintenance of chromoso hypothetical protein FLJ13057 similar to	2.9 2.9
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.9
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fls, clone HE	2.9
	442961	BE614474	Hs.289074	Homo sepiens cDNA FLJ13986 fis, clone Y7	2.9
60	454798 421650	AW821295 AA781795	Hs.122587	gb:PM3-ST0307-241299-002-g03 ST0307 Homo ESTs	2.9
	434398	AA121098	Hs.3838	serum-inducible kinase	29 29
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	2.9
	435706	W31254	Hs.7045	GL004 protein	2.9
65	416065 423250	BE267931	Hs.78996	proliferating cell nuclear antigen	2.9
05	423493	BE061916 Al815965	Hs.125849 Hs.129683		2.8 2.8
	430242	U66669	Hs.236642		. 28
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	2.8
70	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.8
70	437834 400440	AA769294 X83957	N. 02070	gb:nz36g03.s1 NCI_CGAP_GC81 Homo saplens	2.8
	444743	AA045648	Hs.83870 Hs.11817	nebulin mudix (nucleoside diphosphate linked moi	2.8 2.8
	428725	AI565937	Hs.98692	ESTs	2.8 2.8
75	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.8
75	449420	AI854852	Hs.198562	ESTs, Highly similar to TS24 MOUSE PROTE	2.8
	433929 430287	AU375499 AW182459	Hs.27379 Hs.125759	ESTs Mostly similar to tomas successor	28
	423346	Al267677	Hs.127416		2.8 2.8
00	407824	AA147884	Hs.9812	ESTS	2.8
80	408482	NM_000676		adenosine A2b receptor	2.8
	425188 456999	AK002052 AA319798	Hs.155071		2.8
	408875	NM_015434	Hs.172247 Hs.48604	eukaryolic translation etongation factor DKFZP434B168 protein	2.8 2.8
				p	20

	407839	AA045144	Hs.161566	ESTs	2.7
	409012 410762	AL117435 AF226053	Hs.49725	DKFZP434I216 protein	2.7
	426925	NM_001196	Hs.66170 Hs.172894	HSKM-B protein	2.7
5	410116	AW630671	Hs.58636	BH3 interacting domain death agonist squamous cell carcinoma antigen recogniz	2.7
-	428398	AJ249368	Hs.98558	EST8	2.7 2.7
	400048			AFFX control: YEL002c/WBP1	27
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	27
10	435664	AJ032087	Hs.269819	ESTs	2.7
10	405695				2.7
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	2.7
	408670 422576	AF160967 BE548555	Hs.46784	potassium large conductance calcium-acti	2.7
	431379	AA504264	Hs.118554 Hs.182937	CGI-83 protein peptidylprolyl isomerase A (cyclophilin	27
15	429540	M85776	14.102331	gb:EST02297 Fetal brain, Stratagene (cat	2.7 2.7
	426874	N67325	Hs.247132	ESTs	2.7
	433183	AF231338	Hs.222024	transcription factor BMAL2	27
	409902	Al337658	Hs.156351	ESTs	2.7
20	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferese (E2	2.7
20	408434 432328	AW195317	Hs.107716	Homo sapiens cDNA: FLJ22344 fis, clone H	2.7
	407633	AI572739 NM_007069	Hs.195471 Hs.37189	6-phosphotructo-2-kinase/fructose-2,6-bi	2.7
	419216	AU076718	Hs.164021	similar to rat HREV107 small inducible cytokine subfamily 8 (Cy	26 26
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	26
25	445564	AB028957	Hs.12896	KIAA1034 protein	26
	401644			•	2.6
	417479	AI057052	Hs.133554	ESTs	26
	434217 426514	AW014795 BE616633	Hs.23349 Hs.301122	ESTs	2.6
30	414800	8E538690	ns.301122	bone morphogenetic protein 7 (osteogenic	26
	400289	X07820	Hs.2258	gb:601064676F1 NIH_MGC_10 Homo sapiens c matrix metalloproteinase 10 (strometysin	2.6 2.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.6
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-4	2.6
35	430397	AI924533	Hs.105607	ESTs	2.6
23	428048 452092	AA705745	Hs. 185070	ESTs	2.6
	440052	BE245374 AI633744	Hs.27842 Hs.195648	hypothetical protein FLJ11210 ESTs	26
	433077	AA314262	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, done H	2.6 2.6
	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	2.6
40	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	26
	410889	X91662	Hs.66744	twist (Drosophila) homotog (acrocephalos	2.6
	440100 413746	BE382685 AA133243	Hs. 158549	ESTs	26
45	414737	AI160386	Hs.171553 Hs.125087	ESTs ESTs	2.6
-	422063	BE156476	113.12.0001	gb:QV0-HT0368-040100-082-c05 HT0368 Homo	2.6 2.8
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isolo	2.6
	437641	AA811452	Hs.291911	EST\$	2.6
50	436027	AI864053	Hs.39972	ESTs, Weakly similar to 138588 reverse t	2.6
30	444381 452571	8E387335 W31518	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	26
	452862	AW378065	Hs.34665 Hs.8687	ESTs ESTs	26
	411984	NM_005419	Hs.72988	signal transducer and activator of trans	2.6 2.6
	446440	AV658411	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT	2.6
55	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	2.6
	426427	M86699	Hs.169840	TTK protein kinase	2.6
	445848 420022	AA774824 AA256253	Hs.13377	Homo sapiens clone 23649 and 23755 untino	2.6
	451418	BE387790	Hs.120817 Hs.26369	ESTs	2.6
60	428953	AA306610	Hs.194676	hypothetical protein FLJ20287 DKFZP434C013 protein	26 26
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	26
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.6
	414987	AA524394	Hs.165544	ESTs	2.6
65	440249 407966	AI246590 AA295052	Hs. 125325	ESTs	2.6
00	406685	M18728	Hs.38516	ESTs	2.5
	403204			gb:Human nonspecific crossreacting antig	2.5
	436961	AW375974	Hs.156704	ESTs	25 25
70	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	2.5
70	444471	AB020684	Hs.11217	KIAA0877 protein	2.5
	430290	AI734110	Hs.136355	ESTs	2.5
	413670 421928	AB000115 AF013758	Hs.75470 Hs.109643	hypothetical protein, expressed in osteo	2.5
	439580	AF086401	Hs.293847	polyadenylate binding protein-interactin ESTs	2.5
75	439963	AW247529	Hs.6793	platelet-activating factor acetythydrota	2.5 2.5
	457065	AJ476318	Hs.192480	ESTs	25
	439521	A1808955	Hs.58248	ESTs	2.5
	426711	AA383471	Hs.180669		2.5
80	422631 417866	BE218919 AW067903	Hs.118793	hypothetical protein FLJ 10688	2.5
	416975	NM_004131	Hs.82772 Hs.1051	collagen, type XI, alpha 1	2.5
	415947	U04045	Hs.78934	granzyme B (granzyme 2, cytotoxic T-lymp mulS (E. coli) homolog 2 (colon cancer,	2.5
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	2.5 2.5
				The second secon	2.0

	424000	414400000	11- 190110	Harmanian Mala Pi Maggrafia along St	
	424080 426572	AW189983 AB037783	Hs.139119 Hs.170623	Homo sapiens cDNA FLJ10967 fis, clone PL hypothetical protein FLJ11183	2.5 2.5
	440594	AW445167	Hs.126036	ESTs	2.5
5	428264	AA424839	Hs.98484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
3	408750 451177	BE294069 AI969716	Hs.93581 Hs.13034	hypothetical protein FLJ10512 ESTs	2.5 2.5
	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.5
	434414	A1798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	25
10	400240 410519	A14#122C4	LL 42470F	ESTs .	2.5
iÀ	440953	AW612264 AI683036	Hs.131705 Hs.124135	KIAA1618 protein	2.5 2.5
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	2.5
15	442295 420894	AJ827248 AA744597	Hs.224398 Hs.88854	Homo sapiens cDNA FLJ11469 fis, clone HE ESTs	25 25
15	410094	8E147897	Hs.58593	general transcription factor IIF, polype	24
	413998	AW103807	Hs.243933	ESTs	2.4
	412281	AI810054	Hs.14119	ESTS	2.4
20	418105 447335	AW937488 BE617695	Hs.178000 Hs.286192	ESTs protein phosphatase 1, regulatory (inhib	24 24
	446852	AW451643	Hs.257479	ESTs, Wealdy similar to AF147747 1 BOG25	2.4
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	24
	442991 410193	8E281238 AJ132592	Hs.8888 Hs.59757	hypothetical protein FLJ20424 zinc finger protein 281	2.4 2.4
25	410664	NM_006033	Hs.65370	lipase, endotheliai	24
	449264	A1637649	Hs.196105	ESTs	2.4
	423453 433757	AW450737 AI949974	Hs.128791 Hs.152670	CGI-09 protein ESTs	2.4 2.4
	411598	BE336654	Hs.70937	H3 histone family, member K	2.4
30	431657	AJ345227	Hs.105448	ESTs, Weakly similar to 834087 hypotheti	2.4
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosofic,	24
	428242 419559	H55709 Y07828	Hs.2250 Hs.91096	leukemia inhibitory factor (cholinergic ring finger protein	2.4 2.4
26	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.4
35	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.4
	413281 402819	AA861271	Hs.34396	ESTS	2.4 2.4
	431457	NM_012211	Hs.256297	integrin, alpha 11	24
40	422564	Al148006	Hs.222120	ESTs	2.4
40	443683 407242	BE241717 M18728	Hs.9676	uncharacterized hypothalamus protein HT0 gb:Human nonspecific crossreading antig	2.4 2.4
	409235	AA 188827	Hs.7988	ESTs, Weakly similar to endo-alpha-D-man	2.4
	408938	AA059013	Hs.22607	ESTs	2.4
45	422158 423217	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	24
7,7	408321	NM_000094 AW405882	Hs.1640 Hs.44205	collagen, type VII, alpha 1 (epidermotys contistatin	24 24
	419086	NM_000216	Hs.89591	Kalimann syndrome 1 sequence	2.4
	452945	AW978187	Hs.31086	Homo sapiens mRNA for cytochrome b5, par	24
50	452234 427722	AW084176 AK000123	Hs.223296 Hs.180479	ESTs hypothetical protein FLJ20116	2.4 2.4
	430399	AI916284	Hs.199671	ESTs	2.4
	450737	AW007152	Hs.2033330	ESTs	2.4
	428513 405454	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	24 24
55	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.3
	421462 403416	AF016495	Hs.104624	aquaporin 9	2.3
	422039	A1744626 BE567832	Hs.301506 Hs.82148	ESTs, Highly similar to KIAA0564 protein hypothetical protein	2.3 2.3
20	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	2.3
60	429145	AI694923	Hs.49031 Hs.1634	ESTs	23
	423198 442914	M81933 AW188551	Hs.1634 Hs.99519	cell division cycle 25A Horno sapiens cDNA FLJ14007 fls, clone Y7	2.3 2.3
	449042	AW294985	Hs.301148	potassium voltage-gated channel, isk-rel	2.3
65	421308	AA687322	Hs.192843		2.3
UJ	419926 429992	AW900992 AL050053	Hs.93796 Hs.227397	DKFZP586D2223 protein Homo sapiens mRNA; cDNA DKFZp566E103 (fr	2.3 2.3
	440601	N62409	Hs.126688		2.3
	445232	Al281848	Hs.165547		2.3
70	410174 452110	AA306007 T47667	Hs.59461 Hs.28005	DKFZP434C245 protein Homo sapiens mRNA; cDNA DKFZp564G2463 (I	2.3
. •	422493	AW474183	Hs.233816	ESTs	2.3 2.3
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	2.3
	411098 426457	U80034 AW804667	Hs.68583	mitochondrial intermediate peptidase	2.3
75	442029	AW894667 AW956698	Hs.169965 Hs.14456	i chimerin (chimaerin) 1 neural precursor cell expressed, develop	2.3 2.3
	446545	AJ431798	Hs.164192	ESTs, Weakly similar to Y161_HUMAN HYPOT	2.3
	422094	AF129535	Hs.272027	F-box only protein 5	2.3
	421933 430001	R98881 Al580056	Hs.109655 Hs.98992	is sex comb on midleg (Drosophila)-like 1 ESTs	23 23
80	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	23
	402053	L PROPAGA		•	23
	415666 432743	H72693 Al146966	Hs.101656	gb:yu03c11.r1 Soares fetal liver spleen S ESTs	2.3 2.3
	-02, 40	10500			4.3

	433409	AI278802	Hs.25661	ESTs	2.3
	408330	AW182602	Hs.249954	ESTs	2.3
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on	2.3
5	436972	AA284679	Hs.25640	claudin 3	23
3	436747 433730	AW977192 AK002135	Hs.291343 Hs.3542	ESTs	23
	414839	X63692	Hs.77462	hypothetical protein FLJ11273 DNA (cytosine-5-)-methyltransferase 1	23 23
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.3
10	415339	NM_015156	Hs.78398	KIAA0071 protein	2.3
10	449539	W80363	Hs.58446	ESTs	2.2
	412651 450956	AA115333 AW193531	Hs.107968	ESTS Maderately similar to ALMA MURAAN A	22
	430335	D80007	Hs.205647 Hs.239499	ESTs, Moderately similar to ALU1_HUMAN A KIAA0185 protein	2.2 2.2
	417849	AW2915B7	Hs.82733	nidogen 2	2.2
15	454946	AW846376		gb:QV0-CT0179-090200-090-09 CT0179 Homo	2.2
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.2
	408349 424704	BE546947 A1263293	Hs.44276 Hs.152096	homeo box C10	2.2
	419433	AA814807	Hs.7395	cytochrome P450, subfamily IIJ (arachido hypothetical protein FLJ23182	2.2 2.2
20	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.2
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	2.2
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.2
	403137 428479	Y00272	LL 104577	and division and a Columbia Company	2.2
25	430200	8E613337	Hs.184572 Hs.234896	cell division cycle 2, G1 to S and G2 to germinin	2.2 2.2
	433745	AF075320	Hs.28980	Homo sapiens clone HQ0270	2.2
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	22
	408380	AF123050	Hs.44532	diubiquitin	2.2
30	422424 431548	A1186431 A1834273	Hs.116577 Hs.9711	prostate differentiation factor	2.2
50	400298	AA032279	Hs.61635	Homo sapiens cDNA FLJ13018 fis, clone N7 six transmembrane epithelial antigen of	2.2 2.2
	428771	AB028992	Hs.193143	KIAA1069 protein	22
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
25	442573	H93366	Hs.7567	Homo sepiens cDNA: FLJ21962 fis, clone H	2.2
35	412802 412530	U41518 AA766268	Hs.74602 Hs.266273	aquaporin 1 (channel-forming Integral pr	2.2
	414761	AU077228	Hs.77256	Homo sapiens cDNA FLJ13346 fis, clone OV enhancer of zeste (Drosophile) homolog 2	2.2 2.2
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.2
40	440283	A1732892	Hs.190489	ESTs	2.2
40	429568	Al088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	2.2
	424003 425300	BE274717 AW601773	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.2
	448568	AA149121	Hs.270259 Hs.71947	ESTs ESTs	2.2 2.2
	419229	AI827237	Hs.282884	ESTa	2.2
45	420982	AW576160	Hs.100729	KIAA0692 protein	2.2
	403258	4140004400			2.2
	439653 426827	AW021103 AW067805	Hs.6631 Hs.172665	hypothetical protein FLJ20373	22
	444514	A1682905	Hs.270431	methylenetetrahydrofolate dehydrogenase ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2 2.2
50	426298	AW965058	Hs.111583	ESTs	2.2
	425322	U63630	Hs. 155637	protein kinase, DNA-activated, catalytic	2.2
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	22
	412505 438788	AA974491 AA825716	Hs.21734	ESTs gb:od29e10.s1 NCI_CGAP_GCB1 Homo sapiens	2.2 2.2
55	429058	AF138863	Hs.194827	hypothetical protein FLB6421	2.2
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	2.2
	410406	AI969703	Hs.301842	ESTs	2.2
	443180 419235	R15875 AW470411	Hs.70945 Hs.288433	ESTs neurotrim	2.2
60	421379	Y15221	Hs.103982		22
-	422809	AK001379	Hs.121028		22
	415058	AW902848	Hs.273829	ESTs	2.2
	418049	AA211467	Hs.190488		2.2
65	436209 408042	AW850417 AL049233	Hs.254020 Hs.42244	ESTs, Moderately similar to unnamed prot Homo sapiens mRNA; cDNA DKFZp564A023 (fr	2.2 2.2
	425692	D90041	Hs.155956		2.2
	409665	NM_006731	Hs.55777	Fukuyama type congenital muscular dystro	2.2
	428157	A1738719	Hs.298668	ESTs .	2.2
70	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	2.2
, 0	429732 414747	U20158 U30872	Hs.2488 Hs.77204	lymphocyte cytosolic protein 2 (SH2 doma	2.2 2.2
	425843	8E313280	Hs.159627	centromere protein F (350/400kD, mitosin death associated protein 3	2.2
	445299	AI910382	Hs.118727		2.1
75	436251	BE515065	Hs.5092	nucleolar protein (KKE/D repeat)	2.1
75	430066	A1929659	Hs.237825	signal recognition particle 72kD	2.1
	422516 407870	BE258862 AB032990	Hs.117950 Hs.40719		2.1
	416109	AJ420311	Hs.126550	hypothetical protein KIAA1164  suppressor of K+ transport defect 1	2.1 2.1
	427528	AU077143	Hs.179565		2.1
80	448089	A1467945	Hs.173696	ESTs	2.1
	441790 400022	AW294909	Hs.132208		2.1
	400022 428728	NM_016625	Hs.191381	AFFX control: STAT1 I hypothetical protein	2.1 2.1
		0.0020		· ·· · · · · · · · · · · · · · · · · ·	4.1

	414366	BE549143		05-50107645651 NIIU 1400 12 Name and and	•
	409929	R38772	Hs.172619	gb:601076456F1 NIH_MGC_12 Homo sapiens c KIAA1106 protein	2.1 2.1
	405264		1220.0		21
_	445625	BE246743	Hs.288529	Homo sapiens cDNA: FLJ22635 fis, clone H	2.1
5	408949	AF189011	Hs.49163	putative ribonuclease (II)	2.1
	424513 433683	BE385864 Al817723	Hs.149894	mitochondrial translational initiation f	2.1
	442952	A1743261	Hs.22678 Hs.131860	hypothetical protein FLJ21832 ESTs	2.1
	441020	W79283	Hs.35962	ESTS	21 21
10	446770	AV660309	Hs.154986	ESTs, Wealthy similar to AF137386 1 plasm	21
	432378	AJ493046	Hs.146133	ESTs	2.1
	447769	AW873704	Hs.48764	ESTs	2.1
	412654	A1093480	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	21
15	. 445669 417979	A1570830 AU077284	Hs.174870 Hs.83081	ESTS	2.1
	433849	BE465884	Hs.280728	GTP cyclohydrolase I feedback regulatory ESTs	21 21
	437928	NM_005476	Hs.5920	UOP-N-acetylgtucosamine-2-epimerase/N-ac	2.1
	457341	BE181716		gb:QV1-HT0639-150500-198-e03 HT0639 Homo	2.1
20	452833	BE559681	Hs.30736	KIAA0124 protein	2.1
20	403055 414581	AA256213	11- 72010	F07-	21
	432840	AK001403	Hs.72010 Hs.279521	ESTs	21
	418994	AA296520	Hs.89546	hypothetical protein FLJ20530 selectin E (endothetial adhesion molecul	21 21
25	440908	AI915225	Hs.126735	ESTs	2.1
25	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	21
	436895	AF037335	Hs.5338	carbonic anhydrase XII	21
	455716 408420	BE070263 NM_006915	U= 200494	gb:QV4-BT0407-280100-090-e07 BT0407 Homo	2.1
	435849	BE305242	Hs.299481 Hs.112442	Homo sapiens mRNA; cDNA DKFZp\$8680118 (f ESTs, Weakly similar to CLDE_HUMAN CLAUD	2.1
30	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	21 21
	433644	AW342028	Hs.256112	ESTs	21
	400020			AFFX control: STAT1	2.1
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	21
35	410660 404076	Al061118	Hs.65328	Fanconi anemia, complementation group F	2.1
55	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.1 2.1
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.1
	444863	AW384082	Hs.301323	ESTs	2.1
40	445867	AF272663	Hs.13405	gephyrin	2.1
40	441021	AW578716	Hs.7644	H1 histone family, member 2	2.1
	446595 417515	T57448 L24203	Hs.15487 Hs.82237	hypothetical protein FLJ20725	2.1
	412429	AV650262	Hs.75765	ataxia-telangiactasia group O-associated GRO2 oncogene	21 21
	449207	AL044222	Hs.23255	nucleoporin 155kD	21
45	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	21
	400861				2.1
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	2.1
	440591 426181	AA431599 AA371422	H\$.132799	Homo sapiens cDNA: FLJ23451 fis, clone H	2.1
50	452880	AA029332	Hs.69844 Hs.87549	ESTs, Wealdy similar to dJ191N21.1 (H.sa ESTs	2.1 2.1
	421878	AA299652	Hs.111496	Homo sepiens cDNA FLJ11643 fis, clone HE	2.1
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.1
	427224	AL135554	Hs.101937	sine ocutis homeobox (Drosophila) homolo	2.1
55	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.1
33	432487 429534	AA550988 AW976987	Hs.221472 Hs.163327	ESTs ESTs	2.1
	446051	BE048061	Hs.153315	ESTS	21 21
	447760	AI431328	Hs.291179	ESTs, Weakly similar to topoisomerase I	21
60	422675	BE018517	Hs.119140		2.1
60	415173	AW501735	Hs.253015	ESTs	2.1
	425170 453751	AU077315 R38762	Hs.154970		2.1
	426283	NM_003937	Hs.101282		21
	417874	BE616160	Hs.169139 Hs.82829	kynureninase (L-kynurenine hydrolase) protein tyrosine phosphatase, non-recept	2.1 2.1
65	449555	AW450288	Hs.195390	ESTs	21
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	21
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	2.1
	424673 407802	AA345051	Hs.294092		21
70	452834	D84145 AI638627	Hs.39913 Hs.105685	novel RGD-containing protein ESTs	2.0
. •	438895	AW007021	Hs.82894	ESTs ESTS	2.0 2.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	20
	406981	S71129	Hs.296844	Acetylcholinesterase (14-E5 doman) (huma	2.0
75	427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	2.0
, 3	439223	AW238299	Hs.23945	ESTs	2.0
	432343 414890	NM_002960 BE281095	Hs.2961 Hs.77573	S100 calcium-binding protein A3	2.0
	423019	AI840185	Hs.225816	uridine phosphorylase ESTs	2.0
00	435905	AW997484	Hs.5003	KIAA0456 protein	2.0 2.0
80	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.0
	439608	AW864696	Hs.26198	Homo sapiens cDNA: FLJ23363 fis, clone H	2.0
	432114 405545	AL036021	Hs.225597	ESTs	2.0
	-V3343				2.0
				4/1	

	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	2.0
	442528	AF150317	Hs.134217	ESTs	2.0
	445237	AW270515	Hs.149596	ESTs	2.0
5	428074	BE387770	Hs.182378	colony stimulating factor 2 receptor, al	2.0
,	423430 435767	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	20
	432945	H73505 AL043683	Hs.117874 Hs.271357	ESTs ESTs, Wealdy similar to unnamed protein	20 20
	428792	BE535955	Hs.193602	chromosome condensation protein G	20
	404170				20
10	410286	A1739159	Hs.61898	OKFZP586N2124 protein	20
	434565	T52172		gb:yb22d01.s1 Stratagene fetal spieen (9	2.0
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	20
	417933	X02308	Hs.82962	thymidylate synthetase	20
15	441384 437403	AA447849 Al208149	Hs.288660 Hs.121196	protease, serine, 23 ESTs	2.0 2.0
	412673	ALD42957	Hs.31845	ESTs	2.0
	414020	NM_002984		small inducible cytokine A4 (homologous	20
	438426	AA835936	Hs.269763	ESTs	2.0
20	413943	AW294416	Hs.144687	ESTs	20
20	449001	AI619957	Hs.189854		20
	427674 435425	NM_003528		H2B histone family, member Q	20
	433364	H16263 AI075407	Hs.31416 Hs.296083	ESTs ESTs	20 20
	429782	NM_005754		Ras-GTPase-activating protein SH3-domain	20
25	417366	BE185289	Hs.1076	small proline-rich protein 1B (comilin)	20
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.0
	411943	BE502436	Hs.7962	ESTs, Wealthy similar to putative [C.eleg	2.0
	414266	BE267834	LI- 070044	gb:601124428F1 NIH_MGC_8 Homo sapiens cD	2.0
30	432677 450534	NM_004482 AJ570189	Hs.278611 Hs.25132	UDP-N-acetyl-alpha-O-galactosamine:polyp	2.0
50	446715	A1337735	Hs.173919	KIAA0470 gene product ESTs	2.0 2.0
			***************************************	25,0	••
	TABLE 42				
35	Pkey:			set identifier number	
33	CAT numi Accession		ne cluster numt nbank accessio		
	PLACESSILA	. Ge	HOSIK SUCESSEO	in monipers	
	Pkey	CAT numbe	r Accession		
40	408432	1058667_1	AW195262	R27868 AW811262	
40	411479	1247077_1			121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
	411500	*******	AW848214		
	411560 414266	1249443_1 1430984_1		AW996967 BE143456 BE514180 BE\$14096	
	414366	1438636_1		BE390613 BE277344	
45	414727	1481204_1	BE466904		
	414800	1491863_1	BE538690	T40217	
	415666	1543492_1		8673 H72694 F20990 R08580	
	422063 422285	210852_1		BE156473 BE156474 BE156475 AA302839	
50	422689	214669_1 219896_1		N885143 AW470793 AW450703 AI090784 AW271587   AA31 <b>500</b> 6 AW954733	AW236950 AW242783
-	423871	232749_1	AA331906		
	429540	305828_1		A454535 AA456208 H90189	
	431453	333457_1	AW753917	' BE152926 AA505333 BE155673	
55	434414	38585_1			858232 AW861851 AW858382 AA232351 AA218567 AA055556 AW858231
"					AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
			AA157715	WADGESTA WASTOCK! VANCETECE CURSON WINDOWS	ib aa157718 aa157719 aa100472 aa100774 aa130756 aa157705 aa157730 T92637 awb12621 aa206583 aa209204 be156909 aa226824 ab29309 aw991957
			N66951 A	4527374 H66215 AAD45564 AI694265 H60808 AA149	26 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531		
60	434565	38898_1	T52172 AF	147324 T52248	
	436411	419334_1		2 AA715374 Z25205	
	437834	443674_1			293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749295
	438788	465159_1		9 AW749287 BE535498 • AW978859 AA828841	
65	454456	1207088_1	AW85098	AW752836 M86124	
	454678	1228915_1	AW81308		
	454798	1235104_1		5 AWB21272 AWB21282	,
	454946	1245753_1		5 AW846375 AW846434 AW846287 AW846365 AW84	
70	455716 457341	1352695_1		BE070195 BE070265 BE070202 BE070233 BE07039	
, ,	437341	322221_1	05 1017 10	3 AW948314 AW801848 AW948320 AW983981 AA484	444
	TABLE 4				
	Pkey:	U	ujdne unwpet c	orresponding to an Eos probeset	
75	Ref:	S	equence source	. The 7 digit numbers in this column are Genbank Idea	ntifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
,,	Strand:			ian chromosome 22" Dunham, et at. (1999) <u>Nature</u> 402 rand from which exons were predicted.	489-495.
	Nt_posit			ide positions of predicted exons.	
		_			
80	Pkey 400861	Ref 9757506	Strand	Nt_position	
50	401644	8576138	Plus Plus	163855-164016 82655-83959	
	401747	9789672	Minus		20422-120990,130161-130381,130468-130593,131097-131258,131866-31932,132451-
				132575,133580-134011	
					_

	402053	8083229	Plus	62703-63179
	402819	6729581	Plus	29217-29422
	403055	8748904	Minus	109532-110225
_	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
5	403204	7622392	Plus	16214-16439
	403258	7770439	Minus	156251-156619
	403776	7770611	Minus	1414-1513,1624-1756
	404076	9931752	Minus	3848-3967
• •	404170	9930793	Plus	168836-169248
10	405264	7329374	Plus	28556-28684
	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405695	4309958	Plus	51860-52162
15	408434	9256551	Minus	17803-17931
13				

TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER
Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. These were selected as for Table 42A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig. th3, egf. 7tm domains). Predicted protein domains Table 42A and are noted. Picey: ExAccn: UnigenetO: Unigene Title: PSDomain: R1:

20

25

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Protein Structural Domain Ratio of turnor to normal tissue

	Pkey	ExAcco	UnigenetD	I talanna Titla	DCDamaia	
	428368	BE440042	Hs.83326	Unigene Title matrix metallop	PSDomain hemopexin,Peptidase_M10,,SS	R1 60.4
30	428664	AK001666	Hs.189095	similar to SALL	zi-C2H2,TM,SS	26.8
	422330	D30783	Hs.115263	epiregulin	EGF,TM,SS	22.0
	439979	AW600291	Hs.6823	hypothetical or	TM	19.0
	451099	R52795	Hs.25954	interleukin 13	fn3.TM.SS	17.1
	403776				ILB,TM,SS	14.9
35	424905	NM 002497	Hs.153704	NIMA (never in	pkinase.TM.	14.8
	453922	AF053306	Hs.36708	budding uninhib	TM	13.6
	436032	AA150797	Hs.109276	latexin protein	TM	13.1
	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS	12.5
	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain,TM,	12.2
40	414972	BE263782	Hs.77695	KIAA0008 gene p	TM	10.6
	446619	AU076643	Hs.313	secreted phosph	Osteopontin, TM, SS	10.5
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma,TM,SS	9.6
	423020	AA383092	Hs.1608	replication pro	TM	8.6
	408908	BE296227	Hs.48915	serine/threonin	pkinase,TM,SS	8.5
45	419948	AB041035	Hs.93847	NADPH oxidase 4	Ferric_reduct_TM,SS	8.3
	411750	BE562298	Hs.71827	KIAA0112 protei	SS	8.3
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	8.0
	450480	X82125	Hs.25040	zinc finger pro	zf-C2H2,TM,SS	7.6
50	417655	AA780791	Hs.14014	ESTs. Weakly si	TM	7.6
50	430403	AF039390	Hs.241382	tumor necrosis	TMSS	7.5
	428330	L22524	Hs.2256	matrix metallop	Peptidase_M10,,SS	7.3
	452291	AF015592	Hs.28853	CDC7 (cell divi	pkinase,TM,	7.0
	418205	L21715	Hs.83760	troponin I, ske	Troponin,,SS	7.0
55	409757	NM_001898	Hs.123114	cystatin SN	cystatin,,SS	6.9
23	444783	AK001468	Hs.62180	anillin (Drosop	<del>Р</del> Ң,ТМ,	6.5
	416209	AA236776	Hs.79078	MAD2 (mitotic a	HORMA,,SS	6.5
	431958	X63629	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM,SS	5.8
	424345	AK001380	Hs.145479	Homo sapiens cD	TMSS	5.6
60	428227	AA321649	Hs.2248	small inducible	ILB,TM,SS	5,4
UU	424960 400268	BE245380	Hs.153952	5 nucleotidase	5_nucleotidese,TM,SS	4.9
	411274	NM_002776	Hs.69423	toditional and	Myosin_tail,,SS	4.8
	415752	BE314524	Hs.78776	kallikrein 10	trypsin,TM,	4.7
	431806	AF186114	Hs.270737	putative transm	TM	4.6
65	400205	AF 100114	FIG.210131	tumor necrosis	TM,SS SS	4.6
00	422938	NM_001809	Hs.1594	essimmen and	5.5 histone,TM,	4.6
	406687	M31126	Hs.272620	centromere prot pregnancy speci	hemopexin, TM,	4.5
	423871	AA331906	14.272020	gb:EST35805 Emb	TM	4.4 4.4
	431211	M86849	Hs.5566	gap junction or	connexin,TM.	4.4
70	446638	AL133063	Hs.15783	Homo sapiens mR	TM	4.3
	406741	AA058357	Hs.74466	carcinoembryoni	lg,TM,SS	4.3
	411560	AW851186	1.5.1 1.00	gb:IL3-CT0220-1	TM	4.1
	433159	AB035898	Hs.150587	kinesin-fike pr	kinesin, Myosin_tail, TM, SS	4.1
	422285	AI803103		gb:tc14e06.x1 S	TM,SS	4.1
75	451807	W52854	Hs.27099	DXFZP564J0863 p	TM	4.1
	411558	AA102670	Hs.70725	gamma-aminobuty	neur_chan,TM,SS	4.0
	415701	NM_003878	Hs.78619	gamma-glutamyi	TM,SS	4.0
	409420	215008	Hs.54451	laminin, gamma	taminin_EGF_taminin_B_SS	3.9
00	452909	NM_015368	Hs.30985	pannexin 1	TM	3.9
80	407788	BE514982	Hs.38991	S100 calcium-bi	erhand.S_100.TM.SS	3.8
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidaseSS	3.8
	420552	AK000492	Hs.98806	hypothetical pr	SS	3.8
	420727	H75701	Hs.99886	complement comp	sushi	3.7
				•	*	

	422665	AJ011812	Hs.119018	transcription f	R3H,G-pstch,GTP_CDC,TM,SS	3.7
	447425	AJ963747	Hs.18573	acylphosphatase	Acyfphosphatase,TM,	3.7
	406076	AL390179	Hs.137011	Homo sapiens mR	TM	3.6
5	406434				heme_1,TM,	3.6
)	417956	AA210704	Hs.190465	ESTs	sushi,,SS	3.6
	410102	AW248508	Hs.279727	Homo sapiens cD	TM,SS	3.6
	426471	M22440	Hs.170009	transforming gr	EGF,TM,SS	3.5
	425782	U66468	Hs.159525	cell growth reg	\$S	3.5
10	426957	AA393676	Hs.97459	ESTs, Wealdy si	SS	3.5
10	448105	AW591433	Hs.170675	ESTs, Weakly si	trypsin,TM,	3.5
	414998	NM_002543	Hs.77729	oxidised low de	TM	3.5
	442942	AW167087	Hs.131562	ESTs	pkinase,TM,SS	3.4
	416391	AI878927	Hs.79284	mesoderm specif	abhydrolasa,TM,SS	3.4
15	420230	AL034344	Hs.298020	Homo sapiens cD	Fork_head,TM,	3.4
13	408243	Y00787	Hs.624	Interleukin 8	ILB,TM,SS	3.4
	412978	AI431708	Hs.820	homeo box C6	hameobax,TM,	3.4
	412851	AI826502	Hs.106149	ESTs	TM,SS	3.4
	414812	X72755	Hs.77367	monokine induce	il8SS	3.4
20	453884	AA355925	Hs.36232	KIAA0186 gene p	TM	3.4
20	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,	3.4
	421787	AA227068	Hs.108301	nuclear recepto	TM	3.3
	447342 452826	Al199268	Hs.19322	ESTs	TM,SS	3.3
	414821	BE245286 M63835	Hs.301636	ESTs, Moderatel	AAA,TM,	3.3
25	448756	A1739241	Hs.77424	Fc fragment of	ig.TM,SS	3.3
23	421948	L42583	Hs.171480	ESTs	TM	3.3
	438538	AA832203	Hs.111758	keratin 6A	filament,TM,	3.3
	436391	AJ227892	Hs.291955	ESTs	TM	3.3
	418007	M13509	Hs.146274	ESTs	SS	3.3
30	411678	Ai907114	Hs.83169	matrix metallop	hemopexin,Peptidase_M10,,\$\$	3.2
50	422956	BE545072	Hs.71465 Hs.122579	squalene epoxid	Monooxygenase,TM,	3.2
	450400	AI694722	Hs.279744	hypothetical pr	TM	3.2
	440659	AF134160	Hs.7327	ESTs	TM	3.2
	418203	X54942		claudin 1	PMP22_Claudin,TM,SS	3.2
35	416111	AA033813	Hs.83758 Hs.79018	CDC28 protein k	CKS,TM,	3.1
33	445808	AV655234	Hs.298083	chromatin assem	TM,SS	3.1
	421340	F07783	Hs.1369	ESTs	sushi,TM,SS	3.1
	422689	AW856665	ms.1305	decay accelerat gb:RC3-CT0297-2	sushi,,SS	31
	439451	AF086270	Hs.278554	heterochromatin	SNF2_N,TM,	3.1
40	454456	AW850984	FIS.270334	gb:IL3-CT0220-1	chromo_Chromo_shadowSS	3.1
70	429125	AA446854	Hs.271004	ESTs	tn3,TM,SS	3.0
	409361	NM_005982	Hs.54416		TM	3.0
	439453	BE264974	Hs.6566	sine oculis hom	homeoboxSS	3.0
	414696	AF002020	Hs.76918	thyroid hormone Niemann-Pick di	AAA,TM,	3.0
45	422746	NM_004484	Hs.119651		Patched,TM,SS	3.0
	453775	NM_002916	Hs.35120	glypican 3 replication fac	Glypican, TM, SS	3.0
	428862	NM_000346	Hs.2316	SRY (sex-determ	AAA,TM,SS HMG_box,TM,	3.0
	401747		115.2310	ON'I (SEX-DEIGHI)	filament, TM,	2.9 2.9
	429682	NM_006306	Hs.211602	SMC1 (structura	SMC_C,SMC_N,TM,	2.9
50	413385	M34455	Hs.840	indoleamine-pyr	IDO,TM,	2.9
	442961	BE614474	Hs.289074	Homo sapiens cD	TM	2.9 2.9
	421650	AA781795	Hs.122587	ESTs	TM	2.9
	434398	AA121098	Hs.3838	serum-inducible	pkinase,POLO_box,TM,	2.9
	435706	W31254	Hs.7045	GL004 protein	PDEase,TM,	2.9
55	416065	BE267931	Hs.78996	proliferating c	TM	2.9
	423493	AI815965	Hs.129683	ubiquitin-conju	UQ_con,,SS	2.8
	430242	U66669	Hs.236642	3-hydroxyisobut	TM	2.8
	411770	NM_014278	Hs.71992	heat shock prot	HSP70,TM,	28
	400440	X83957	Hs.83870	nebulin	TM	2.8
60	444743	AA045648	Hs.11817	nudix (nucleosi	mulT,TM,	28
	417771	AA804698	Hs.82547	retinoic acid r	TM	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly si	TM.SS	2.8
	408482	NM_000676	Hs.45743	adenosine AZb r	7tm_1,TM,SS	2.8
٠.	425188	AK002052	Hs.155071	hypothetical pr	TM	2.8
65	456999	AA319798	Hs.172247	eukaryotic tran	SS	2.8
	408875	NM_015434	Hs.48604	DKFZP434B168 pr	TM	2.8
	409012	AL117435	Hs.49725	DKFZP434I216 pr	RhoGEF,TM,	27
	410762	AF226053	Hs.66170	HSKM-B protein	zi-MYNDSS	27
	426925	NM_001196	Hs.172894	BH3 interacting	TM	27
70	410116	AW630671	Hs.58636	squamous cell c	TMSS	2.7
	428398	AJ249368	Hs.98558	ESTs	SS	2.7
	412140	AA219691	Hs.73625	RAB6 interactin	kinesin,TM,SS	2.7
	456655	AJ376736	Hs.111779		kazal, SS	27
~-	408670	AF160967	Hs.46784	potassium large	TM,SS	2.7
75	422576	BE548555	Hs.118554		lactamase_B,,SS	2.7
	431379	AA504264	Hs.182937		TM	2.7
	433183	AF231338	Hs.222024		HLH,PAS,TM,SS	2.7
	432328	A1572739	Hs.195471		PGAM,6PF2K,TM,	2.7
0.0	407633	NM_007069	Hs.37189	similar to rat	TM,SS	26
80	419216	AU076718	Hs.164021	small inducible	IL8,TM,SS	26
	422363	T55979	Hs.115474		TM	2.6
	401644				zf-C2H2,TM,	26
	417479	AI057052	Hs. 133554	ESTs	CARD,TM,	2.6
					•	<u>-</u>



	426514	BE616633	Hs.301122	hana mambanana	TOP 1 TOP	
	400289	X07820	Hs.2258	bone morphogene matrix metallop	TGF-beta,TGFb_propertide,TM,SS hemopexin,.SS	2.6
	418478	U38945	Hs.1174	cyclin-dependen	ank,TM,SS	2.6 2.6
-	421246	AW582962	Hs.300961	ESTs. Highly si	PalyA_pal,TM,	2.6
5	428048	AA705745	Hs.185070	ESTs	AMP-binding,TM,	2.6
	452092	8E245374	Hs.27842	hypothetical pr	Acyltranslerase,TM,SS	26
	440052	AI633744	Hs.195648	ESTs .	PAC,TM,SS	2.6
	452401 451813	NM_007115	Hs.29352 Hs.27182	tumor necrosis	Xlink,CUB,TM,SS	26
10	410889	NM_016117 X91662	Hs.66744	phospholipase A twist (Drosophi	WD40,.\$\$	26
	422063	BE156476	113.00144	gb:QV0-HT0368-0	HLH,TM, SS	2.6
	418250	U29926	Hs.83918	adenosine monop	A_deaminase,TM,	26 26
	437641	AA811452	Hs.291911	ESTs	TM	26
	452571	W31518	Hs.34665	ESTs	TM	2.6
15	411984	NM_005419	Hs.72988	signal transduc	SH2,STAT,,SS	2.6
	426427	M86699	Hs.169840	TTK protein kin	pkinase,TM,	2.6
	445848	AA774824	Hs.13377	Homo sapiens of	TM	2.6
	420022	AA256253	Hs.120817	ESTs	SS	2.6
20	451418	8E387790	Hs.26369	hypothetical pr	TM	2.6
20	428953 424008	AA306610 R02740	Hs.194676	DKFZP434C013 pr	arf,TNFR_c6,DEAD,Stathmin,TM,SS	2.6
	417863	A8000450	Hs.137555 Hs.82771	putative chemok vaccinia relate	7tm_1,TM,	2.6
	436961	AW375974	Hs.156704	ESTs	pkinase,TM,SS TM	2.6
	413670	AB000115	Hs.75470	hypothetical pr	TM	2.5 2.5
25	421928	AF013758	Hs.109643	polyadenylate b	SS	2.5
	439963	AW247529	Hs.6793	platelet-activa	PAF-AH, HMG_box pkinase, TM,	25
	426711	AA383471	Hs.180669	conserved gene	TM	2.5
	422631	BE218919	Hs.118793	hypothetical pr	TM	2.5
30	417866	AW067903	Hs.82772	collagen, type	TSPN,Collagen,COLFL,SS	2.5
30	416975 415947	NM_004131 U04045	Hs.1051	granzyma B (gra	trypsin,,SS	25
	454678	AW813089	Hs.78934	mutS (E. coli)	Muis_C.Muis_N,TM,	25
	426572	AB037783	Hs.170623	gb:RC3-ST0186-2 hypothetical pr	TPR, Ribosomal_SS, TM, SS PH, FYVE, TM,	2.5
	428264	AA424839	Hs.98484	ESTs. Weakly si	TM	· 2.5 2.5
35	444478	W07318	Hs.240	M-phase phospho	kinesin, SS	2.5
	442295	AJ827248	Hs.224398	Homo sapiens cD	Collagen, COLFI, vwc, TM, SS	25
	410094	BE147897	Hs.58593	general transcr	TFIIF_beta,TM,	24
	413998	AW103807	Hs.243933	ESTs	TPR,TM,SS	2.4
40	412281	AI810054	Hs.14119	ESTs	Ribosomal_S7e,TM,	2.4
70	446852 408915	AW451643	Hs.257479	ESTs, Weakly si	TM	2.4
	442991	NM_016651 BE281238	Hs.48950 Hs.8886	heptacellular c	TM,SS	2.4
	410193	AJ132592	Hs.59757	hypothetical pr zinc finger pro	TM	2.4
	410664	NM_006033	Hs.65370	lipase, endothe	zi-C2H2,TM, Ribosomal_L22,lipase,PLAT,TM,SS	2.4
45	423453	AW450737	Hs.128791	CGI-09 protein	Granin,COP-OH_P_transf,TM,	2.4 2.4
	411598	BE336654	Hs.70937	H3 histone fami	histone,,SS	24
	429663	M68874	Hs.211587	phospholipase A	C2,PLA2_B,TM,	2.4
	428242	H55709	Hs.2250	leukemia inhibi	LIF_OSM,SS	24
50	419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4.zf-B_box,TM,	24
30	419839 402819	U24577	Hs.93304	phospholipase A	SS	2.4
	431457	NM_012211	Hs.256297	laterada ataba	IBR,TM,	2.4
	443683	BE241717	Hs.9676	integrin, alpha uncharacterized	FG-GAP,vwa,TM,SS	2.4
	422158	L10343	Hs.112341	protease inhibi	DUF157,TM, wap,.SS	2.4 2.4
55	423217	NM_000094	Hs.1640	collagen, type	fn3,Collagen,Kunitz_BPTI,vwa,,SS	24
	408321	AW405882	Hs.44205	cortistatin	TM	24
	419086	NM_000216	Hs.89591	Kalimann syndro	fn3,wap.,SS	24
	427722	AK000123	Hs.180479	hypothetical pr	PH,,S\$	24
60	405454 422168	44500004	11- 140400	0400	TM	2.4
00	421462	AA586894 AF016495	Hs.112408 Hs.104624	S100 calcium-bi aquaporin 9	efhand,TM,	2.3
	403416	AI744626	Hs.301506	ESTs, Highly si	MIP,TM, SS	2.3
	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.3
	423198	M81933	Hs.1634	cell division c	Rhodanese, SS	2.3 2.3
65	419926	AW900992	Hs.93796	DKFZP586D2223 p	SS	2.3
	429992	AL050053	Hs.227397	Homo sapiens mR	fn3,TM,SS	2.3
	446232	AI281848	Hs.165547	ESTs	7tm_3,TM,	2.3
	422493	AW474183	Hs.233816		TM	2.3
70	407047	X65965	11- 00000	gb:H.sapiens SO	sodfe,TM,	2.3
, ,	411096 426457	U80034 AW894667	Hs.68583	mitochondrial i	Peptidase_M3,,	23
	446545	A4431798	Hs.169965 Hs.164192		DAG_PE-bind,RhoGAP,TM,	23
	422094	AF129535	Hs.272027		TM TM	2.3
	421933	R98881	Hs.109655		SAM,TM,	23 23
75	430001	A1580056	Hs.98992	ESTs	TM	23
	420802	U22376	Hs.1334	v-myb avian mye	TM	2.3
	402053			•	gpdh,,SS	2.3
	432743	A1146966	Hs.101656		ŠS	2.3
80	433409	AI278802	Hs.25661	ESTs	PWWP.PHD.bromodomain,TM,	2.3
30	408330 407807	AW182602 AL031427	Hs.249954		TMSS	23
	436972	AA284679	Hs.40094 Hs.25640	Human DNA seque claudin 3	T4_deiodinase,TM,	2.3
	433730	AK002135	Hs.3542	hypothetical pr	PMP22_Claudin,TM,SS TM,SS	2.3
					· m,oo	2.3

	414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	2.3
	438192	AI859065	Hs.16808	ESTs, Weakly si	TM,SS	23
	415339	NM_015156	Hs.78398	KIAA0071 protei	ELM2,TM,	2.3
5	449539	WB0363	Hs.58446	ESTs	pkinase,Furin-like,Recep_L_domain,TM,SS	2.2
,	450956 430335	AW193531	Hs.205647	ESTs, Moderatel	pkinase,TM,SS	2.2
	417849	D80007 AW291587	Hs.239499	KIAA0185 protei	S1,TM,	2.2
	412326	R07566	Hs.82733 Hs.73817	nidogen 2	EGF,ld1_recept_b,thyroglobulin_1,TM,SS	2.2
•	408349	BE546947	Hs.44276	small inducible homeo box C10	(LB,,SS homeobox,TM,	2.2
10	424704	AI263293	Hs.152096	cytochrome P450	p450,,SS	2.2
	409632	W74001	Hs.55279	serine (or cyst	serpin,TM,	2.2 2.2
	415323	BE269352	Hs.949	neutrophil cyto	SH3,TPR,TM,	2.2
	417531	NM_003157	Hs.1087	serine/threonin	pkinase,TM,	22
	403137	_			mm,TM,SS	2.2
15	428479	Y00272	Hs.184572	cell division c	pkinase,TM,SS	22
	430200	BE613337	Hs.234896	geminin	TM,SS	2.2
	425390	AI092634	Hs.156114	protein tyrosin	ig, Optods_neuropep, TM, SS	22
	408380	AF123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,	2.2
20	422424	AI186431	Hs.116577	prostate differ	TGF-beta,,SS	2.2
20	400298	AA032279	Hs.61635	six transmembra	TM	2.2
	411571 412802	AA122393	Hs.70811	hypothetical pr	SS	2.2
	414761	U41518 AU077228	Hs.74602	aquaporin 1 (ch	MIP,TM,	2.2
	408432	AW195262	Hs.77256	enhancer of zes	SET,TM,	2.2
25	429568	AI088691	Hs.208414	gb:xn67b05.x1 N Homo sepiens mR	TMSS	2.2
	425300	AW601773	Hs.270259	ESTs	mito_cart,TM, TM	2.2
	439653	AW021103	Hs.6631	hypothetical pr	TM,SS	2.2 2.2
	426827	AW067805	Hs.172665	methylenetetrah	THF_DHG_CYH,FTHFS,TM,	22
30	444514	AI682905	Hs.270431	ESTs, Wealdy si	cNMP_binding,TM,SS	2.2
30	425322	U63630	Hs.155637	protein kinase,	MCM,TM,	2.2
	421662	NM_014141	Hs.106552	cett recognitio	taminin_G,TM,SS	2.2
	438788	AA825716		gb:od29e10.s1 N	ank,death,RHD,TM,	2.2
	429058	AF138863	Hs.194827	hypothetical pr	TM	2.2
35	423104 410406	AJ005273 AI969703	Hs.123647	antigenic deter	TM	2.2
55	421379	Y15221	Hs.301842 Hs.103982	ESTS	FGGY,TM,	2.2
	422809	AK001379	Hs.121028	small inducible	ILB,TM,SS	2.2
	418049	AA211467	Hs.190488	hypothetical pr hypothetical pr	IQ,TM, TM	2.2
	436209	AW850417	Hs.254020	ESTs, Moderatel	TM,SS	2.2 2.2
40	408042	AL049233	Hs.42244	Homo sapiens mR	TM	2.2
	425692	D90041	Hs.155956	N-acetyltransfe	Acetyltransf2,TM,	2.2
	409665	NM_006731	Hs.55777	Fukuyama type c	SS	2.2
	428157	AJ738719	Hs.298668	EST8	hexokinase,TM,	2.2
45	410480	R97457	Hs.63984	cadherin 13, H-	cadherin,TM,SS	2.2
73	429732 414747	U20158 U30872	Hs.2488	lymphocyte cyto	SH2,TM,	2.2
	425843	BE313280	Hs.77204 Hs.159627	centromere prot death associate	SS	2.2
	445299	AI910382	Hs.118727	Homo sapiens cD	TM HLH,TM,	2.2
	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.1 2.1
50	430066	AI929659	Hs.237825	signal recognit	TPR.SS	2.1
	427528	AU077143	Hs.179565	minichromosome	MCM,TM,SS	2.1
	448089	AI467945	Hs.173696	ESTs	TM,SS	21
	428728	NM_016625	Hs.191381	hypothetical pr	TM	2.1
55	409929	R38772	Hs.172619	KIAA1106 protei	TM	2.1
,,	405264 445625	DE040740			SS	2.1
	408949	BE246743 AF189011	Hs.288529 Hs.49163	Homo sapiens cD	TM	21
	424513	BE385864	Hs.149894	putative ribonu	Ribonuclease_3,TM,SS	2.1
	433583	AI817723	Hs.22678	milochondrial t hypothetical pr	GTP_EFTU,IF2,TM, SS	2.1
60	442952	AJ743261	Hs.131860	ESTs	TM	2.1
	432378	AI493046	Hs.146133	ESTs	TM	21 21
	417979	AU077284	Hs.83081	GTP cyclohydrol	TM.SS	21
	433849	BE465884	Hs.280728	EŞTs	SS	21
65	437928	NM_005476	Hs.5920	UDP-N-acetylglu	ROK,Epimerase_2,TM,	2.1
03	403055				filament, TM, SS	2.1
	432840	AK001403	Hs.279521	hypothetical pr	TM_	21
	418994	AA296520	Hs.89546	selectin E (end	EGF,lectin_c.aushi,TM,SS	21
	440908 417621	AI915225 AV654694	Hs.126735	ESTs	TM	2.1
70	435895	AF037335	Hs.82316 Hs.5338	interferon-Indu	TM	21
. •	408420	NM_006915	Hs.299481	carbonic anhydr Homo sapiens mR	carb_anhydrase,TM,SS TM	21
	434064	AL049045	Hs.180758	hypothetical pr	cadherin,TM,SS	21
	404076			, p	RmaAD,TM,	2.1 2.1
7.5	422515	AW500470	Hs.117950	multifunctional	AIRC, SAICAR_SYRLTM	21
75	445867	AF272663	Hs.13405	gephyrin	MoCF_biosynth,TM	2.1
	441021	AW578716	Hs.7644	H1 histone fami	finker_histone, TM,	2.1
	446595	T57448	Hs.15467	hypothetical pr	TM,SS	21
	417515	124203	Hs.82237	ataxia-telangle	zf-B_box.,SS	21
80	412429 449207	AV650262	Hs.75765	GRO2 oncogene	ILB.TM.SS	2.1
	412095	AL044222 AI624707	Hs.23255 Hs.5921	nucleoporin 155	TM,SS	2.1
	400861		.19.3361	Homo sapiens cD	TM,SS phinges TM	2.1
	440591	AA431599	Hs.132799	Homo sapiens cD	pkinase,TM, TM	21
		•				2.1



	442104	L20971	Hs.168	phasphodiestere	PDEase,TM,	2.1
	446921	AB012113	Hs.16530	small inducible	ILB,,SS	2.1
	446051	BE048061	Hs.153315	ESTs	Reprolysin, Pep_M128_propep, TM, SS	2.1
5.	422675	BE018517	Hs.119140	eukaryotic tran	elF-Sa,TM,	2.1
J.	425170 453751	AU077315	Hs.154970	transcription (	TM	21
	426283	R36762 NM_003937	Hs.101282 Hs.169139	Homo sapiens mR	TM TM	21 21
	417874	BE616160	Hs.82829	kynureninase (L. protein tyrosin	Y_phosphatase,TM,	21
	449555	AW450288	Hs.195390	ESTS	TM	21
10	439699	AF086534	Hs.187561	ESTs. Moderatel	TM	2.1
	427413	BE547647	Hs.177781	superoxide dism	sodfa,TM,	21
	407802	D84145	Hs.39913	novel RGD-conta	haxapep,TM,SS	20
	446035	NM_006558	Hs.13565	Sam68-like phos	TM	20
16	406981	S71129	Hs.296844	Acetylchofinest	COesterase,TM,SS	2.0
15	432343	NM_002960	Hs.2961	\$100 calcium-bi	S_100,efhand,TM,SS	2.0
•	414890 423019	BE281095	Hs.77573	uridine phospho	PNP_UDP_1,TM,SS	20
	423019	AI840185 AF072873	Hs.225816 Hs.114218	ESTs	SS S- S	20
	405545	AFUI 2013	FIS. 114210	trizzled (Oroso	Fz,Frizzled,TM,SS ABC_tran,ABC_membrane,TM,SS	2.0 2.0
20	446237	AW270515	Hs.149596	ESTS	bZIP,TM,	20
	428074	BE387770	Hs.182378	colony stimulat	SS SS	2.0
	423430	AF112481	Hs.128501	RAD54, S. cerev	SNF2_N,helicase_C,TM,	20
	435767	H73505	Hs.117874	ESTs	Pepiidase_S8,P,TM,	20
26	432945	AL043683	Hs.271357	ESTs, Wealtly si	PK,SS	2.0
25	404170				sodfe,TM,	2.0
	422610	AF153820	Hs.1547	potassium inwar	IRK,TM,	2.0
	417933	X02308	Hs.82952	thymidylate syn	thymidylat_synt,.SS	2.0
	441384 414020	AA447849 NM_002984	Hs.288660 Hs.75703	protease, serin small inducible	TM ILB.,SS	2.0
30	427674	NM_003528	Hs.2178	H28 histone fam	histone, TM, SS	2.0 . 2.0
	435425	H16263	Hs.31416	ESTS	TM	2.0
	429782	NM_005754	Hs.220689	Ras-GTPase-acti	rm,NTF2,.SS	2.0
	417366	BE185289	Hs.1076	small proline-r	Cornifin, T.M.	2.0
20	426746	J03626	Hs.2057	uridine monopho	Pribosyltran, OMPdecase, TM,	20
35	432677	NM_0044B2	Hs.278611	UDP-N-acetyl-al	Glycos_transf_2,Ricin_B_tectin,TM,	2.0
	TABLE 43	a.				
	Pkey:		o Coe amba	set identifier number		
	CAT numb		e cluster numb			
40	Accession		ank accessio			
•	Pkey	CAT number	Accession			
	408432	1058667_1		R27868 AW811262		
.45	411560 422063	1249443_1 210852_1		AW996987 BE143456	22475 44200000	
.73	422285	214669_1		BE156473 BE156474 BE15	0703 A1090784 AW271587 AW236950 AW24278;	
•	422689	219896_1		AA315006 AW954733	U1U3 MU3U104 MYZ11301 MYZ3033U MYZ4Z10.	•
	423871	232749_1	AA331906			
	438788	465159_1		AW978859 AA828841		
50	454456	1207088_1		AW752836 M86124		
	454678	1228915_1	AW813089	W28102		
	TABLE 43					
		c.				
				rdina to on Eas ambassa		
55	Pkey:	Unique nun	nber correspon	nding to an Eos probeset	in are Gooksak Montifer (CH aumbers "Thinkam	of all maters to the authorities askilled "The DNA secures of
55		Unique nun Sequence :	source. The 7	digit numbers in this colum	in are Genbank Identifier (GI) numbers. "Dunham, ne 407-489-495.	et al." refers to the publication entitled "The ONA sequence of
55	Pkey:	Unique nun Sequence : human chri	source. The 7 omosome 22°	digit numbers in this colum Dunham, et al. (1999) Natu	<u>re</u> 402:489-495.	et al." refers to the publication entitled "The ONA sequence of
55	Pikey: Ref: Strand:	Unique nun Sequence : human chri Indicates D	source. The 7 omosome 22° NA strand from	digit numbers in this colum	<u>re</u> 402:489-495.	et al." refers to the publication entitled "The DNA sequence of
	Pkey: Ref: Strand: Nt_positio	Unique nun Sequence : human chn Indicates 0 in: Indicates n	source. The 7 omosome 22° NA strand from ucleotide positi	digit numbers in this colum Dunham, et al. (1999) <u>Natu</u> n which exons were predictions of predicted exons.	<u>re</u> 402:489-495.	, et al." refers to the publication entitled "The ONA sequence of
<b>5</b> 5	Pkey: Ref: Strand: NL position	Unique nun Sequence : human chn Indicates 0 in: Indicates n	source. The 7 omosome 22° NA strand from ucleotide positions.	digit numbers in this colum Dunham, et al. (1999) Natu in which exons were predictions of predicted exons. Nt_position	<u>re</u> 402:489-495.	et al." refers to the publication entitled "The ONA sequence of
	Pkey: Ref: Strand: NL_position Pkey 400861	Unique nun Sequence : human chri Indicates D In: Indicates n Ref 9757505	source. The 7 omosome 22° NA strand from ucleotide positions Strand Plus	digit numbers in this colum Dunham, et al. (1999) Natu n which exons were predic- tions of predicted exons. Mt_position 163855-164016	<u>re</u> 402:489-495.	et al." refers to the publication entitled "The ONA sequence of
	Pkey: Ref: Strand: NL position Pkey 400861 401644	Unique nun Sequence : human chn Indicates 0 Indicates n Ref 9757505 8576138	source. The 7 omosome 22° NA strand froi ucleotide positi Strand Plus Plus	digit numbers in this cotum Dunham, et al. (1999) <u>Natu</u> m which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959	<u>re</u> 402489-495. led.	
60	Pkey: Ref: Strand: NL_position Pkey 400861	Unique nun Sequence : human chri Indicates D In: Indicates n Ref 9757505	source. The 7 omosome 22° NA strand from ucleotide positions Strand Plus	digit numbers in this cotum Dunham, et al. (1999) Natu, n which exons were predic- tions of predicted exons. Nt_position 163855-164016 82655-83959 118596-118816,119115	<u>ne</u> 402:489-495. led. - 119244,119609-119761,120422-120990,130161-	et al." refers to the publication entitled "The DNA sequence of
	Pkey: Ref: Strand: NL position Pkey 400861 401644	Unique nun Sequence : human chn Indicates 0 Indicates n Ref 9757505 8576138	source. The 7 omosome 22° NA strand fros ucleotide positi Strand Plus Plus Minus	digit numbers in this colum Dunham, et al. (1999) Natu which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959 118596-118816, 119115 131932, 132451-132575	<u>ne</u> 402:489-495. led. - 119244,119609-119761,120422-120990,130161-	
60	Pkey: Ref: Strand: NL position Pkey 400861 401644 401747 402053 402819	Unique nun Sequence : human chn Indicates D Indicates n Ref 9757506 8576138 9789672	source. The 7 omosome 22° NA strand froi ucleotide positi Strand Plus Plus	digit numbers in this cotum Dunham, et al. (1999) Natu, n which exons were predic- tions of predicted exons. Nt_position 163855-164016 82655-83959 118596-118816,119115	<u>ne</u> 402:489-495. led. - 119244,119609-119761,120422-120990,130161-	
60	Pkey: Ref: Strand: Ni_position Pkey 400861 401644 401747 402053 402819 403055	Unique nun Sequence : human chri Indicates D Indicates n Ref 9757505 8576138 9789672 8083229 6729581 8748904	source. The 7 proscorne 22* proscorne 20* Na strand froi ucleotide posit  Strand Plus Plus Minus  Plus Plus Minus Minus Minus	digit numbers in this colum Dunham, et al. (1999) Natu n which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959 118598-118816, 119115 131932, 132451-132575 62703-63179 29217-29422 109532-110225	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-
60	Pkey: Ref: Strand: Nt_position Pkey 400861 401644 401747 402053 402053 403055 403137	Unique nun Sequence : human chri Indicates 0 Indicates n Ref 9757505 8576138 9789672 8083229 6729581 8748904 9211494	source. The 7 proscome 22* NA strand fror ucleotide posit Strand Plus Plus Minus Plus Minus Minus Minus Minus	digit numbers in this colum Dunham, et al. (1999) Natu in which sexors were predictions of predicted exons. NL position 163855-164016 82655-83999 118596-118816, 119115 131932, 132451-132575 62703-63179 29217-29422 109532-110225 92349-92572,92958-93	<u>ne</u> 402:489-495. led. - 119244,119609-119761,120422-120990,130161-	-130381,130468-130593,131097-131258,131866-
60	Pkey: Ref: Strand: NL positio Pkey 400861 401644 401747 402053 402819 403053 403137	Unique nun Sequence : human chri Indicates D Indicates n Ref 9757506 8576138 9789672 8083229 6729581 8748904 9211494 7770611	source. The 7 mosome 22* Ma strand froi ucleotide posit  Strand Plus Plus Minus Plus Minus Minus Minus Minus Minus Minus	digit numbers in this colum Dunham, et al. (1999) Natu n which exons were predic- tions of predicted exons. Mt_position 163855-164016 82655-83959 118598-118816, 119115 131932, 132451-132575 62703-63179 29217-29422 195532-110225 92349-92572,92958-93 1414-1513, 1624-1756	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-
60	Pkey: Ref: Strand: NL position Pkey 400861 401644 401747 402053 402053 403055 403137 403776 404076	Unique nun Sequence: human chri Indicates D Indicates n Ref 9757505 8576138 9769672 8083229 6729581 8748904 9211494 7770611 9931752	source. The 7 moreover 22* NA strand froucleotide position Strand Plus Plus Minus Plus Minus	digit numbers in this colum Dunham, et al. (1999) Natu n which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959 118598-118816, 119115 131932, 132451-132575 62703-63179 29217-29422 109532-110225 92349-92572,92958-93 1414-1513, 1624-1756 3848-3967	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-
60 65	Picey: Reaf: Strand: NL_posibic Picey 400861 401747 402053 402053 402053 403137 403776 404076 404170	Unique nun Sequence : human chri Indicates n Indicates n 8576138 9789672 8083229 6729581 8748904 9211494 7770611 9931752 9930793	source. The 7 mosorme 22* NA strand fros ucleotide posit Strand Plus Plus Minus Plus Minus Minus Minus Minus Minus Minus Minus Minus Ptus	digit numbers in this colum Ounham, et al. (1999) Natu n which exons were predic- tions of predicted exons. Nt_position 163955-164016 82655-83959 118596-118816,119115 131932,132451-132576 62703-63179 29217-29422 199532-110225 92349-92572,92958-93 1414-1513,1624-1756 3848-3967 168835-169248	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-
60 65	Pikey: Raf: Strand: NL posibic Pikey 400851 401644 401747 402053 402819 403055 403137 404076 404076 404170 405264	Unique nun Sequence : human chri Indicates D Indicates n Ref 9757505 8576138 9789672 8083229 6729581 8748904 9211494 7770611 9931752 9930793 7329374	pource. The 7 moreover 22* NA strand froucleotide position Strand Plus Plus Minus Plus Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	digit numbers in this colum Dunham, et al. (1999) Natu n which exons were predic- tions of predicted exons. Mt_position 163855-164016 82655-83959 118598-118816,119119 131932,132451-132579 62703-63179 29217-29422 199532-110225 92349-92572,92958-93 1414-1513,1624-1756 3848-3967 168836-169248 28556-28684	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-
60 65 70	Picey: Ref: Strand: NL posible 400861 401644 401747 402053 402013 402076 404170 405464 405454	Unique num Sequence: human chri Indicates D Indicates n Ref 9757505 8576138 9789672 8083229 6729581 8748904 9211494 7770611 9931752 9930793 7329374 7556875	source. The 7 moreover 22* NA strand froucleotide position Strand Plus Plus Minus Plus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	digit numbers in this colum Dunham, et al. (1999) Natu, n which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959 118598-118816, 119115 131932-132451-132575 62703-63179 92317-29422 109532-110225 92349-92572,92958-93 1414-1513, 1624-1756 3848-3967 168836-169248 28556-28684 133807-134053	ng 402-489-495. led. 9-119244,119609-119761,120422-120990,130161- 5,133580-134011 084,93579-93712,93949-94072,94591-94748,952	-130381,130468-130593,131097-131258,131866-
60 65	Pikey: Raf: Strand: NL posibic Pikey 400851 401644 401747 402053 402819 403055 403137 404076 404076 404170 405264	Unique nun Sequence : human chri Indicates D Indicates n Ref 9757505 8576138 9789672 8083229 6729581 8748904 9211494 7770611 9931752 9930793 7329374	pource. The 7 moreover 22* NA strand froucleotide position Strand Plus Plus Minus Plus Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	digit numbers in this colum Dunham, et al. (1999) Natu, n which exons were predictions of predicted exons. Nt_position 163855-164016 82655-83959 118598-118816, 119115 131932-132451-132575 62703-63179 92317-29422 109532-110225 92349-92572,92958-93 1414-1513, 1624-1756 3848-3967 168836-169248 28556-28684 133807-134053	ng 402:489-495. led. 9-119244,119609-119761,120422-120990,130161- 1,133580-134011	-130381,130468-130593,131097-131258,131866-

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER
Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and denominator were switched.

Pikey:

Linduce Eos probeset identifier number

Exacts:

Linduce Eos probeset identifier number

Unique enumber 80

	Unigena T R1:		ene gene title of turnor to nor	mal tissue	
_	Pkey	ExAcon	UnigenelD	Unigene Tide	RI
5	412859	NM_000705	Hs.813	ATPase, H+/K+ exchanging, beta polypepti	0.01
	415447	297171	Hs.78454	myocilin, trabecular meshwork inducible	0.05
	427469	AA403084	Hs.269347	ESTs	0.05
	407486	S69741		gb:hSCG-3=stomach cancer gene-3 (oncogen	0.06
10	428602	AL137479	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (1	0.06
10	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e	0.07
	443547	AW271273	Hs.23767	Homo sapiens cDNA FLJ12666 fls, clone NT	0.07
	430130	AL137311	Hs.234074	Homo sepiens mRNA; cDNA DKFZp761G02121 (	0.07
	435473	N53650	Hs.260881	ESTs	0.07
15	455826 402015	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	0.07
13	430664	AW969834		-L-F07001010101010	0.08
	444515	AW204908	Hs.169979	gb:EST381912 MAGE resequences, MAGK Horno ESTs	0.09
	429201	X03178	Hs.198246		0.09
	434424	AI811202	Hs.125385	group-specific component (vitamin D blnd Homo sapiens cDNA: FLJ23523 fis, clone L	0.10
20	450940	A1744943	Hs.300744	ESTs, Moderately similar to ALU7_HUMAN A	0.10 0.10
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	0.10
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	0.10
	403670			• • • • • • • • • • • • • • • • • • • •	0.11
25	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	0.12
25	407462	AJ252011		gb:Homo sapiens partial mRNA for amilori	0.13
	405110				0.13
	402760	44 000000	11. 10115		0.13
	408947 413724	AL080093	Hs.49117	Homo sepiens mRNA; cDNA DKFZp564N1662 (f	0.13
30	431514	AA131466 AW972383	Hs.23767	Homo sapiens cDNA FLJ12666 fls, clone NT	0.14
20	451103	R52804	Hs.25956	gb:EST384454 MAGE resequences, MAGL Homo	0.14
	452033	AW273741	Hs.246977	DKFZP564D206 protein ESTs	0.14
	440058	AJ932662	Hs.164073	ESTs	0.16
	405645			2013	0.16 0.17
35	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	0.17
	445627	AW818475	Hs.7363	ESTs	0.19
	425679	X05997	Hs.159177	lipase, gastric	0.19
	417296	L36196	Hs.81884	sulfotransferase family, cytosolio, 2A,	0.19
40	443537 435654	013305	Hs.203	cholecystokinin B receptor	0.20
40	406326	AW139612	Hs.131041	ESTs	0.20
	454120	AB032990	Hs.40719	Secretarian	0.20
	455541	AW993005	110.40713	hypothetical protein KIAA1164 gb:RC2-BN0032-160200-013-d04 BN0032 Homo	0.20
	453989	M63962	Hs.36992	ATPase, H+/K+ exchanging, alpha polypept	0.21 0.23
45	407261	L03172		gb:Homo sapiens cell-type T-cell immunog	0.23
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 [1	0.23
	429350	A1754634	Hs.131987	ESTs	0.23
	411021	F00055	Hs.172004	tiin	0.24
50	441212 450572	AW242447	Hs.146182	ESTs, Wealdy similar to lactase phlorizi	0.24
50	444922	A1700863 A1921750	Hs.202494	Homo sapiens cDNA FLJ13245 fis, clone OV	0.25
	421562	AA530994	Hs.144871 Hs.105803	Homo sapiens cDNA FLJ13752 fls, clone PL	0.26
	457432	NM_005136	Hs.268538	ghrelin precursor potassium voltage-gated channel, lsk-rel	0.26
	418421	R58620	Hs.85050	phospholamban	0.26
55	424104	AA669515	Hs.144950	ESTs	0.26 0.26
	422582	AA312660		gb:EST183335 Jurket T-cells VI Homo sepi	0.26
	417332	AW972717	Hs.288462	Homo sapiens cDNA: FLJ21511 fis, clone C	0.27
	432440	X63597	Hs.2996	sucrase-isomaltase	0.27
60	448520	AB002387	Hs.21355	doublecortin and CaM kinase-like 1	0.28
00	401989 452528				0.28
	412569	AA742457 H63789	Hs.291479 Hs.296288	ESTs	0.28
	434779	AF153815		ESTs, Wealdy similar to KIAA0638 protein	0.28
_	406255	m 199619	Hs. <b>50</b> 151	potassium inwardly-rectifying channel, s	0.28
65	419293	AA746282	Hs.255659	ESTs	0.29
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fts, clone PL	0.29
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	0.29 0.29
	414502	AL133721	Hs.224680	EST\$	0.29
20	432113	AA935065	Hs.152385	EST ₅	0.29
70	413808	J00287	Hs.182183	caldesmon 1	0.29
	451406	A1694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	0.29
	434745	AW974445 AI905985	Hs.185155	ESTs, Wealdy similar to HuEMAP (H.sapien	0.30
	420444 445200	A1905985 AA084460	Hs.111805	ESTs	0.30
75	415314	N88802	Hs.12409 Hs.5422	somatostatin	0.30
	427019	AA001732	Hs.173233	glycoprotein M68 hypothetical protein FLJ10970	0.30
	431152	AW970998		gb:EST383083 MAGE resequences, MAGK Horno	0.30
	432306	Y18207	Hs.274315	protein phosphatase 1, regulatory (inhib	0.30 0.31
90	401775			· · · · · · · · · · · · · · · · · · ·	0.31
80	440059	AW467335	Hs.257676	ESTs	0.31
	436089	AA804957	Hs.119840	ESTs	0.31
	447071 435604	AW236867 AA625279	Hs.244376 Hs.26892	ESTs	0.32
			· w.20034	uncharacterized bone marrow protein BM04	0.32



	423968	AF098277	Hs.136529	solute carrier family 23 (nucleobase tra	0.32
	445487	AI806287	Hs.201217	ESTs	0.32
	421296	NM_002668	Hs.103253	perilipin	0.32
5	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 28	0.33
)	449916	T50525	Hs.299221	ESTs	0.33
	446393	AW014174	Hs.151707	ESTs	0.33
	445632	AI333565	Hs.159073	diacylglycerol kinase, eta	0.33
	428070	T63918	Hs.182313	refinal-binding protein 2, cellular	0.33
10	421451	AA291377	Hs.50831	ESTs	0.33
10	405817	414000000		-b-D00 070001 400000 044 445 07000	0.33
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
	413679	BE156765		gb:RC1-HT0370-120100-012-009 HT0370 Homo	0.34
	404121	*****	11- 2022CC	Ends and Abba Para anneals de la south	0.34
15	433084 413079	M18079	Hs-282265	fatty acid binding protein 2, intestinal	0.34
13	403059	BE064382		gb:RC4-8T0310-110300-015-c12 BT0310 Homo	0.34
	458987	AW750067	I - 005000	COV.	0.35
	429609	AF002246	Hs.205386 Hs.210863	ESTs	0.35
	423371	AU076819	Hs.1650	cell adhesion molecule with homology to	0.35
20	424765	AA428211	Hs.284256	solute carrier family 26, member 3	0.35
20	451818	AI819018	NS.204230	hypothetical protein FLJ 14033 similar to	0.35
	438380	T06430	Hs.6194	gb:ts54f01.x1 NCI_CGAP_Kid8 Homo sapiens chondroitin suffate proteoglycan BEHAB/b	0.35
	405742	100-30	NS.0134	Cholicidan satistis proteogrycen och Abro	0.35
	403429				0.35 0.35
25	443622	AI911527	Hs.11805	ESTs	0.35
	404973	74311021	113.11003	2010	0.36
	444567	AV654020	Hs.184261	ESTs, Weakly similar to putative type II	0.36
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	0.35
	407110	AA018042	Hs.95078	ESTs	0.36
30	411671	BE049094	Hs.278567	ESTs	0.36
	430800	NM_000805	Hs.2681	gastrin	0.36
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	0.36
	444536	AI161068	Hs.14780	ESTs	0.36
	454042	H22570	Hs.172572	hypothetical protein FLJ20093	0.37
35	444102	AV647953	Hs.282379	ESTs	0.37
	424122	AA335593	Hs.116147	ESTs	0.37
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	0.37
	436277	R88520	Hs.120917	ESTs	0.37
	456350	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.37
40	451027	AW519204	Hs.40808	ESTs	0.37
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	0.38
	410023	AB017169	Hs.57929	stit (Drosophila) homolog 3	0.38
	436802	N34486	Hs.170504	ESTs	0.38
4.5	448142	AI521768	Hs.164586	ESTs	0.38
45	442378	R54033	Hs.21245	EST8	0.38
	446406	AI553681	Hs.25248	ESTs	0.38
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	0.38
	424903	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.38
50	406714	AJ219304	Hs.283108	hemoglobin, gamma G	0.39
50	434340	AJ193043	Hs.128685	ESTs	0.39
	406036				0.39
	431078	U82827	Hs.249195	homeo bax A13	0.39
	457663	AW371946	Hs.116119	ESTa	0.39
55	451880	AI821032	Hs.209387	ESTs	0.39
75	419219 446414	AW583139 W93248	Hs.89717	carboxypeptidase A2 (pancreatic)	0.39
	442317	AI915599	Hs.59187 Hs.129225	ESTs	0.39
	447261	NM_006691	Hs.17917	ESTs	0.39
	439569	AW602166	Hs.222399	lymphatic vessel endothelial hyaluronan CEGP1 protein	0.39
60	433485	AI493076	Hs.78183	aldo-keto reductase family 1, member C1	0.39 0.40
	432753	NM_014075	Hs.278915	PRO0593 protein	0.40 0.40
	420200	Al271429	Hs.88142	ESTs	0.40
	421853	AI952677	Hs.108972	Homo sapiens mRNA: cDNA DKFZo434P228 (fr	0.40
	453950	AA156998	Hs.211568	eukaryotic translation initiation factor	0.40
65	407408	AF054830		gb:Homo sapiens interleukin-1 type I rec	0.40
	410732	AW984328		gb:PM3-HN0010-050400-001-h12 HN0010 Homo	0.40
	458272	AJ797360	Hs.264899	ESTs. Weakly similar to ALU3_HUMAN ALU S	0.40
	401514	AF147188		gb:AF147186 Horno sepiens library (Schere	0.40
	436363	AA843926	Hs.124434	ESTs	0.40
70	434445	Al349306	Hs.11782	ESTs	0.40
	413272	AA127923	Hs.293256	ESTs	0.40
	409681	N51508	Hs.143718	ESTs	0.40
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.40
7.	450891	AI743118	Hs.238914	ESTs. Wealdy similar to neurogulin-4 sho	0.40
75	452078	AA022620	Hs.52170	ESTs	0.41
	419278	AU076799	Hs.1247	apolipoprotein A-IV	0.41
	433637	AW024214	Hs.135405	ESTS	0.41
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	0.41
00	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	0.41
80	453139	AA330620	Hs.240559	ESTs	0.41
	408614	AL137698	Hs.46531	Homo saplens mRNA; cDNA DKFZp434C1915 (f	0.41
	437931	A1249468	Hs.145274	ESTs	0.41
	402759				0.41

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	450888	AW021446	Hs.80714	<b>ESTs</b>	0.41
	417318	AW953937	Hs.12891	ESTs .	0.41
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	0.41
_	424884	AW299437	Hs.225717	ESTs	0.41
5	439024	R96696	Hs.35598	EST ₅	0.42
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	0.42
	409300	AA126190		gb:zm78f03.r1 Stratagene neuroepithelium	0.42
	444237	AA336878	Hs.9842	Human DNA sequence from clone RP4-788L20	0.42
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	
10	447021	AI356564	Hs.161406	ESTs	0.42
	422270	AF114494			0.42
	407850		Hs.114062	protein tyrosina phosphatase-like (profi	0.42
		AW086230	Hs.244912	ESTs	0.42
	449884	AI673110	Hs.222195	ESTs	0.42
15	436327	AA813075	Hs.120181	ESTs	0.42
13	415972	H11436	Hs.260201	ESTs	0.42
	400917				0.43
	435309	AW089050	Hs.187993	ESTs	0.43
	424410	W79027	Hs.271762	ESTs .	0.43
20	445577	N40696	Hs.146077	EST8	0.43
20	411069	AL133092	Hs.68055	hypothetical protein DKFZp434l0428	0.43
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	0.43
	451123	A1927224	Hs.213480	ESTs .	0.43
	457151	AW206116	Hs.253538	ESTs	0.43
	459185	AI908222		gb:RC-BT165-300399-020 BT165 Homo sapien	0.43
25	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	0.43
	424815	AA347287	Hs.104573	ESTs	0.43
	429704	AA584440	Hs.185812	ESTs	0.43
	411067	AI681006	Hs.301543	ESTs	0.43
	430172	AA468591	Hs.161889	ESTs	0.43
30	435124	AA725362	Hs.120456	ESTs	0.43
	445966	L17330	Hs.280	pre-T/NK cell associated protein	
	443741	AW451759	Hs.145420	ESTs	0.43
	416275	H42823	Hs.155742		0.43
	451138	W92287	Hs.40268	głyczylate reductase/hydroxypyruvate red	0.44
35	409038	T97490		ESTs	0.44
33	426730		Hs.50002	small inducible cytokine subfamily A (Cy	0.44
	410066	AL040738 AL117664	11- 50440	gb:DKFZp43481615_r1 434 (synonym; htes3)	0.44
	427965		Hs.58419	DKFZP586L2024 protein	0.44
		D00306	Hs.183864	elastase 38	0.44
40	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.44
40	408479	BE047329	Hs.144483	ESTa	0.44
	457994	AW136239	Hs.132922	ESTs	0.44
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dNT-2); nucl	0.45
	435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.45
AE	434399	AAB78845	Hs.125769	ESTs	0.45
45	415797	Al291896	Hs.72800	ESTs	0.45
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sagiens	0.45
	409435	AI810721	Hs.95424	ESTs	0.45
	433542	AA598869	Hs.173770	ESTs	0.45
	455400	AW936342		gb:QV4-DT0021-281299-070-h12 DT0021 Homo	0.45
50	412047	AA934589	Hs.49695	ESTs	0.45
	443948	T56148	Hs.9997	Homo sapiens mRNA full length Insert cDN	0.45
	450307	AW450336	Hs.201783	ESTs	0.45
	434500	AF143877	Hs.215047	Homo sapiens clone (MAGE:113431 mRNA seq	0.45
	420460	AA262331	Hs.135503	ESTs	0.45
55	450752	AA012986	Hs.60456	ESTs	0.45
	418138	AA213626	Hs.136204	EST	0.45
	441088	AA916548	Hs.126546	ESTs	0.46
	410990	AW812929		gb:RC3-ST0188-250200-018-c05 ST0186 Homo	0.46
	438211	T08401		gb:EST06292 Infant Brain, Bento Soares H	0.46
60	434349	NM_015678	Hs.3821	neurobeachin	0.46
-	409824	AW501063		gb:UI-HF-BP0p-eiz-c-01-0-UI.r1 NIH_MGC_5	0.46
	403279			Property of the Property of th	0.46 0.45
	434882	AW974752	Hs.269497	ESTs	
	404529		110.203431	E010	0.46
65	427393	A8029018	Hs.177635	MIAA1006	0.46
••	454651	AW812091	ns.117033	KIAA1095 protein qb:RC4-ST0173-191099-032-b04 ST0173 Homo	0.46
	401992	A11012031		80:WC4-2101/3-131039-032-004 2101/3 HOMO	0.46
		AA463422	11- 200424	COX	0.46
	457275 403710	~~~~~~~	Hs.209431	ESTs	0.46
70		4.00004			0.46
, 0	419728	L36861	Hs.92858	guanylate cyclase activator 1A (retina)	0.46
	401075				0.46
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	0.46
	453404	AA035446	Hs.261224	ESTs	0.46
75	407208	T10695	Hs.102948	enigma (LIM domain protein)	0.46
75	440681	AW449696	Hs.166547	ESTs	0.46
	454206	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	0.47
	402466				0.47
	429996	N90822	Hs.48969	ESTs	0.47
00	403680				0.47
80	428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapi	0.47
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	0.47
	402851				0.47
	438421	AAB06907	Hs.194451	ESTs	0.47
				<del>-</del>	V. **

# PCT/US02/29560

	454661	BE244138		gb:TCBAP1E1218 Pediatric pre-8 cell acut	0.47
	408753	A/337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.47
	409106 413199	AW337854 M62843	Hs.177386 Hs.75236	ESTs	0.47
5	442799	MD2043 ALS64739	Hs.68505	ELAV (embryonic lethal, abnormal vision,	0.47
3	457955	AI208986	Hs.143945	ESTs ESTs	0.47 0.47
	458147	AW752597	18.14040	abdL3-CT0214-161299-045-806 CT0214 Horno	0.47
	407938	AA905097	Hs.85050	phospholamban	0.47
	414141	BE255083		gb:601111390F1 NIH_MGC_16 Homo sapiens c	0.47
10	448869	AI792798	Hs.12496	ESTs	0.47
	400749				0.47
	458745	AW207347	Hs.211101	ESTs	0.48
	418437	AA771738	Hs.295351	ESTs	0.48
1.5	452286	A1358570	Hs.123933	ESTs	0.48
15	430369	AA477631	Hs.119484	ESTs .	0.48
	453572	AA382590	Hs.31848	ESTs, Weakly similar to hypothetical pro	0.48
	455175	AW993247	11- 443000	gb:RC2-BN0033-180200-014-h09 BN0033 Homo	0.48
	445765	AV655102 AF045576	Hs.117266	ESTs	0.48
20	400322 412526	M90366	Hs.247758 Hs.73982	offactory receptor, family 5, subfamily	0.48
20	407986	U32659	Hs.41724	zona pellucida glycoprotein 2 (sperm rec interleukin 17 (cytotoxic T-lymphocyte-a	0.48 0.48
	455479	AW948312	115.41724	ab:RCO-MT0015-280300-021-h04 MT0015 Homo	0.48
	450308	Al692571	Hs.201681	ESTs	0.48
	411149	N68715	Hs.269128	ESTS	0.48
25	453982	AW014252	Hs.252837	ESTS	0.48
	410971	AW812258		gb:RC0-ST0174-191099-031-b02 ST0174 Homo	0.48
	410839	NM_006849	Hs.66581	protein disuffide isomerase	0.48
	421553	AA536080	Hs.97302	ESTs	0.48
~~	442376	W95588	Hs.129982	Homo sapiens cONA FLJ12228 ffs, clone MA	0.48
30	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Hamo	0.48
	447858	AW080339	Hs.211911	ESTs	0.49
	422639	Al929377	Hs.173724	creatine kinase, brain	0.49
	402449				0.49
26	420440	NM_002407	Hs.97644	mammaglobin 2	0.49
35	435056	AW023337	Hs.5422	glycoprotein M68	0.49
	419543	AA244170	Hs.188719	ESTs	0.49
	407033	U78628		gb:Human leukemia inhibitory factor rece	0.49
	437468	AA457619		gb:ea89d11.r1 Stratagene fetal retina 93	0.49
40	412639	AW961284	Hs.296235	ESTs	0.49
40	406109				0.49
	404519 410285	44003000		-h	0.49
	406014	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	0.49
	400938				0.49 0.49
45	414290	AI568801	Hs.71721	ESTs	0.49
45	432433	AW014734	Hs.157969	ESTS	0.49
	405273	A11011134	113.137303	C310	0.49
	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.49
	414383	BE279406		gb:601157981F1 NIH_MGC_21 Homo sapiens c	0.49
50	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	451241	AI767545	Hs.209572	ESTs	0.49
	428336	AA503115	Hs.183752	microseminoprotein, beta-	0.49
	418310	AA814100	Hs.86693	ESTS	0.49
	452152	AL046755	Hs.28219	protein phosphatase 2 (formerly 2A), reg	0.49
55	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	0.49
	400332	\$66407	Hs.248032	FLT4	0.49
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	0.49
	408221	AA912183	Hs.47447	ESTs	0.49
60	440179	Al990151	Hs.125904	ESTs	0.50
UU	425360	BE547704		gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.50
	406600	41777007	15 403040	cor.	0.50
	418594 432128	A1732083 AA127221	Hs.187619	ESTs	0.50
	458611	A1268407	Hs.117037	ESTs	0.50
65	426495	NM_001151	Hs.211458	ESTs	0.50
05	441068	AA913897	Hs.2043 Hs.233559	solute carrier family 25 (mitochondrial ESTs	0.50 0.50
	428108	AA421452	Hs.164851	ESTs	
	400803	W451405	ris. 104631	C218	0.50 0.50
	439996	AA916565	Hs.221675	ESTs	0.50 0.50
70	100000	74131444	110.22.1013	6015	0.30
. •	TABLE 4	4R-			
	Pkey:		ique Eos probece	t identifier number	
	CAT nur		ne cluster number		
	Accessio			ession numbers	
75				' <del></del>	
_	Pkey	CAT numbe	r Accession		
	409300	111676_1		N074486 AA074707 AA070059 AA084885	
	409824	1155499_1		W503034 AW501523	
00	410285	119128_1		N083790 AA112048	
80	410495	1205826_1		040 AW751366 H81987	
	410732	1218556_1		W984322 AW984318 AW984330 R58427 AW984332 AW7998	
	410971	1228216_1		W812252 AW812261 AW812263 AW812285 AW812277 AW8	12264
	410990	1228649_1	AW812929 A	W812779 AW813088	

	*****			
	411607	1251251_1	AW853498 AV	WB53442 AWB53590 AWB53433 AWB53592
	413079	1348528_1		064387 BE064385 BE064381 BE153367 BE153366 BE153401 BE153385 BE064372
	413679	1382784_1	BE156765 BE	156770 BE156767 BE156769 BE156803 BE156802 BE156847 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779
_			BE156789 BE	156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
5	414141	1420715_1	BE255083 BE	
	414383	1440279_1	BE 279406 BE	280100
	422582	218132_1	AA312660 AI4	
	425360	250631_1	BE547704 AA	
	426730	271055_1	AL040738 AA	
10	428151	287658_1	AA422028 W	
10	430264			
		315008_1		303010 BE302954 BE384120
	430664	321423_1		AS28493 AA483165 AW969842
	431152	328675_1		W971004 AA574217 AA493538
15	431514	334213_1		A506335 A1077445
15	437468	43743_1	AA457619 AL	390167
	438211	45225_1	T08401 Z839	34 T16897
	449923	81926_1	BE258051 R4	I5758 AA004732 BE255126
	451818	887271_1	AI819018 RO	5492 W27615
	454206	1050848_1	AW810279 B	E145684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515
20				W810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263
				W810443 AW810198 AW810321 AW810265 AW810567 AW810447 AW810328 AW810513 BE146674 AW810257 AW810185 AW810281
				E062400 AW810323 AW810293 BE145652 AW810516 BE146689 AW810289 AW810566 AW810636 AW178842 BE062434 BE146563
			AW810536 A	
	454554	1223842_1		W811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156
25	404004	1223042_1	AMPRODA A	110 1 (1 32 DECO 142 DECO 1433 A1104/300 A1104/333 A1104/330 DECO 1430 DECO 1430 DE 142400 DE 142403 A1104/3 A1104/33 A1
23				W814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431
			BEU01435 AV	M847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330
				E051434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998
			BE061745 BE	
20	454560	1223940_1		W807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
30	454651	1228069_1	AW812091 A	W812228 AW812106 AW938581 AW812080
	454661	1228527_1	8E244138 81	E244727 AWB12636 AWB12647
	454738	1232449_1	BE072139 BI	E157977 BE157974 AW857974 AW817778
	454754	1233580_1		W819252 AW819183 AW819175 AW819177 AW819188 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265
				W819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454790	1234752_1		W820773 AW821088
	454869	1238137 1		W836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
				W836078 AW836161 AW862135 AW836165 AW836003
	455175	1257335_1	AW993247 A	
	455400	1288135_1	AW936342 A	
40	455479	1293163_1		W948266 AW948289 AW948297 AW948279 AW948295
70	455541			
		1323705_1		W993285 AW993290
	455753	1356070_1		E075229 BE075278
	455826	1373392_1	BE144228 B	
15	458147	488021_1		\W848781 AW849062 AW848490 AW752699 AW752604 AW752700
45	459185	922823_1	A1908222 AF	908224 AI908217
		_		
	TABLE 44			
	Pkey:	Unic	ine unuper cou	responding to an Eos probeset
50		Seq	uence source. `	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA
50	Pkey: Ref;	Seq	uence source. `	esponding to an ece proceser. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
50	Pkey:	Seq seq:	uence source. ' uence of human	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA
50	Pkey: Ref;	Seq sequ India	uence source. ' uence of human cates ONA stran	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
50	Pkey: Ref; Strand: Nt_positio	Seq sequ India	uence source. ' uence of human cates ONA stran	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Id from which exons were predicted.
	Pkey: Ref; Strand:	Seq sequ India	uence source. ' uence of human cates ONA stran	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  Id from which exons were predicted.  Positions of predicted exons.  NL_position
50 55	Pkey: Ref; Strand: Nt_positio	Seq sequ India in: India	uence source.  uence of human cates DNA strar cates nucleofide Strand	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  Id from which exons were predicted.  Positions of predicted exons.  NL_position
	Pkey: Ref: Strand: Nt_positio	Seq sequ India in: India Ref	uence source. ' Jence of human cates DNA strar cates nucleotide Strand Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Id from which exons were predicted. In positions of predicted exons.  Nil. position 9162-9293
	Pkey: Ref: Strand: Nt_positio Pkey 400749	Seq sequ India in: India Ref 7331445	uence source. ' uence of human cates DNA stran cates nucleotide Strand Minus Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Id from which exons were predicted. positions of predicted exons.  Nt_position 9162-9293 18267-19088
	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917	Seq seq: India n: India Ref 7331445 8567875 7283186	uence source. ' uence of human cates ONA strar cates nucleotide Strand Minus Minus Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA otherwise to the DNA oth
	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938	Seq seq; India n: India Ref 7331445 8567875 7283186 7652890	uence source. ` uence of human cates ONA strar cates nucleotide Strand Minus Minus Minus Minus Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  It from which exons were predicted.  Positions of predicted exons.  Nil position  9162-9293  18267-19088  173258-173631  92074-92423
55	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938 401075	Seq sequindia n: India Ref 7331445 8567875 7283186 7652890 3687273	uence source. ' uence of human cates ONA stran cates nucleotide Strand Minus Minus Minus Minus Minus Plus Plus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495. d from which exons were predicted. exons.  Ni_positions of predicted exons.  Ni_position 9162-9293 18257-19088 173258-173631 930774-92423 81218-81335
	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938 401075 401514	Seq sequ India n: India Ref 7331445 8567875 7283186 7652890 3687273 7622355	uence source. Lence of humanicates DNA strancates nucleotide Strand Minus Minus Minus Minus Plus Plus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA otherwise and predicted exons.  Nt_position 9162-9293   18257-19088   173258-173631   92074-92423   31218-81395   93224-93292-94913-95065,95163-95334
55	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938 401075 401775	Seq sequ India Ref 7331445 8567875 7283186 7652890 3687273 7622355 9966311	uence source. I uence of human zates NNA strar zates nucleofide Strand Minus Minus Minus Plus Plus Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA otherwise the chromosome 22" Dunham, et al." (1999) Nature 402:489-495.  Id from which exons were predicted.  Positions of predicted exons.  NI_position  9162-9293  18267-19068  173258-173631  92074-92423  81218-81395  93224-93292,94913-95065,95163-95334  110228-110340
55	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938 401075 401514 401775 401989	Seq sequindii Indii Ref 7331445 8567875 7283186 7652890 3687273 7622355 9966311 4309964	uence source, uence of human cates DNA strancates nucleofide Strand Minus Minus Minus Plus Plus Minus	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA othromosome 22" Dunham, et al. (1999) Natura 402:489-495.  Id from which exons were predicted.  Positions of predicted exons.  Ni_position 1162-9293 118267-19088 173258-173631 1792074-92423 181218-61395 19324-93292-94913-95065,95163-95334 110228-110340 110228-110340
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<ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>	Pkey: Ref: Strand: Nt_position Pkey 400749 400803 400917 400938 401075 401514 40175 401989 401992 402015 402049 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40205 40	Seq sequi India India Ref 7331445 8567875 7283186 7552890 3687273 7622355 9965311 4309964 4153858 7417802 9796674 9796919 9213869 9650753 8954192 8072597 9719566 7259739 7331517 6437516 9796219 8152000 9796665 3213020 8095688	uence source	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA ot normosome 22" Dunham, et al. (1999) Natura 402:489-495.  Id from which exons were predicted.  positions of predicted exons.  Ni_position 18267-19088 173258-173631 92074-92423 1218-81395 93224-93292_94913-95065,95163-95334 110228-110340 110228-110340 110621-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 99887-60099,62588-5280,63465-63623,64923-65108 57659-57866,58839-58908 134117-134281 138829-13952_1373356-137521 63022-63136,63683-63783 99553-69702 162569-162768,163918-164168 52789-52917 88377-88537 157184-157415 27413-28978 99256-59401 12817-13000 55584-55796 101602-102591 118840-119100
55 60 65 70 75	Pkey: Ref: Strand: Nt_positio Pkey 400749 400803 400917 400938 4019075 401514 401775 401989 401973 402449 402469 402759 402759 402759 403770 403880 403710 404121 404529 404973 40519 405273	Seq sequindi India Ref 7331445 8567875 7283186 7652890 3687273 7622355 9966311 4309964 4153858 7417802 9796674 9796919 9213869 9213869 9650753 8954192 8072597 9719566 7259739 7331517 6437516 9796219 8152000 9796665 3213020 8096888 4156137	uence source, and expense of humanizates DNA strand attes nucleofide Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA ot from which exons were predicted.  In chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  In this column are greated exons.  Nt_position 9162-9293 18267-19088 173258-173631 92074-92423 181218-81395 18218-81395 18218-81395 18218-81395 18218-81395 18324-93292-94913-95065,95163-95334 110228-110340 118611-118821 31452-31649 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 59867-60009,62588-52828,63465-63623,64923-65108 57569-57866,5839-58908 134117-134281 136829-136952,137336-137521 136829-136952,137336-137521 136928-136952,137336-137521 136928-136952-137738-137521 157184-157415 27413-28978 19526-59401 12817-13000 55584-55796 101602-102591 118940-119100 93141-98754
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	405817	4071056	Plus	19914-20112,25655-25810
	406014	6758904	Minus	23738-24076
	406036	6758919	Plus	17942-18163
_	406109	9127147	Minus	58328-58485
5	406255	7417729	Ptus	2959-3200
	406326	9212385	Plus	84508-84655
	406600	8248616	Minus	36296-36610

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TABLE 45A: ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES

Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Aflymetrix/Eos Hu/03

GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" stomach cancer level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levets of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play:

Unique Eos probeset identifier number

Exacm:

Unique Eos probeset identifier number

Unique Table:

Unique Fate:

Unique a gene title

Ratio of stomach cancer compared to normal stomach

15

20

	Pkey	ExAcon	UnigenelD	Unigene Title	R1
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	66.80
0.0	411243	AB039886	Hs.69319	CA11	61.16
25	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	42.36
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	35.80
	425679	X05997	Hs.159177	lipase, gastric	28.34
	409041	AB033025	Hs.50081	KIAA1199 protein	26.91
30	452121	NM_004081	Hs.70936	deleted in azoospermia	26.22
30	403776	44/004 400	11. 60400	NA .	25.00
	444783 422956	AK001468 BE545072	Hs.62180 Hs.122579	anilin (Drosophila Scraps homolog), act	23.90
	409187	AF154830	Hs.50966	hypothetical protein FLJ10461	23.90
	424252	AK000520	Hs.143811	carbamoyl-phosphate synthetase 1, mitoch	23.35
35	439759	AL359055	Hs.67709	hypothetical protein FLJ20513 Homo sapiens mRNA full length insert cDN	22.26 21.06
	415989	AI267700	Hs.317584	ESTs	20.72
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeas), h	19.84
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	15.50
	438639	AJ278360	Hs.31409	ESTs	15.16
40	426427	M86699	Hs.169840	TTK protein kinase	14.54
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	14.26
	443211	Al128388	Hs.143655	ESTs	14.22
	421470	R27496	Hs.1378	annexin A3	13.96
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	13.94
45	424086	Al351010	Hs.102267	lysyl oxidase	13.73
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.38
	409757	NM_001898	Hs.123114	cystatin SN	13.33
	447033	Al357412	Hs.157601	ESTs	13.20
60	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	12.80
50	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	12.66
	432596	AJ224741	Hs.278461	matrilin 3	12.64
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	12.46
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	12.32
55	423020 448693	AA383092	Hs.1608	replication protein A3 (14kD)	12.18
55	442660	AW004854 AW138174	Hs.228320	hypothetical protein FLJ23537	11.74
	441693	AA384673	Hs.130651 Hs.7943	ESTs RPB5-mediating protein	11.73
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	11.16 11.08
	414142	AW368397	Hs.150042	Homo sapiens cONA FLJ14438 fis, clone HE	10.90
60	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.48
	443715	AI583187	Hs.9700	cyclin E1	10.44
	420900	AL045633	Hs.44269	ESTs	10.38
	453922	AF053308	Hs.36708	budding uninhibited by benzimidazotes 1	10.36
	415076	NM 000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.20
65	452291	AF015592	Hs.28853	COC7 (cell division cycle 7, S. cerevisi	10.18
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	10.14
	414422	AA147224	Hs.337232	ESTs	10.12
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.02
70	414972	BE263782	Hs.77695	KIAA0008 gene product	10.02
70	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	9.80
	428365	AA295331	Hs.183861	Homo sepiens cDNA FLJ20042 fis, clone CO	9.72
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.68
	400195	NA		NA	9.66
75	418738	AW388533	Hs.6682	solute carrier family 7, (cationic amino	9.64
15	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	9.60
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	9.58
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	9.34
	446998 429485	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (1	9.26
80	429486 428227	AF155827 AA321649	Hs.203963	hypothetical protein FLJ 10339	9.16
50	431810	X67155	Hs.2248 Hs.270845	small Inducible cytokine subfamily B (Cy	8.95
	419261	X07876	Hs.89791	kinesin-like 5 (mitotic kinesin-like pro wingless-type MMTV integration site fami	8.84
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.80 8.78
			. 10. 102211	and a serial tales a free had resulted	0.70

	424834	AK001432	Hs.153408	Morno conince allata El Lagraga a	
	413268	AL039079	Hs.75256	Homo sapiens cDNA FLJ10570 fls, clone NT regulator of G-protein signating 1	8.69 8.68
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	8.68
_	452461	N78223	Hs.108106	transcription factor	8.68
5	425916	NM_006786	Hs.162200	urotensin 2	8.64
	42 <i>2</i> 805 438394	AA435989	Hs.121017	HZA histone family, member A	8.54
	441377	BE379623 BE218239	Hs.27693 Hs.202656	peptidylprolyl isomerase (cyclophāin)-l ESTs	8.52
	445891	AW391342	Hs.199460	ESTs	8.41 8.31
10	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.30
	439521	A1808955	Hs.58248	ESTs	8.30
	425087	R62424	Hs.126059	ESTs	8.28
	424653 441795	AW977534 N58115	Hs.151469	calcium/calmodulin-dependent serine prot	6.22
15	427878	C05766	Hs.21137 Hs.181022	AD024 protein CGI-07 protein	8.02 8.00
	413583	AL120806	Hs.5888	ESTs	7.98
	407853	AA338797	Hs.40499	dickkopf (Xenopus taevis) homolog 1	7.98
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	7.97
20	404996 400289	V07020	44- 2050	NA	7.96
20	410044	X07820 BE566742	Hs.2258 Hs.58169	matrix metalloproteinase 10 (strometysin highly expressed in cancer, rich in leuc	7.96
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.94 7.92
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	7.91
25	418895	AA894638	Hs.14600	ESTs	7.90
25	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	7.88
	423123 434539	NM_012247 AW748078	Hs.124027 Hs.214410	SELENOPHOSPHATE SYNTHETASE; Human selen	7.82
	447505	AL049266	Hs.18724	ESTs, Weakly similar to MUC2_HUMAN MUCIN Homo sapiens mRNA; cDNA DKFZp564F093 (tr	7.80 7.72
20	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.70
30	447289	AW247017	Hs.36978	metanoma antigen, family A, 3	7.70
	443354	AW970672	Hs.9247	protein klnase, AMP-activated, alpha 1 c	7.69
	427718 434032	AJ798680 AW009951	Hs.25933 Hs.206892	EST8 ESTs	7.66
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	7.60 7.58
35	450480	X82125	Hs.25040	zinc finger protein 239	7.51
	418678	NM_001327	Hs.167379	cancer/testis antigen	7.49
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	7.44
	452705 443846	H49805 Al085198	Hs.246005	ESTs	7.36
40	425420	BE536911	Hs.164226 Hs.234545	ESTs hypothetical protein NUF2R	7.32 7.30
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	7.28
	421155	H87879	Hs.102267	lysyl oxidase	7.24
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.24
45	447254 435473	NM_004153 NS3550	Hs.17908	origin recognition complex, subunit 1 (y	7.22
73	413293	AL047483	Hs.260881 Hs.302498	ESTs GTP-binding protein homologous to Saccha	7.20
	449347	AV649748	Hs.295901	KIAA0493 protein	7.14 7.11
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.11
50	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.11
30	408660 453688	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	7.10
	426890	AW381270 AA393167	Hs.194110 Hs.41294	hypothetical protein PRO2730 ESTs	7.02
	404440	7000.01	14,412,54	NA	6.98 6.97
~ ~	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.96
55	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.95
	413833 426249	Z15005 F05422	Hs.75573	centromere protein E (312kD)	6.94
	441421	AA356792	Hs.168352 Hs.334824	nucleoporin-like protein 1 hypothetical protein FLJ14825	6.94
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.92 6.85
60	423903	M57765	Hs.1721	interleukin 11	6.84
	431041	AA490967	Hs.197955	KIAA0704 protein	6.74
	417256 426921	U94332 AA037145	Hs.81791 Hs.172865	tumor necrosis factor receptor superfami	6.74
	407771	AL138272	Hs.62713	cleavage stimulation factor, 3 pre-RNA, ESTs	6.70
65	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.69 6.66
	407162	N63855	Hs.142634	zinc finger protein	6.64
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	6.64
	427920	Z11502	Hs.181107	annexin A13	6.59
70	450159 427401	AJ702416 U20582	Hs.200771 Hs.2149	ESTs, Moderately similar to A Chain A, T actin like protein	6.58
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	6.55 6.54
	431806	AF186114	Hs.270737	turnor necrosis factor (figand) superfami	6.54
	435159	AA668879	Hs.116649	ESTs	6.54
75	440209 418134	H05049	Hs.22269	neurexin 3	6.54
	451807	AA397769 W52854	Hs.86617 Hs.27099	ESTS	6.50
	434894	AW977850	Hs.23856	hypothetical protein FLJ23293 similar to hypothetical protein MGC5297	6.47 6.40
	422505	AL120862	Hs.124165	ESTs	6.34
80	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	6.32
30	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	6.31
	408380 420218	AF123050 AW958037	Hs.44532 Hs.286	diubiquitin	6.31
	405817	NA NA	113.200	ribosomal protein t.4 NA	6.29 6.29
					6.28

	406747	AJ925153	Hs.217493	annexin A2	6.24
	448743 434636	A8032962	Hs.21896	KIAA1138 protein	6.24
_	424602	AA083764 AK002055	Hs.6101 Hs.151046	hypothetical protein MGC3178 hypothetical protein FLJ11193	6.20 6.17
5	412661	N32860	Hs.24611	ESTs. Weakly similar to 154374 gene NF2	6.17
	401644 423248	AA380177	Hs.125845	NA	6.16
	427335	AA448542	Hs.251677	ribulose-5-phosphate-3-epimerase G antigen 78	6.13 6.12
10	450375	AA009647	Hs.8850	a disintagrin and metafloproteinase doma	6.07
10	422420 419752	U03398 AA249573	Hs.1524 Hs.152618	tumor necrosis factor (ligand) superfami	6.06
	413573	A1733859	Hs.149089	ESTs, Moderately similar to ZN91_HUMAN 2 ESTs	6.06 6.06
	408758	NM_003686	Hs.47504	exonuclease 1	6.02
15	444188 407746	Al393165 AK001962	Hs.699 Hs.38114	peptidylprolyl isomerase B (cyclophilin hypothetical protein FLJ11100	6.02 6.00
	446364	AB006624	Hs.14912	KIAA0286 protein	5.98
	418939	AW630603	Hs.89497	lamin B1	5.90
	424839 434377	AI917494 AW137148	Hs.9812 Hs.306593	Homo sapiens cDNA FLJ14388 ffs, clone HE Homo sapiens cDNA FLJ11382 ffs, clone HE	5.88 5.86
20	419863	AW952691	Hs.93485	Homo sepiens mRNA; cDNA DKFZp761D191 (fr	5.84
	430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.82
	428822 448776	W28418 BE302464	Hs.30715 Hs.30057	potassium voltage-gated channel, tst-rel MRS2 (S. cerevisiae)-like, magnesium hom	5.80 5.74
26	442957	Al949952	Hs.49397	ESTs	5.72
25	444577 424565	AI207721 AW102723	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.72
	433330	AW207084	Hs.75295 Hs.132816	guanylate cyclase 1, soluble, atpha 3 hypothetical protein MGC14801	5.71 5.68
	428618	AA885360	Hs.160199	NADPH oxidase, EF hand calcium-binding d	5.68
30	432867 412140	AW016936 AA219691	Hs.233364 Hs.73625	ESTs	5.64
50	433133	AB027249	Hs.104741	RAB6 Interacting, kinesin-like (rabkines PDZ-binding kinase; T-cell originated pr	5.63 5.62
	418379	AA218940	Hs.137516	fidgetin-like 1	5.57
	434551 442353	BE387162 BE379594	Hs.280858 Hs.49136	ESTs, Highly similar to A35661 DNA excis ESTs, Moderately similar to ALU7_HUMAN A	5.57 5.56
35	427386	AW836261	Hs.337717	ESTs	5.54
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.52
	428479 449370	Y00272 AK002114	Hs.184572 Hs.23495	cell division cycle 2, G1 to S and G2 to hypothetical protein FLJ11252	5.51 5.50
40	431118	BE264901	Hs.250502	carbonic anhydrase VIII	5.50
40	423673 453931	BE003054 AL121278	Hs.1695	matrix metalloproteinase 12 (macrophage	5.50
	409044	Al129586	Hs.25144 Hs.33033	ESTs hypothetical protein FLJ14623	5.49 5.48
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.45
45	448336 454018	R53848 AW016892	Hs.44976 Hs.100855	ESTs ESTs	5.44
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	5.42 5.42
	412246	AI150873	Hs.69233	zinc finger protein	5.40
	432193 437319	AA372264 BE410958	Hs.273193 Hs.56406	hypothetical protein FLJ10706 Homo sapiens cONA FLJ13549 fis, clone PL	5.40 5.40
50	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.40
	452862 409327	AW378065	Hs.8687	ESTs	5.38
	412811	L41162 H06382	Hs.53563 Hs.21400	collagen, type tX, alpha 3 ESTs	5.36 5.34
55	448390	AL035414	Hs.21068	hypothetical protein	5.32
55	428187 450434	AI687303 AA166950	Hs.285529 Hs.195870	G protein-coupled receptor 49 hypothetical protein FLJ14991	5.30 5.29
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	5.29
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	5.27
60	446638 444743	AL133063 AAD45648	Hs.15783 Hs.301957	Homo sapiens mRNA; cDNA DKFZp434P1115 (f nudix (nucleoside diphosphate linked mol	5.26 5.25
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	5.24
	452150 432865	W42490 AJ753709	Hs.260844 Hs.152484	ESTS	5.24
	453382	AA709285	Hs.5997	ESTs, Wealdy similar to I38022 hypotheti hypothetical protein FLJ13078	5.24 5.22
65	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	5.22
	426518 453884	Z43039 AA355925	Hs.170198 Hs.36232	KIAA0009 gene product	5.22
	429625	AA455568	Hs.193814	KIAAD185 gene product ESTs	5.20 5.20
70	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	5.20
,,	449318 444059	AW236021 R69743	Hs.78531 Hs.116774	Homo sapiens, Similar to RIKEN cDNA 5730 integrin, atpha 1	5.19 5.18
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	5.17
	412719 444342	AW016610 NM_014398	Hs.129911 Hs.10887	ESTs	5.15
75	425739	T19016	Hs.159410	similar to lysosome-associated membrane molybdopterin synthase sulfurylase	5,14 5.12
	452198	A1097560	Hs.61210	ESTs, Wealty similar to 138022 hypotheti	5.12
	445657 434699	AW812141 AA643687	Hs.279575 Hs.149425		5.10
00	424296	AI631874	Hs.155140		5.09 5.08
80	441645	A1222279	Hs.201555	ESTs, Wealty similar to T23406 hypotheti	5.06
	412723 448811	AA648459 Al590371	Hs.335951 Hs.174759		5.06 5.05
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.04

	411835	U29343	Hs.72550	husbannan madistrat marris	
	421373	AA808229	Hs.167771	hyaluronan-mediated motility receptor (R ESTs	5.04 5.04
	448991	AW771565	Hs.189594	ESTS	5.02
-	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	5.00
5	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.98
	405770 421110	AJ250717	Hs.1355	NA	4.96
	452588	AA889120	Hs.110637	cathepsin E homeo box A10	4.96 4.92
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.92
10	420952	AA282067	Hs.88972	ESTs. Moderately similar to A46010 X-fin	4.88
	408321	AW405882	Hs.44205	cortistatin	4.87
	441801 450568	AW242799 AL050078	Hs.86366	ESTs	4.84
•	452909	NM_015368	Hs.25159 Hs.30985	Homo sapiens cONA FLJ10784 fis, clone NT pannexin 1	4.83 4.82
15	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.82
	451105	A1761324	_	gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	4.80
	418203 418994	X54942 AA296520	Hs.83758 Hs.89546	CDC28 protein kinase 2	4.80
20	436982	AB018305	Hs.5378	selectin E (endothelial adhesion molecul spondin 1, (f-spondin) extracellular mat	4.78 4.78
•	432874	W94322	Hs.279651	melanoma inhibitory activity	4.78
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.78
	431956 442980	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.77
25	432437	AA857025 W07088	Hs.8878 Hs.293685	kinesin-like 1 ESTs	4.76
	414869	AA157291	Hs.21479	ubinuclein 1	4.76 4.74
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	4.74
	418380	AA425473	Hs.84429	KIAA0971 protein	4.74
30	419343 418478	AA456245 U38945	Hs.85603 Hs.1174	down-regulated by Ctrinb1, a	4.74
	425813	AA364136	Hs.210553	cyclin-dependent kinase inhibitor 2A (me hypothetical protein DKFZp7611172	4.72 4.71
	425071	NM_013989	Hs.154424	delodinase, lodothyronine, type ()	4.71
	412733	AA984472	Hs.74554	KIAA0080 protein	4.68
35	444325 407638	AW152618 AJ404572	Hs.16757	ESTs	4.66
	430345	AK000282	Hs.334483 Hs.239681	hypothetical protein FLJ23571 hypothetical protein FLJ20275	4.66 4.66
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.64
	449448	D60730	Hs.57471	ESTs	4.62
40	409732 432415	NM_016122 T16971	Hs.58148 Hs.289014	NY-REN-58 antigen	4.62
. •	421987	AJ133161	Hs.286131	ESTs, Wealthy similar to A43932 mucin 2 p CGI-101 protein	4.62 4.60
	430217	N47863	Hs.336901	ribosomal protein S24	4.58
	429597 425932	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	4.57
45	408728	M81650 AL137379	Hs.1968 Hs.47125	semenogelin I hypothetical protein FLJ13912	4.57
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	4.56 4.55
	451254	A1571016	Hs.172967	ESTs	4.54
	422426 439483	W79117 T69980	Hs.58559 Hs.58323	ESTS	4,54
50	435420	AI928513	Hs.59203	Homo sapiens cDNA FLJ11613 fis, clone HE ESTs	4.53 4.53
	447519	U48258	Hs.339665	ESTs	4.52
	424176	AL137273	Hs.142307	hypothetical protein	4.52
	414812 438069	X72755 N80701	Hs.77367 Hs.33790	monokine induced by gamma interferon ESTs	4.51
55	450096	A1682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	4.50 4.50
	438159	Z83947		gb:H.sapiens mRNA; clone CD 117	4.50
	433925	Al183551	Hs.26481	S8BI26 protein	4.48
	417866 433384	AW067903 Al021992	Hs.82772 Hs.124244	collagen, type XI, atpha 1 ESTs	4.48
60	421863	AI952677	Hs.108972	Homo sepiens mRNA; cDNA DKFZp434P228 (tr	4.47 4.47
	453941	U39817	Hs.36820	Bloom syndrome	4.45
	423401	NM_001992	Hs.128087	coagulation factor (I (thrombin) recepto	4.44
	430510 424084	AW162916 AI940675	Hs.241576 Hs.20914	hypothetical protein PRO2577	4.43
65	459587	AA031956	N3.2V314	hypothetical protein FLJ23056 gb:zk15e04.s1 Soares_pregnant_uterus_NbH	4.42 4.42
	417956	AA210704	Hs.190465	ESTs	4.42
	449433	AJ672096	Hs.9012	ESTs, Weakly similar to \$26650 DNA-bindi	4.42
	421477 406687	A1904743 M31126	Hs.104650	hypothetical protein FLJ10292	4.42
70	451813	NM_016117	Hs.272620 Hs.27182	pregnancy specific beta-1-glycoprotein 9 phospholipase A2-activating protein	4.41
-	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.41 4.40
	425142	AW954397	Hs.154762	HTV-1 rev binding protein 2	4.40
	441720	A1346487	Hs.28739	ESTs	4.40
75	409683 411571	U33317 AA122393	Hs.711 Hs.70811	defensin, alpha 6, Paneth cell-specific hypothetical protein FLJ20516	4.39
-	430044	AA454510	Hs.152812	ESTs	4.38 4.37
	436246	AW450963	Hs.119991	ESTs	4.37
	409582 453652	R27430	Hs.271565	ESTs	4.37
80	453652 425211	AW009640 M18667	Hs.28368 Hs.1867	ESTs, Moderately similar to \$65657 alpha	4.35
	448692	AW013907	Hs.167531	progastricsin (pepsinogen C) methylcrotonoyl-Coenzyme A carboxylase 2	4.34
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.34
	442470	AW273860	Hs.5759	ESTs	4.33

	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	4.32
	422867	L32137	Hs.1584	cartilage ofigomeric matrix protein (pse	4.31
	436396	A1683487	Hs.152213	wingless-type MMTV integration sita fami	4.31
5	433397 417576	AW079768	Hs.134880	ESTs, Wealty similar to unnamed protein	4.30
,	413278	AA339449 BE563085	Hs.82285 Hs.833	phosphoribosylglycinamide formyltransfer	4.29
	451592	AI805416	Hs.213897	interferon-stimulated protein, 15 kDa ESTs	4.29 4.28
	453900	AW003582	Hs.226414	ESTs. Wealthy similar to ALUS_HUMAN ALU S	4.28
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.26
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	4.26
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	4.24
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.23
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	4.22
16	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4,21
15	445640	AW969626	Hs.31704	ESTs, Wealty similar to KIAAD227 [H.sapi	4.20
	422232 442655	D43945	Hs.113274	transcription factor EC	4.18
	444381	AW027457 BE387335	Hs.30323 Hs.283713	ESTs, Wealdy similar to B34087 hypotheti	4.18
	434217	AW014795	Hs.23349	ESTs, Wealdy similar to S64054 hypotheti ESTs	4.16
20	413384	NM_000401	Hs.75334	exostoses (multiple) 2	4.16 4.14
	407768	AW002841	Hs.29475	ESTs	4.14
	419168	Al338132	Hs.33718	Homo sapiens cONA FLJ12641 fis, clone NT	4.13
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	4.12
25	443691	AI081724	Hs.17267	ESTs	4.12
25	409640	U78722	Hs.55481	zinc finger protein 165	4.12
	438176	AW138970	Hs.122113	ESTs	4.10
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	4.10
	419606 452824	AW294795 W27643	Hs.198529	ESTs	4.08
30	414152	NM_003248	Hs.73965 Hs.75774	splicing factor, arginine/serine-rich 2 thrombospondin 4	4.08
	418688	T85017	Hs.1192	KIAA0074 protein	4.08 4.07
	404253		1.5.1152	NA Protesti	4.06
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	4.06
0.5	428218	AA424266	Hs.123642	EphA3	4.06
35	428858	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	4.06
	428336	AA503115	Hs.183752	microseminoprotein, beta-	4.05
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.04
	421841	AA908197	Hs.108850	MAK-related kinase	4.04
40	451177 425188	AI969716 AK002052	Hs.13034	ESTs	4.04
70	421262	AA286746	Hs.155071 Hs.9343	hypothetical protein FLJ11190 Homo sapiens cDNA FLJ14265 fis, clone PL	4.04
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	4.03 4.02
	438777	AA825487	Hs.142179	ESTs	4.02
	423343	AA324643	Hs.246106	ESTs	4.02
45	425788	BE466417	Hs.231899	ESTs, Wealty similar to rab3 effector-6	4.02
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.01
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	4.01
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	4.00
50	433225	AW816515	Hs.173540	ATPase, Class V, type 100	4.00
20	411765 452022	H43346 AW072330	U- 202075	gbyp09a04.r1 Soares breast 3NbHBst Homo	4.00
	451806	NM_003729	Hs.293875 Hs.27076	ESTs	4.00
	423541	AA296922	Hs.129778	RNA 3-terminal phosphate cyclase gastrointestinal peptide	3.99 3.99
	414132	AI801235	Ha.48480	ESTs	3.99
55	452453	AI902519		gb:QV-8T009-101198-051 8T009 Homo sapien	3.98
	418454	AA315308	Hs.195870	hypothetical protein FLJ 14991	3.98
	430134	BE380149	Hs.105223	ESTs, Wealdy similar to T33188 hypotheti	3.98
	453160	AI263307	Hs.239884	H2B histone family, member L	3.97
60	417235	AA810278	Hs.24250	ESTs	3.96
50	425398 414136	AL049689 AA812434	Hs.156369	hypothetical protein similar to tenascin	3.95
	436608	AA628980	Hs.119023 Hs.192371	SMC2 (structural maintenance of chromoso	3.94
	431753	X76029	Hs.2841	down syndrome critical region protein DS neuromedin U	3.94 3.94
	453161	AA628608	Hs.61656	ESTs	3.94
65	454821	AW833504		gb:QV4-TT0008-091199-025-f03 TT0008 Homo	3.94
	427961	AW293165	Hs.143134	ESTs	3.94
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.93
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.93
70	418396	A1765805	Hs.26691	ESTs	3.92
70	451411	AAD17492	Hs.135655	EST	3.92
	445885 407698	A1734009 AA058900	Hs.127699		3.92
	407696 442896	R37725	Hs.32646 Hs.261108	hypothetical protein FLJ21901	3.91
_	433361	AW469373	Hs.300141	ESTs	3.90
75	419926	AW900992	Hs.93796	ribosomal protein L39 DKF2P586D2223 protein	3.90
• -	413775	AW409934	Hs.75528	nucleolar GTPase	3.89 3.88
	452943	BE247449	Hs.31082	hypothetical protein FLJ10S25	3.86
	428549	AA430064	Hs.220929	Homo sepiens cDNA FLJ14369 fis, clone HE	3.86
٥٨	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	3.86
80	452194	AI594413	Hs.332649	offactory receptor, family 2, subfamily	3.85
	421247	BE391727	Hs.102910		3.85
	417720	AA205625	Hs.208067		3.85
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	3.84

	430899	BE018217	Hs.183528	hundhatiant protein EL 114000	204
	421246	AW582962	Hs.102897	hypothetical protein FLJ14906 CGI-47 protein	3.84 3.83
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	3.83
-	428698	AA852773	Hs.334838	KIAA1866 protein	3.82
5	435202	AI971313	Hs.170204	KIAA0551 protein	3.82
	454074	R63503	Hs.28419	EST ₅	3.82
	448917 410507	A1583598 AA355288	Hs.201615 Hs.40834	ESTs	3.82
	452571	W31518	Hs.34665	transitional epithelia response protein ESTs	3.82 3.82
10	445663	AJ247343	Hs.149232	ESTs	3.82
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ 12280 fis, clone MA	3.80
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	3.80
	425656	AB018284	Hs.158688	KIAA0741 gene product	3.80
15	407168	R45175	Hs.117183	ESTs	3.79
כו	403422 425492	NA AL021918	Hs.158174	NA	3.79
	432239	X81334	Hs.2936	zinc finger protein 184 (Kruppel-like) matrix metafloproteinase 13 (collagenase	3.79 3.79
	457325	AA744550	Hs.136345	ESTs	3.78
••	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	3.77
20	428865	BE544095	Hs.164960	Bartt-like homeobox 1	3.76
	424188	AW954552	Hs.142634	zinc finger protein	3.75
	424638	AJ472106	Hs.49303	Homo saplens cDNA FLJ11663 fis, clone HE	3.75
	451099 448105	R\$2795 AW591433	Hs.25954 Hs.298241	interleukin 13 receptor, alpha 2	3.75
25	452785	AL359942	Hs.296434	Transmembrane protease, serine 3 erythroid differentiation and denucleati	. 3.74 3.74
	459000	AA903705	Hs.4190	Homo sepiens cDNA: FLJ23269 fis, clone C	3.74
	432653	N62096	Hs.293185	ESTs. Weakly similar to JC7328 amino aci	3.73
	409632	W74001	Hs.55279	serina (or cysteine) proteinase inhibito	3.73
30	414883	AA926960	Hs.334883	CDC28 protein kinase 1	3.73
30	415064	AA159804	Hs.149305	hypothetical protein MGC2603	3.72
	432198 458194	AI475306 AW383618	Hs.50458 Hs.265459	ESTs ESTs, Moderately similar to ALU2_HUMAN A	3.72 3.72
	415263	AA948033	Hs.130853	ESTS	3.71
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.71
35	408460	AA054726	Hs.285574	ESTs	3.71
	437496	AA452378	Hs.170144	Homo seplens mRNA; cDNA DKFZp547J125 (fr	3.70
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.68
	432021 420092	AA524470 AA814043	Hs.58753 Hs.88045	ESTs ESTs	3.68
40	414923	AW445008	Hs.77637	homeo box A4	3.68 3.68
	429432	Al678059	Hs.202676	synaptonemal complex protein 2	3.68
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.67
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.67
45	432542	AW083920	Hs.16098	claudin 2	3.67
43	410782 421106	AW504860 AA877124	Hs.288836	hypothetical protein FLJ12673	3.66
	439107	AL046134	Hs.172844 Hs.13944	ESTs adrenergic, beta, receptor kinase 2	3.64 3.64
	418735	N48769	Hs.44609	ESTS	3.64
	411598	BE336654	Hs.70937	H3 histone family, member A	3.63
50	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase 8	3.63
	436411	AW67#352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.63
	429774 448844	AI522215	Hs.50883	KIAA1804 protein	3.62
	402473	AI581519 AB033035	Hs.177164 Hs.51965	ESTs	3.61
55	441085	AW136551	Hs.181245	KIAA1209 protein Homo sapiens cDNA FLJ12532 ffs, clone NT	3.61 3.61
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.60
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.60
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.59
60	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.59
UU	451381 428664	BE241831 AK001666	Hs.172330 Hs.189095	hypothetical protein MGC2705	3.58
	424345	AK001380	Hs.145479	similar to SALL1 (sal (Drosophila)-like Homo sapiens cDNA FLJ10518 fis, clone NT	3.58 3.58
	440717	AA904527	Hs.42207	ESTs	3.58
	450698	W31489	Hs.95044	ESTs. Wealty similar to 138022 hypotheti	3.58
65	423675	A1990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.58
	424882	AJ379461	Hs.153636		3.57
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	3.55
	411096 430294	U80034 AI538226	Hs.68583 Hs.32976	mitochondrial intermediate peptidase	3.55
70	439225	AA192669	Hs.45032	guanine nucleotide binding protein 4 ESTs	3.54 3.54
	429183	AB014604	Hs.197955		3.54
	419948	AB041035	Hs.93847	NADPH oxidase 4	3.53
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.52
75	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	3.52
75	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	3.52
	432101 419216	AI918950 AU076718	Hs.123642		3.52
	444754	T83911	Hs.164021 Hs.11881	small inducible cytokine subfamily B (Cy transmembrane 4 superfamily member 4	3.51
• •	422093	AF151852	Hs.111449		3.51 3.50
80	404766	NA		NA	3.50
	441513	AW014557	Hs.112420	ESTs .	3.50
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.50
	417315	A1080042	Hs.336901	ribosomal protein \$24	3.50



	407182	********	11- 030453	FOT-	• • •
	443204	AA312551 AW205878	Hs.230157 Hs.29643	ESTs Homo sapiens cDNA FLJ13103 fis, clone NT	3.49 3.49
	432289	AI860145	Hs.55118	ESTs	3.49
_	453644	AI813444	Hs.42197	ESTS	3.48
5	427986	N45214	Hs.282387	Homo saplens cDNA: FLJ21837 fis, clone H	3.48
	405466 410804	1154000	N- CCC04	NA	3.48
	430357	U64820 AW976789	Hs.66521 Hs.165607	Machado-Joseph disease (spinocerebellar ESTs	3.48 3.46
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.46
10	422260	AA315993	Hs.105484	regenerating gene type IV	3.46
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.48
	451403 406117	AA885569	Hs.40919	Homo saplens cDNA FLJ14511 fis, clone NT	3.46
	458242	8E299588	Hs.28465	NA Homo sepiens cDNA: FLJ21859 fis, clone H	3.46 3.48
15	408562	AI436323	Hs.31141	Homo sepiens mRNA for KIAA1568 protein,	3.45
	440105	AA594010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	3.45
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	3.45
	426320 444478	W47595 W07318	Hs.169300 Hs.240	transforming growth factor, beta 2 M-phase phosphoprotein 1	3.45 3.45
20	425904	AI805990	Hs.82238	POP4 (processing of precursor, S. cerev	3.44
	416702	AA186428	Hs.85591	ESTs	3.44
	448668	AJ560305	Hs.199852	ESTs	3.42
	410004 428771	AI298027 AB028992	Hs.5057 Hs.193143	carboxypeptidase D KIAA1069 protein	3.42 3.42
25	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.42
	429628	H09604	Hs.13268	ESTs	3.40
	448816	AB033052	Hs.22151	KIAA1226 protein	3.40
	456032 439635	AW957446	Hs.301711	ESTs	3.39
30	414275	AA477288 AW970254	Hs.94891 Hs.889	hypothetical protein FLJ22729 Charot-Leyden crystal protein	3.39 3.38
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	3.38
	416057	AI927382	Hs.29857	ESTs	3.38
	430704	AW813091	Hs.335799	ESTs .	3.38
35	423600 453891	A1633559 AB037751	Hs.310359 Hs.36353	ESTs Homo sapiens mRNA full length insert cDN	3.38 3.38
-	430178	AW449612	Hs.152475	ESTs	3.37
	417791	AW965339	Hs.111471	ESTs	3.37
	408867	AA437199	Hs.656	cell division cycle 25C	3.37
40	449802 457003	AW901804 S78234	Hs.23984 Hs.172405	hypothetical protein FLJ20147 cell division cycle 27	3.37 3.36
	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.36
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.36
	418782	AJ792648	Hs.14665	ESTs	3.34
45	449722 447984	BE280074 AI457263	Hs.23960 Hs.37244	cyclin B1 ESTs	3,34 3.34
	451103	R52804	Hs.25956	DKFZP564D206 protein	3.34
	408812	BE397160	Hs.254763	ESTs, Wealthy similar to A42442 integrin	3.34
	448305 418849	AA625207 AW474547	Hs.264915 Hs.53565	Homo sapiens cDNA FLJ12908 fis, clone NT Homo sapiens PIG-M mRNA for mannosytiran	3.34 3.33
50	450531	AW301032	Hs.203800	ESTs	3.32
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.32
	416530	U62801	Hs.79361	kallikrain 6 (neurosin, zyme)	3.31
	425746 421037	NM_001701 A1684808	Hs.159440 Hs.197653	bile acid Coenzyme A: amino acid N-acylt ESTs	3.30 3.30
55	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.30
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.30
	447078 402408	AW885727	Hs.301570	ESTs	3.30
	437044	NA AL035864	Hs.69517	NA cDNA for differentially expressed CO16 a	3.29 3.29
60	423126	AA322245	Hs.290165	ESTs	3.28
	446223	BE300091	Hs.119699		3.27
	451917 419335	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.27
	411078	AW960146 AJ222020	Hs.284137 Hs.182384	hypothetical protein FLJ 12888 CocoaCrisp	3.26 3.26
65	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	3.26
	427119	AW880562	Hs.114574	ESTs	3.26
	400250	NA ADELIO	11- 445600	NA SOT-	3.26
	429044 451050	Al261490 AW937420	Hs.145527 Hs.69662	ESTs ESTs	3.25 3.24
70	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.24
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.23
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.22
	442028 409110	AI239437 AA191493	Hs.48945 Hs.48778	ESTs niban protein	3.22 3.22
75	418926	AA232658	Hs.105794		3.22
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.21
	445417	AK001058	Hs.12680	Homo sepiens cDNA FLJ10196 fis, clone HE	3.20
	442979 439292	AW440782 AA090421	Hs.174743 Hs.5555	l ESTs hypothetical protein MGC5347	3.20
80	440953	A1683036	Hs.124135		3.20 3.20
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	3.20
	451181	AI796330	Hs.207461		3.19
	422809	AK001379	Hs.121028	hypothetical protein FLJ 10549	3.19

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	411573	AB029000	Hs.70823	KIAA1077 protein	3.19
	424539	L02911	Hs.150402	activin A receptor, type I	3.18
	443179 452545	AJ928402 N31940	Hs.6933 Hs.14434	hypothetical protein FLJ12684 ESTs, Weakly similar to I38022 hypotheti	3.18
5	433024	AA573847	Hs.26549	KIAA1708 protein	3.18 3.18
	414737	AI160386	Hs.125087	ESTs	3.18
	444230	H95537	Hs.146067	ESTs	3.18
	419741 428945	NM_007019 AW192803	Hs.93002	ubiquitin carrier protein E2-C	3.17
10	424085	NM_002914	Hs.98974 Hs.139226	ESTs, Wealdy similar to \$65824 reverse t replication factor C (activator 1) 2 (40	3.17 3.17
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.17
	443598	AW499970	Hs.14822	ESTs, Weakly similar to 178885 serine/th	3.16
	413518	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.16
15	434389 431322	AA971235 AW970622	Hs.128098	ESTS	3.16
	432158	W33165	Hs.22983	gb:EST382704 MAGE resequences, MAGK Horno UDP-glucose:glycoprotein glucosyltransfe	3.15 3.15
	453331	AI240665	Hs.8895	ESTs :	3.15
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	3.14
20	408687 422789	AL110280 AK001113	Hs.301152 Hs.120842	Homo sepiens mRNA; cDNA DKFZp434F053 (fr	3.14
	419078	M93119	Hs.89584	hypothetical protein FLJ 10251 insulinoma-associated 1	3.14 3.14
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.14
	451525	AW001757	Hs.14005	ESTs	3.13
25	453775 433183	NM_002916 AF231338	Hs.35120 Hs.222024	replication factor C (activator 1) 4 (37	3.13
	424783	AA913909	Hs.153088	transcription factor BMAL2 TATA box binding protein (TBP)-associate	3.12 3.12
	413170	BE068819		gb:MR0-BT0374-Z20300-001-b03 BT0374 Homo	3.12
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	3.12
30	442991 453867	BE281238 AI929383	Hs.8886 Hs.33032	hypothetical protein FLJ20424	3.11
		AAB11452	Hs.291911	hypothetical protein DKFZp434N185 ESTs	3.11 3.10
	428651	AF196478	Hs.188401	annexin A10	3.09
	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.09
35	419196 414569	AF110908 AF109298	Hs.297660 Hs.118258	TNF receptor-associated factor 3	3.09
-	408633	AW863372	Hs.46677	prostate cancer associated protein 1 PRO2000 protein	3.09 3.09
	403381			NA	3.08
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	3.08
40	422363 434138	T55979 AA625804	Hs.115474	replication factor C (activator 1) 3 (38 gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.08
. •	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.07 3.07
	436556	Al364997	Hs.7572	ESTs	3.07
	427043 443055	AA397679 AV653742	Hs.3991	ESTs	3.06
45	419229	AI827237	Hs.15536 Hs.282884	hypothetical pratein DKFZp761J139 ESTs	3.06 3.05
	414718	H95348	Hs.107987	ESTs	3.05
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	3.05
	448587 448595	AJ539652 AB014544	Hs.28338 Hs.21572	KIAA1546 protein KIAA0644 gene product	3.04 3.04
50	407201	N31998	Hs.164256	hypothetical protein FLI20657	3.04
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	3.04
	431980 416198	AA523696 H27332	Hs.324507	hypothetical protein FLJ20986	3.04
	429410	X98494	Hs.99598 Hs.201676	hypothetical protein MGC5338  M-phase phosphoprotein 10 (U3 small nucl	3.04 3.04
55	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.03
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	3.03
	446142 402167	A1754693	Hs.145968	ESTs NA	3.02
	402299			NA NA	3.02 3.02
60	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.02
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.02
	424001 413930	W67883 M86153	Hs.137476 Hs.75618	paternally expressed 10	3.01
	439924	AI985897	Hs.125293	RAB11A, member RAS oncogene family ESTs	3.01 3.01
65	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.01
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	3.00
	445845 420727	AI261870 H75701	Hs.145555 Hs.99886	ESTs	3.00
	427510	Z47542	Hs.179312	complement component 4-binding protein, small nuclear RNA activating complex, po	3.00 3.00
70	403637	NA		NA	3.00
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	3.00
	413430 423575	R22479 C18863	Hs.167073 Hs.163443	Homo sepiens cDNA FLJ13047 fis, clone NT	3.00
	426711	AA383471	Hs.180669	Homo sapiens cDNA FLJ11576 fis, clone HE conserved gene amplified in osteosarcoma	2.99 2.99
75	442204	A1635450	Hs.21914	ESTs	2.98
	429682	NM_006306	Hs.211602		2.98
	419227 447233	BE537383 AW246333	Hs.89739 Hs.17901	cholinergic receptor, nicolinic, beta po	2.97
00	441826	AW503603	Hs.129915	Homo sapiens, clone iMAGE:3937015, mRNA, phosphotriesterase related	2.97 2.97
80	433404	T32982	Hs.102720	ESTS	2.96
	450506 423880	NM_004460 BE278111	Hs.418	fibroblast activation protein, alpha	2.96
	411750	BE562298	Hs.134200 Hs.71827	DKFZP564C186 protein KIAA0112 protein; homolog of yeast ribos	2.96 2.96
				and the second section of the second of the	£. 30

	408155 424131	AB014528	Hs.43133	KIAA0628 gene product ESTs	2.96
	451250	AA335714 AA491275	Hs.199665 Hs.236940	hypothetical protein FLJ12542	2.96 2.96
	425154	NM. 001851	Hs.154850	collagen, type IX, alpha 1	2.96
5	447829	AI433029	Hs.164104	ESTs	2.95
	410561	BE\$402\$\$	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.95
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.95
	452693 407742	T79153 AF186252	Hs.48589	zinc finger protein 228	2.95
10	421430	AF 100232 AW207555	Hs.38084 Hs.97093	suffotransferase family, cytosofic, 1C, Homo sapiens cDNA: FLJ23004 fis, clone L	2.94 2.94
	407995	AID94748	Hs.100134	hypothetical protein FLJ 12787	294
	413281	AA861271	Hs.222024	transcription factor BMAL2	294
	452381	H23329	Hs.290880	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.94
1.5	441020	W79283	Hs.35962	ESTs	2.94
15	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	294
	420005 412530	AW271106 AA766268	Hs.133294 Hs.266273	ESTs hypothetical protein FLJ13346	2.93
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein 8M03	2.93 2.93
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	293
20	443341	AW631480	Hs.8688	ESTs	2.92
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.92
	410144	W07189	Hs.68185	ESTs, Weakly similar to ARL3_HUMAN ADP-R	2.92
	434450	S78664	Hs.87	retinoblastoma-lika 1 (p107)	2.92
25	450402 422026	BE218027 U80736	Hs.89969 Hs.110826	ESTs trinucleotide repeat containing 9	2.92 2.92
	421562	AA530994	Hs.334471	ghrelin precursor	2.92
	410434	AF051152	Hs.63668	toll-like receptor 2	2.92
	422665	AJ011812	Hs.119018	transcription factor NRF	2.91
20	428966	AF059214	Hs.194687	cholesteral 25-hydroxylase	2.90
30	412416	AI628253	Hs.22580	alkylglycerone phosphate synthase	2.90
	446232 454600	AI281848 AW810001	Hs.194691	retinoic acid induced 3 gb:MR4-ST0124-270300-005-b11 ST0124 Homo	2.90 2.90
	438018	AKD01160	Hs.5999	hypothetical protein FLJ10298	2.90
	433252	AB040957	Hs.151343	KIAA1524 protein	2.90
35	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALUS_HUMAN A	2.90
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.89
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.89
	411643 419559	Af924519 Y07828	Hs. 192570 Hs. 91096	hypothetical protein FLJ22028 ring finger protein	2.89
40	433527	AW235613	Hs.133020	ESTs	2.89 2.88
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	2.88
	406182	NA		NA	2.88
	432731	R31178	Hs.287820	fibronectin 1	2.88
45	429274	AI379772	Hs.99206	ESTs	2.87
43	418216 410166	AA662240	Hs.283099	AF15q14 protein	2.87
	452665	AK001376 AW839326	Hs.59346 Hs.330414	hypothetical protein FLJ10514 ESTs, Moderately similar to S65657 atpha	2.86 2.86
	424696	BE439547	Hs.151903	GrpE-like protein cochaperone	2.86
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.85
50	443640	AJ872643	Hs.134218	ESTs	2.85
	432912	BE007371	Hs.200313	ESTs	2.85
	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.85
	446565 424770	D13757 AA425562	Hs.311 Hs.11065	phosphoribosyl pyrophosphate amidotransi Homo sepiens HDCME13P mRNA, partial cds	2.85 2.84
55	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	2.84
	403639	NA		NA (STOCKET	2.84
	451110	AI955040	Hs.265398	ESTs, Weattly similar to transformation-r	2.84
	415185	AW975861	Hs.47367	KIAA1785 protein	2.84
60	444565 423441	BE613126	Hs.47783	B aggressive lymphoma gene	2.83
oo	450584	R68649 AA040403	Hs.278359 Hs.60371	absent in melanoma 1 like ESTs	2.83
	420191	AW003565	Hs. 192323		2.83 2.83
	425599	AW366745	Hs.214140		2.83
	424408	AJ754813	Hs.146428		2.83
65	448769	N66037	Hs.38173	ESTS	2.82
	444946	AW139205	Hs.156457		2.82
	435347 438435	AW014873	Hs.116963		2.82
	427687	AA807142 AW003867	Hs.42194 Hs.1570	hypothetical protein FLJ22649 similar to histamine receptor H1	2.82 2.82
70	426951	AA393636	Hs.97454	ESTs	2.82
-	427970	AA418187	Hs.330515		2.82
	442577	AA292998	Hs.163900	ESTS	2.82
	441016	AW138653	Hs.25845	ESTs	2.81
75	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.81
, 5	417160 409346	N76497 AL162066	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	261
	410407	X66839	Hs.54320 Hs.63287	hypothetical protein DKF2p7620096 carbonic anhydrase IX	2.81 2.81
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.81
00	435849	BE305242	Hs.15098	claudin 2	2.80
80	426695	AW118191	Hs.112729	ESTs	2.80
	428301	AW628666	Hs.98440	ESTs, Wealdy similar to I38022 hypotheti	2.80
	420759 421341	T11832 AJ243212	Hs.127797		2.80
	421341	M243212	Hs.279611	deleted in malignant brain tumors 1	2.80

	410422	020400	N- 00315	MA 40007	
	419423 452355	D26488 N54926	Hs.90315 Hs.29202	KIAA0007 protein G protein-coupled receptor 34	2.79 2.79
	425826	U97698	Hs.159593	mucin 6, gastric	2.79
_	457465	AW301344	Hs.122908	DNA replication factor	2.79
5	426472	BE246138	Hs.30853	ESTs	2.79
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.78
	425851 419236	NM_001490 AA330447	Hs.159642	glucosaminyi (N-acetyi) transferase 1, c	2.78
	423430	AF112481	Hs.135159 Hs.128501	Homo sapiens cDNA FLJ11481 fis, clone HE RAD54, S. cerevisiae, homolog of, B	2.78 2.78
10	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.78
	453700	AB009426	Hs.560	apolipoprotain B mRNA editing enzyme, ca	2.78
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	2.77
	414043	AI521210	Hs.97977	ESTS	2.77
15	418054 439223	NM_002318 AW238299	Hs.83354	lysyl oxidase-like 2	2.77
13	439223 425956	M60828	Hs.250618 Hs.164568	UL16 binding protein 2 fibroblast growth factor 7 (keratinocyte	2.76 2.75
	437612	AA827715	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	2.76
	426119	W94997	Hs.189917	ESTs	2.76
20	459574	AI741122	Hs.101810		2.76
20	442339	BE299668	Hs.227591	ESTs. Wealthy similar to 1901303A Leu zip	2.76
	414334 418217	AA824298	Hs.21331	hypothetical protein FLJ10036	2.76
	420022	AI910647 AA256253	Hs.13442 Hs.120817	ESTs ESTs	2.76
	408243	Y00787	Hs.624	Interleukin 8	2.76 2.75
25	421346	Z34277	Hs.103707	apornucin	2.75
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.75
	425773	N21279	Hs.237749	ESTs	2.75
	449611 424827	AI970394	Hs.197075	ESTs	2.74
30	448621	AJ057094 AJ097144	Hs.96867 Hs.5250	Homo sepiens cDNA: FLJ23155 fis, clone L ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74 2.74
-	428523	AW974540	Hs.98626	ESTs	2.73
	410839	NM_006849	Hs.66581	protein disutfide isomerase	2.73
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (tr	2.73
35	424641	AB001106	Hs.151413	glia maturation factor, beta	2.73
33	431708 436209	A1698136 AW850417	Hs.108873 Hs.254020	ESTs	2.73
	441790	AW294909	Hs.132208	ESTs, Moderately similar to unnamed prot ESTs	2.73 2.73
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	273
40	409506	NM_006153	Hs.54589	NCK adaptor protein 1	2.73
40	423482	BE280172	Hs.129228	galactokinase 2	2.73
	417015	M83772	Hs.80876	flavin containing monocxygenase 3	2.72
	448165 448826	NM_005591 AI580252	Hs.202379 Hs.293246	meiotic recombination (S. cerevisiae) 11	2.72
	447803	BE620578	Hs.30858	ESTs, Weakly similar to putative p150 (H ESTs, Weakly similar to S65657 alpha-1C-	2.72 2.72
45	429703	T93154	Hs.28705	ESTs	2.72
	448796	AA147829	Hs.301431	endothefial zinc finger protein induced	2.72
	410902	AW809665		gb:MR4-ST0124-261099-015-g07 ST0124 Homo	2.72
	424745 454469	AA214618	Hs.152759	activator of S phase kinase	2.72
50	458632	AW792775 AI744445	Hs.167073	gb:CM0-UM0001-010300-258-g10 UM0001 Homo Homo saplens cDNA FLJ13047 fis, clone NT	272 272
•	452012	AA307703	Hs.279766	kinesin family member 4A	2.72
	422109	\$73265	Hs.1473	gastrin-releasing peptide	2.72
	438008	AA775026	Hs.203802	ESTs	2.72
55	420552	AK000492	Hs.98806	hypothetical protein	271
22	427038 409239	NM_014633	Hs.173288	KIAA0155 gene product	2.71
	425371	AA740875 D49441	Hs.44307 Hs.155981	ESTs, Moderately similar to 138022 hypot mesothelin	2.71 2.71
	439857	AA847194	Hs.232002	EST8	2.71
-	455309	AW894017		gb:RC4-NN0027-150400-012-g04 NN0027 Hamp	2.71
60	439580	AF086401	Hs.293847	ESTs, Moderately similar to \$65657 alpha	2.70
	437257	AJ283085	Hs.290931	ESTs, Wealtly similar to YFJ7_YEAST HYPOT	2.70
	435039 438796	AW043921 W67821	Hs.130526 Hs.109590	ESTs genethonin 1	2.70
	407013	U35637	16.105550	gb:Human nebulin mRNA, partial cds	2.70 2.70
65	445413	AA151342	Hs.12677	CGI-147 protein	270
	418416	U11700	Hs.84999	ATPase, Cu↔ transporting, beta polypept	2.70
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.69
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.69
70	441858 449076	A1400276 A1627826	Hs.183485 Hs.209109	ESTs ESTs	2.69
. •	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.69 2.69
	427617	D42063	Hs.199179	RAN binding protein 2	2.69
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.69
75	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.58
,,	419310	AA235233	Hs.188716		2.68
	445279 439741	R41900 BE379646	Hs.22245 Hs.6904	ESTs Homo sapiens mRNA full length insert cON	2.68
	446692	Z44514	Hs.156829	Homo sepiens mRNA for KtAA1763 protein,	2.68 2.68
00	449300	AI656959	Hs.222165		2.68
80	444585	AW170015	Hs.6594	ESTs	2.68
	444384 448104	BE174527	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	2.68
	446839	A1674818 BE091926	Hs.316433 Hs.16244		2.67
		OEV\$1320	113.10244	mitoric spindle colled-coil related prot	2.67



	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.67
	418971	AA360392	Hs.87113	ESTs	2.66
	446152 441553	AI292036 AA281219	Hs.150028 Hs.121296	ESTs ESTs	2.66 2.66
5	403548			NA	2.66
	452699	AW295390	Hs.213062	ESTs	2.66
	449532 45 <b>3</b> 985	W74653 N44545	Hs.271593 Hs.251865	ESTs, Moderately similar to A47582 B-cel ESTs	2.66 2.65
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.65
10	409446	AJ561173	Hs.67688	ESTs	2.65
	422094 445462	AF129535 AA378776	Hs.272027 Hs.288649	F-box only protein 5 hypothetical protein MGC3077	2.65 2.64
	432670	AA806536	Hs.291841	ESTs	2.64
16	418634	AK000064	Hs.86905	ATPase, H+ transporting, lysosomal (vacu	2.64
15	453628 442117	AW243307 AW664964	Hs.83937 Hs.128899	hypothetical protein ESTs	2.64 2.64
	416248	H99169	Hs.23450	mitochondrial ribosomal protein \$25	2.64
	414631	AW970130	Hs.65408	ESTs	2.64
20	423268 413597	BE386898 AW302885	Hs.131162 Hs.117183	ESTs, Wealtry similar to ALU5_HUMAN ALU S ESTs	2.64 2.63
20	445031	AI271704	Hs.18987	Homo sapiens BAC clone RP11-505D17 from	263
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	2.63
	436304 439832	AA339622 TB1829	Hs.108887 Hs.14870	ESTS	2.63
25	449207	AL044222	Hs.23255	Horno sapiens, Similar to hect domain and nucleoporin 155kD	2.63 2.62
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	2.62
	414747 423811	U30872 AW299598	Hs.77204 Hs.50895	centromere protein F (350/400kD, mitosin	2.62
	439474	AI824060	Hs.211501	hameo bax C4 ESTs	2.62 2.62
30	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.62
	408031 442821	AA081395 BE391929	Hs.42173	Homo sapiens cDNA FLJ10366 fls, clone NT	2.62
	418245	AA088767	Hs.8752 Hs.83883	transmembrane protein 4 transmembrane, prostate androgen induced	2.62 2.62
25	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	2.61
35	424840 443268	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.61
	403056	AI800271 R58624	Hs.129445 Hs.2186	hypothetical protein FLJ12498 eukaryotic translation elongation factor	261 261
	433037	NM_014158	Hs.279938	HSPC067 protein	2.61
40	410358 426181	AW975168	Hs.13337	ESTs, Wealthy similar to unnamed protein	2.60
70	414853	AA371422 U31116	Hs.334371 Hs.77501	hypothetical protein MGC13096 sarcoglycan, beta (43kD dystrophin-assoc	2.60 2.60
	457233	Al355009	Hs.221698	ESTs	2.60
	416049	AI970536	Hs.16603	hypothetical protein FLJ 13163	2.60
45	418946 441891	AI798841 AW129145	Hs.164526 Hs.128076	ESTs ESTs	2.60 2.60
	443742	AW627805	Hs.145421	ESTs	2.60
	433868	AA612960	Hs.337300	ESTs	2.60
	442717 444542	R88362 Al161293	Hs.180591 Hs.280380	ESTs, Wealdy similar to T23976 hypotheti aminopeptidase	2.59 2.59
50	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	2.59
	429170	NM_001394		dual specificity phosphatase 4	2.59
	417531 401458	NM_003157	Hs.1087	serine/threonine kinase 2 NA	2. <del>5</del> 9 2.58
	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	2.58
55	430980	AW971904	Hs.122164	diaphanous (Drosophila, homolog) 3	2.58
	441581 435693	BE551408 Al033134	Hs.127196 Hs.119887	ESTs ESTs	2.58 2.58
	431814	BE256242	Hs.270847	delta-tubulin	2.58
60	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.58
60	422765 456999	AW409701 AA319798	Hs.1578 Hs.298581	baculoviral IAP repeat-containing 5 (sur eutkaryotic translation elongation factor	2.58 2.58
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.58
	434423	NM_006769		LIM domain only 4	2.57
65	425782 433929	U66468 Al375499	Hs.159525 Hs.27379	cell growth regulatory with EF-hand doma ESTs	2.57 2.57
05	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	2.57
	411789	AF245505	Hs.72157	DKFZP564/1922 protein	2.57
	435627 432168	W88774 AK000563	Hs.118370		2.57
70	432375	BE536069	Hs.272805 Hs.2962	hypothetical protein FLJ20556 S100 calcium-binding protein P	2.57 2.57
	424057	A1339874	Hs.126593	ESTs	2.57
	424315 435663	AW614850 AJ023707	Hs.193384		2.57
	439277	R80051	Hs.134273 Hs.164478		2.56 2.56
75	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.56
	438182	AW342140 AJ470093	Hs.182545		2.56
	421102 445725	AK000956	Hs.283085 Hs.13209	protocadherin beta 6 hypothetical protein FLJ 10094	2.56 2.56
00	448243	AW369771	Hs.52620	integrin, beta 8	2.56
80	442881	AJ023175	Hs.167022	ESTs .	2.56
	422165 425843	AL041199 BE313280	Hs.1481 Hs.159627	histidine decarboxytase death associated protein 3	2.56 2.56
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.55
					·

	410000				
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	2.55
	438113	AJ467908	Hs.8882	ESTs	2.55
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.55
5	448275	BE514434	Hs.20830	kinesin-like 2	2.55
,	419987	NM_005014	Hs.94070	osteomodulin	2.55
	439929 452240	S73205	64000	gb:insulin activator factor (human, pane	2.55
	417806	AI591147	Hs.61232	ESTs	2.55
	421482	A1867277 Al.135462	Hs.183733	ESTs	255
10	456884	AA054679	Hs.104715	inversin ribonuclease P (14kD)	2.55
10	442961	BE614474	Hs.155150 Hs.289074		2.55
	411274	NM_002776	Hs.59423	F-box only protein 22 kallikrein 10	2.55
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.55
	448666	NM_014953	Hs.323346	KIAA1008 protein	254
15	428911	Z43848	Hs.194478	Homo sapiens mRNA; cONA DKFZp43401572 (f	254 254
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fls, clone C	2.54 2.54
	430733	AW975920	Hs.283361	ESTs	2.54
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	254
	435361	AI168596	Hs.117117	ESTs	2.54
20	452833	BE559681	Hs.30736	KIAA0124 protein	2.54
	422330	D30783	Hs.115263	epiregulin	2.54
	424962	NM_012288	Hs.153954	TRAM-like protein	254
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Horno saplens	253
0.5	447178	AW594541	Hs.192417	ESTs	2.53
25	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.53
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.53
	419449	H1B417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	2.53
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	2.53
30	409435	AJ810721	Hs.95424	ESTs	2.52
30	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.52
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.52
	422314	K01900	Hs.73890	interferon, alpha 8	2.52
	441343 417185	AI970348	Hs.132230	ESTs	2.52
35	401747	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	2.52
55	448526	AB028946	Hs.21361	NA	2.52
	419488	AA316241	Hs.90691	KIAA1023 protein nucleophosmin/nucleoplasmin 3	2.52
	413627	BE182082	Hs.246973	ESTs	2.52
	441285	NM_002374	Hs.167	microtybule-associated protein 2	251
40	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.51 2.51
	429357	AA779725	Hs. 164589	ESTs	2.51
	443171	BE281128	Hs.9030	TONDU	2.50
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	2.50
	420795	AA323037	Hs.128645	sorting nexin 16	2.50
45	448582	AI538880	Hs.94812	ESTs	2.50
	445459	AI478629	Hs.158465	likely artholog of mouse putative IKK re	2.50
	423909	AJ223183	Hs.135194	immunoglobutin superfamily, member 6	2.50
	414315	Z24878		gb:HSB650052 STRATAGENE Human skeletal m	2.50
50	407568	AA740964	Hs.62699	ESTs	2.50
30	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	2.50
	431571	AW500486	Hs. 180610	splicing factor proline/glutamine rich (	2.50
	433843	AW021423	Hs.112819	EST8	2.50
	456254 403137	T19844		gb:B711F Heart Homo sapiens cDNA clone B	2.50
55	425895	AI269484	Hs.161427	NA	2.50
-	418612	AB037788	Hs.224961	zinc finger protein 215	2.50
	410012	AD037706	T13.224301	cleavage and polyadenylation specific fa	2.50
	TABLE 45	a.			
	Pkey:		ue Eos probes	set identifier number	
60	CAT num		cluster numb		
	Accession		ank accession		
	Pkey	CAT Number	Accessions		
65	410784	1221005_1		BE079700 BE062940	
05	410902	1226078_1		AW810108 AW809781 AW809844	
	411765	125700_1		248302 AA095182	
	413170	1351880_1	BE058819 (	BE068821 BE068825	
	413516	1374595_1	BE1459071	BE145796 BE145803 BE145851 BE145923 BE145812	BE145809 BE145852 BE145856
70	414315 428858	143512_1		494098 F13654 AA494040 AA143127	
70	430264	296453_1		AW237453 BE327496 N47347 N56967	
	431322	315008_1 331543_1		BE303010 BE302954 BE384120	
	434138	380572 1	VACAEDU4	AAS03009 AAS02998 AAS02989 AAS02805 T92188	
	436411	419334_1	VANCOOR I	AW418787 AW074833 AI675842 AI393368 AA715374 Z25205	
75	438159	451062	Z83947	nni 13314 42343	
	439929	480591	S73205		
	451105	859083_1		W880941 AW880937	
	452453	918300_1		1902518 A1902516	
00	454469	1213727_1	AW792775	BE072509 AW792958	
80	454600	1226077_1	AW810001	AW810092 AW810170 AW809884 AW809664 AW810	353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006
		_	AW809672	AW809694 AW810552 AW810345 AW810432 AW809	360
	454821	1238365_1	AW833504	AW833751 AW833493 AW833341	<del></del>
	455309	1278153_1		AW893956 AW894032	

	456254	456254 1699246_1 T19844 T11755 T11830 T20136 T11957 R45834 R45828 R15595										
	TABLE 45	C:										
5	Pkey: Ref:	Seq	rique number corresponding to an Eos probeset quence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA objects of human chromosome 20" Dunbarge et al. (1990) Met Novel (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA									
	Strand:											
	M_position	raios	Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.									
10	Pkey	Ref	Strand	All according								
- •	401458	9187886	Plus	Nt_position 76485-77597								
	401644	8576138	Ptus	82655-83959								
	401747	9789672	Minus		1,120422-120990,130161-130381,130468-130593,131097-131258,131866-							
15	400407		_	121205 12542 1125212 122200-124011	**************************************							
IJ	402167 4022 <del>9</del> 9	8571795	Plus	109122-110357								
	402408	6693370 9796239	Plus	23367-25175								
	403137	9211494	Minus Minus	110326-110491								
	403381	9438267	Minus	92349-92572,92958-93084,93579-93712,93949- 26009-26178	-94072,94591-94748,95214-95337							
20	403422	9665041	Minus	151169-151561								
	403548	8081591	Minus	38760-39352								
	403637	8671936	Minus	142647-142771,145531-145762								
	403639 403778	8671948	Plus	113234-113326,115186-115287,119649-119788	<b>}</b>							
25	404253	7770611 9367202	Minus Minus	1414-1513,1624-1756								
	404440	7528051	Plus	55675-56055 80430-81581								
	404766	7882612	Minus	158681-158882,160838-160973		•						
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-	AD67A A2351 A2460							
30	405466	7767904	Minus	04438-040/5								
20	405770 405817	2735037	Plus	61057-62075								
	405117	4071056 9142932	Plus Plus	19914-20112,25655-25810								
	406182	5923650	Minus	54304-54584 28256-28935	•							
3.6				m130-20333								
35												
	TABLE 48A: ABOUT 1303 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH											
	Table 46A 8sts about 1303 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 45A except using non-matignant stomach specimens in determining the denominator value and the ratio was equal to or greater than 5.0.											
	Pkey:			or value and the ratio was equal to or greater than : el idantifier number	5.0.	•						
40	ExAcon:	Exe	notar Arcessio	n number, Genbank accession number								
	UnigenelD	: Unig	ene number	Trial lacification accession number								
	Unigene T	itle: Unig	ene gene tide									
	R1:	Ratio	of tumor to no	ormal body tissue								
45	Pkey	ExAcon	UnigenelD	i balanca Wina								
	446619	AU076643	Hs.313	Unigene Title secreted phosphoprotein 1 (osteopontin,	R1							
	414152	NM_003248	Hs.75774	thrombospondin 4	80.50							
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	70.52 65.30							
50	428698	AA852773	Hs.334838	KIAA1866 protein	61.90							
50	428368 409041	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	50.60							
	452281	AB033025 T93500	Hs.50081 Hs.28792	KIAA1199 protein	44.50							
	452862	AW378065	Hs.8687	Homo sapiens cDNA FLJ11041 fis, clone PL ESTs	41.10							
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	33.50 32.10							
55	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ 10570 fis, clone NT	26.90							
	428398	A1249368	Hs.98558	ESTS	26.40							
	409757 403776	NM_001898	Hs.123114	cystatin SN	25.48							
	427674	NM_003528	Hs.2178	NA U20 biologo foreita accessor a	24.90							
60	419968	X04430	Hs.93913	H2B histone family, member Q interleutin 6 (interferon, bete 2)	23.80							
	427108	AB028976	Hs.173571	KIAA1053 protein	23.10 21.76							
	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro	20.70							
	400419 415989	AF084545		NA .	20.40							
65	432101	AI267700 AI918950	Hs.317584 Hs.123642	ESTS	19.80							
	418994	AA296520	Hs.89546	EphA3 selectin E (endothelial adhesion molecul	19.70							
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	19.00							
	412652	AI801777	Hs.6774	ESTs	18.40 18.20							
70	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	17.71							
422100 AASS894 Hs.112408 S100 calcium-binding protein A7 (psorias 17.38				17.38								
	437446	AA788946	Hs.22785 Hs.16869	gamma-aminobutyric acid (GABA) A recepto	17.36							
	440594	AW445167	Hs.126036	ESTs, Moderately similar to CA1C RAT COL ESTs	17.00							
75	430044	AA464510	Hs.152812	ESTs	17.00 17.00							
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	17.00 16.90							
	414737	AI160386	360 HS 125087 ESTS 16.50									
	427335 423453	AA448542 AW450737	Hs.251677	G antigen 7B	16.30							
• -	414569	AV450737 AF109298	Hs.128791 Hs.118258	CGI-09 protein	15.50							
80	401961	NA	ns. i 10438	prostate cancer associated protein 1 NA	15.40							
	434551	BE387162	Hs.280858	ESTs. Highly simitar to A35661 DNA excis	15.40							
	432069	AW975868	Hs.294100	ESIS	15.40 15.30							
	434699	AA643687	Hs.149425	Homo sapiens cONA FLJ11980 fis, clone HE	15.30							
					• • •							



	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	15.30		
	400289 415138	X07820 C18356	Hs.2258 Hs.295944	matrix metalloproteinase 10 (stromelysin tissue factor pathway inhibitor 2	15.20 15.20		
_	428820	AA436187	Hs.172631	integrin, glpha M (complement component	15.19		
5	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	15.10		
	438639 458997	AI278360 AW937420	Hs.31409 Hs.69662	ESTs ESTs	15.10		
	432731	R31178	Hs.287820	fibronectin 1	15.00 14.90		
10	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	14.70		
10	451099 452242	R52795 R50956	Hs.25954	Interleukin 13 receptor, alpha 2	14.70		
	426427	M86699	Hs.159993 Hs.169840	gycosyftransferase TTK protein kinase	14.70 14.50		
	439924	AI985897	Hs.125293	ESTs	14.45		
15	414869	AA157291	Hs.21479	ubinuclein 1	14.40		
13	411573 418693	AB029000 AI750878	Hs.70823 Hs.87409	KIAA1077 protein thrombospondin 1	14.40 14.37		
	421823	N40850	Hs.28625	ESTs	14.30		
	423903	M57765	Hs.1721	interleukin 11	14.20		
20	419227 447417	BE537383 AW732858	Hs.89739 Hs.143067	chofinergic receptor, nicotinic, beta po KIAA1602 protein	14.10		
	416406	D86961	Hs.79299	Epoma HMGIC fusion partner-like 2	13.96 13.90		
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	13.90		
	412863 449509	AA121673	Hs.59757	zinc finger protein 281	13.90		
25	440953	AA001615 AI683036	Hs.84561 Hs.124135	ESTs Horno sapiens cDNA FLJ13051 fis, clone NT	13.80 13.80		
	432415	T16971	Hs.289014	ESTs, Wealthy similar to A43932 mucin 2 p	13.60		
	428769	AW207175	Hs.106771	ESTs	13.60		
	416292 424580	AA179233 AA446539	Hs.42390 Hs.339024	nasopharyngeat carcinoma susceptibility ESTs, Wealdy similar to A46010 X-linked	13.41 13.40		
30	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13555 fls, clone PL	13.30		
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	13.26		
	406972 432368	M32053 AW970244	Hs.162188	gb;Human H19 RNA gene, complete cds. ESTs	13.19 13.16		
~ ~	424806	AA382523	Hs.105689	MSTP031 protein	13.08		
35	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	12.98		
	437789 447164	Al581344 AF026941	Hs.127812 Hs.17518	ESTs, Weakly similar to T17330 hypotheti	12.90		
	417412	X16896	Hs.82112	Homo sapiens cig5 mRNA, partial sequence interleukin 1 receptor, type I	12.80 12.80		
40	402363	NA		NA	12.78		
40	444301 416783	AK000135 AA206186	Hs.10760 Hs.79889	asporin (LRR class 1)	12.76		
	435706	W31254	Hs.7045	monocyte to macrophage differentiation-a GL004 protein	12.60 12.50		
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	12.50		
45	439737	AJ751438	Hs.41271	Homo sapiens mRNA full length insert cDN	12.49		
73	405770 418678	NM_001327	Hs.167379	NA cancer/testis antigen	12.48 12.45		
	414132	AI801235	Hs.48480	ESTs	12.40		
	410434	AF051152	Hs.63668	toll-like receptor 2	12.30		
50	451092 407891	A1207256 AA486620	Hs.13766 Hs.41135	Homo sapiens mRNA for FLJ00074 protein, endomucin-2	12.26 12.20		
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	12.01		
	411213	AA676939	Hs.69285	neuropäin 1	12.00		
	436476 413582	· AA326108 AW295647	Hs.33829 Hs.71331	bHLH protein DEC2 hypothetical protein MGC5350	12.00 11.90		
55	449318	AW235021	Hs.78531	Homo sepiens, Similar to RIKEN cONA 5730	11.90		
	401747			NA .	11.88		
	409619 432596	AK001015 AJ224741	Hs.55220 Hs.278481	BCL2-associated athanogene 2 matrilin 3	11.84		
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	11.80 11.73		
60	425688	U48361	Hs.159223	NGFI-A binding protein 2 (ERG1 binding p	11.72		
	407938 419948	AA905097 AB041035	Hs.85050	phospholamban	11.70		
	459645	AA074346	Hs.93847 Hs.250715	NADPH oxidase 4 ESTs	11.70 11.51		
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	11.50		
65	434851 418699	AA806164 BE539639	Hs.116502 Hs.173030	ESTS	11.50		
	413453	AA129640	Hs.173030 Hs.128065		11.47 11.40		
	442028	AI239437	Hs.48945	ESTs	11.40		
70	428479	Y00272	Hs.184572		11.39		
70	453313 421633	BE005771 AF121860	Hs.153746 Hs.106260		11.20 11.20		
	410339	AI916499	Hs.298258		11.20		
	448111	AA053486	Hs.20315	Interferon-induced protein with tetratri	11.15		
75	453857 430217	AL080235 N47863	Hs.35861 Hs.336901	DKFZP586£1621 protein ribosomal protein S24	11.15		
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	11.10 11.10		
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	11.06		
	416854	H40164	Hs.80296	Purkinje cell protein 4	10.90		
80	447072 424882	D61594 Al379461	Hs.17279 Hs.153636	tyrosytprotein sulfotransferase 1 far upstream element (FUSE) binding prot	10.90 10.80		
	448693	AW004854	Hs.228320		10.80		
	408750	8E294069	Hs.93581	hypothetical protein FLJ10512	10.80		
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	10.80		
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	436411	AW674352		abba63a07 v1 billy 1400 1211	40.00
	441693	AA384673	Hs.7943	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD RPB5-mediating protein	10.80 10.80
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	10.80
•	441801	AW242799	Hs.86366	ESTs	10.80
5	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	10.80
	415727 414142	BE501389	Hs.20848	ESTs, Weakly similar to APAF_HUMAN APOPT	10.80
	421650	AW368397 AA781795	Hs.150042 Hs.122587	Homo sapiens cDNA FLJ14438 fis, clone HE ESTs	10.80 10.80
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.80
10	421814	L12350	Hs.108623	thrombospondin 2	10.69
	415060	AJ223810	Hs.43213	ESTs, Wealdy similar to IEFS_HUMAN TRANS	10.67
	421462 410444	AF016495 W73484	Hs.104624	aquaporin 9	10.66
	409743	N48721	Hs.183506	gbzd54e04.s1 Soares_fetal_heart_NbHH19W hypothetical protein FLJ14213	10.61
15	448142	A1754693	Hs.145968	ESTs	10.60 10.60
	444114	T58003	Hs.10323	Homo sapiens mRNA from chromosome 5q31-3	10.60
	423020	AA383092	Hs. 1608	replication protein A3 (14kD)	10.55
	453891 417352	AB037751 AA195919	Hs.36353	Homo sapiens mRNA full tength insert cDN	10.50
20	417866	AW067903	Hs.82772	gb:zp95h09.r1 Stratagene muscle 937209 H collagen, type XI, atpha 1	10.46 10.42
	427718	AJ798680	Hs.25933	ESTs	10.42
	412589	R28660	Hs.24305	ESTS	10.40
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	10.40
25	424717 450434	H03754 AA166950	Hs.152213 Hs.195870	wingless-type MMTV integration site fami	10.30
	409044	AJ129586	Hs.33033	hypothetical protein FLJ14991 hypothetical protein FLJ14623	10.30 10.30
	423600	AI633559	Hs.310359	ESTs	10.30
	433819	AW511097	Hs.112765	ESTs	10.18
30	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.10
30	410503 433800	AW975746 AI034361	Hs.188662	KIAA1702 protein	10.10
	429357	AA779725	Hs.135150 Hs.164589	lung type-I cell membrane-associated gly ESTs	10.10 10.00
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	10.00
25	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	10.00
35	416198 413918	H27332	Hs.99598	hypothetical protein MGC5338	10.00
	400570	AW015898 NA	Hs.71245	ESTS NA	10.00
	439333	AW384710	Hs.125258	Homo sapiens cDNA FLJ13795 ffs, clone TH	10.00 9.97
40	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	9.93
40	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	9.90
	434352	AF129505	Hs.86492	small muscle protein, X-linked	9.90
	453160 433929	AI263307 AI375499	Hs.239884 Hs.27379	H2B histone family, member L ESTs	9.90
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	9.89 9.81
45	437536	X91221	Hs.144465	ESTs	9.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	9.80
	452291 438913	AF015592 Al380429	Hs.28853	CDC7 (cell division cycle 7, S, cerevisi	9.80
	417849	AW291587	Hs.172445 Hs.82733	ESTs nidogen 2	9.80
50	424086	AI351010	Hs.102267	lysyl oxidase	9.78 9.72
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	9.70
	414422 419197	AA147224	Hs.337232	ESTs	9.70
	427660	N48921 Al741320	Hs.27441 Hs.114121	KIAA1615 protein Homo sapiens cDNA: FLJ23228 fis, clone C	9.70
55	449347	AV649748	Hs.295901	KIAA0493 protein	9.70 9.70
	409643	AW450866	Hs.257359	ESTs	9.70
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	9.70
	439608 430290	AW864696 AJ734110	Hs.301732 Hs.136355	hypothetical protein MGC5306	9.60
60	447124	AW976438	Hs.17428	ESTs RBP1-like protein	9.60 9.60
	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fis, clone H	9.60
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	9.58
	418067 424001	AI127958 W67883	Hs.83393	cystatin E/M	9.54
65	443037	AW500305	Hs.137476 Hs.299166	paternally expressed 10 syntaxin 7	9.50 9.50
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	9.50 9.50
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	9.50
	409269	AA576953	Hs.22972	hypothetical protein FLJ 13352	9.50
70	443162 444381	T49951 BE387335	Hs.9029 Hs.283713	DKFZP434G032 protein	9.45
. •	424026	Al798295	Hs.137576	ESTs, Wealdy similar to \$64054 hypotheti ribosomal protein L34 pseudogene 1	9.43 9.40
	440052	AI633744	Hs.195648	ESTs. Weakly similar to 138022 hypotheti	9.40
	403137	4144444		NA .	9.37
75	418051 418701	AW192535	Hs.19479	ESTs	9.35
, 5	430291	AA814948 AV660345	Hs.96343 Hs.238126	ESTs, Weakly similar to ALUC_HUMAN !!!! CGI-49 protein	9.30
	426137	AL040683	Hs.167031	OKFZP566D133 protein	9.30 9.30
	400195	NA		NA .	9.30
80	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	9.20
-00	423936 414259	U77629 W44633	Hs.135639 Hs.301296		9.20
	416661	AA634543	Hs.79440	Homo sapiens cDNA: FLJ23131 fis, clone L IGF-IJ mRNA-binding protein 3	9.20 9.20
	405543	NA	• • • • •	NA .	9.20

	420900	AL045633	Hs.44269	ESTs	
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	9.11 9.10
	410929	H47233	Hs.30643	ESTs	9.10
-	427319	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	9.10
5	443745	A8039670	Hs.9728	ALEX1 protein	9.10
	436574 407192	AW293527 AA609200	Hs.126465	ESTs	9.10
	426075	AW513691	Hs.270149	gb:af12e02.s1 Soares_testis_NHT Homo sap ESTs, Wealdy similar to 2109260A B cell	9.08 9.07
	408778	AI500519	Hs.63382	hypothetical protein PRO2714	9.03
10	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	9.00
	404440			NA .	9.00
	407168 451678	R45175 AA374181	Hs.117183 Hs.26799	ESTs	9.00
	431946	AI018336	Hs.131730	DKFZP564D0764 protein ESTs	9.00 8.92
15	408875	NM_015434	Hs.48604	DKFZP434B168 protein	8.90
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	8.90
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	8.89
	445029 442717	AF196481 R88362	Hs.12256	midline 2	8.86
20	409089	NM_014781	Hs.180591 Hs.50421	ESTs, Wealdy similar to T23976 hypotheti KiAA0203 gene product	8.80 8.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.80
	418190	N54000		gb:yy99d02.r1 Soares_multiple_sclerosis_	8.80
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.77
25	416440 421262	Al823912 AA286746	Hs.79335	Homo sepiens, Similar to SW/SNF related	8.76
23	441031	Al110684	Hs.9343 Hs.7645	Homo sapiens cONA FLJ14265 fis, clone PL fibrinogen, B beta polypeptide	8.70 8.70
	452234	AW084176	Hs.223296	ESTs. Weatly similar to I38022 hypotheti	8.70
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	8.70
30	430462	AI584156	Hs. 105640	Homo sapiens, clone IMAGE:4139775, mRNA,	8.65
30	426457 412054	AW894667 W87482	Hs.169965 Hs.302209	chimerin (chimaerin) 1	8.65
	450238	AW162998	Hs.24684	ESTs KIAA1376 protein	8.64 8.63
	418782	AI792648	Hs.14665	ESTs	8.60
25	452631	Al188658	Hs.87498	ESTs	8.60
35	425268	AIB07883	Hs.180059	Homo sapiens cDNA FLJ20653 ffs, clone KA	8.60
	432014 440270	H\$6741 NM_015986	Hs.38540 Hs.7120	ESTs, Weakly similar to ALU4_HUMAN ALU S cytokine receptor-like molecule 9	8.60
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	8.60 8.60
40	426809	BE313114	Hs.29706	ESTs	8.60
40	419704	AA429104	Hs.45057	ESTs	8.60
	452909	NM_015368	Hs.30985	pannexin 1	8.60
	432639 430418	AW973785 R98852	Hs.36029	gb:EST385886 MAGE resequences, MAGM Homo heart and neural crest derivatives expre	8.60 8.58
	450480	X82125	Hs.25040	zinc finger protein 239	8.58
45	444984	H15474	Hs.132898	fatty acid desaturase 1	8.58
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	8.57
	430518 424735	AW363687 U31875	Hs.82916 Hs.272499	chaperonin containing TCP1, subunit 6A (	8.50
	414061	NM_000699	Hs.300280	short-chain alcohol dehydrogenase family amylase, alpha 2A; pancreatic	8.50 8.50
50	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	8.50
	441079	AW150697	Hs.107418	ESTS	8.50
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	8.50
	418618 416565	U66097 AW000960	Hs.86724 Hs.44970	GTP cyclohydrofase 1 (dopa-responsive dy endoplasmic reticulum resident protein 5	8.50
55	441540	C01367	Hs.127128	ESTs	8.50 8.50
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	8.50
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	8.50
	426855 436515	AL117427 AJ278111	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	8.48
60	416315	AA179483	Hs.195292 Hs.73605	putative tumor antigen ESTs	8.43 8.42
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	8.40
	410094	BE147897	Hs.58593	general transcription factor (IF, polype	8.40
	419198	AA234938	Hs.87384	ESTs	8.36
65	448920 410305	AW408009 AF030409	Hs.22580 Hs.62185	alkylglycerone phosphate synthase solute carrier family 9 (sodium/hydrogen	8.36 8.31
	408687	AL110280	Hs.301152	Homo sepiens mRNA; cDNA DKFZp434F053 (fr	8.30
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	8.30
	459060	HB9244	Hs.303627	heterogeneous nuclear ribonucleoprotein	8.30
70	451957 443977	A1796320 AL120986	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	8.30
	457997	AA806616	Hs.150627 Hs.209523	ESTs, Wealdy similar to I38022 hypotheti ESTs	8.30 8.30
	451934	AI540842	Hs.61082	ESTs	8.30
	404335			NA .	8.30
75	445073	AW291389	Hs.13056	hypothetical protein FLJ 13920	8.30
, 5	431566 446307	AF176012 T50083	Hs.260720 Hs.9094		8.29
	423928	AA332680	110.3034	ESTs gb:EST36768 Embryo, 8 week t Homo sapien	8.28 8.26
	436420	AA443966	Hs.31595	ESTs	8.25
80	426110	NM_002913			8.25
ov	442988 402408	AI026130 NA	Hs.131683		8.25
	438707	L08239	Hs.5326	NA amino acid system N transporter 2; porcu	8.24 8.23
	425770	NM_014363			8.22

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	448704	AM090033	Un 240247	hotomassassassassassassassassassassassassass	
	452682	AW080932 AA456193	Hs.249247 Hs.9071	heterogeneous nuclear protein similar to progesterone membrane binding protein	8.21
	411984	NM_005419	Hs.72988	Signal transducer and activator of trans	8.20 8.20
_	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin t	8.20
5	437048	AA743240	Hs.91582	ESTs	8.20
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.20
	447066	8E167667	Hs.32163	ESTs	8.20
	425932	M81650	Hs.1968	semenogelin I	8.20
10	431819 431810	AA515995 X67155	Hs.152334 Hs.270845	ESTs	8.20
10	459702	A1204995	ns.2/0043	kinesin-like 5 (mitotic kinesin-like pro	8.20
	406687	M31126	Hs.272620	gb:an03c03.x1 Stratagene schizo brain S1 pregnancy specific beta-1-glycoprotein 9	8.20 8.18
	413109	AW389845	Hs.110855	ESTs	8.17
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	8.16
15	424335	AW021508	Hs.28170	ESTs	8.10
	453096	AW294631	Hs.11325	ESTs	8.10
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	8.10
	457796 429340	AA913389	Hs.126691	ESTs	8.10
20	445165	N35938 AV652831	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	8.10
	418048	W49670	Hs.56044	gb:AV552831 GLC Homo sapiens cDNA clone ESTs	8.08 8.06
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.04
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.02
26	419559	Y07828	Hs.91096	ring finger protein	8.02
25	409268	AA625304	Hs.188554	ESTs	8.00
	447207 446977	AA442233	Hs.17731	hypothetical protein FLJ12892	8.00
	424565	AW863613 AW102723	Hs.156798	ESTs	8.00
	407013	U35637	Hs.75295	guanylate cyclase 1, soluble, alpha 3 gb:Human nebulin mRNA, partial cds	8.00 7.99
30	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	7.98
	440637	AW900115	Hs.7309	Nomo sapiens clone 23741 mRNA sequence	7.96
	417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	7.95
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	7.94
35	415585	R59946	Hs.184852	KIAA1553 protein	7.92
55	453331 445527	AI240665 W39694	Hs.8895	ESTs	7.92
	417318	AW953937	Hs.83286 Hs.12891	ESTs, Weakly similar to S14747 sphingomy ESTs	7.90
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	7.90 7.90
40	444769	Al191650	Hs.221436	ESTs	7.90
40	444272	AI138596	Hs.154619	ESTs	7.90
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	7.90
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A:	7.90
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	7.90
45	421558 446444	AB011125 AJ743737	Hs.105749 Hs.24370	KIAA0553 protein	7.90
1.5	420000	AB035063	Hs.94262	ESTs p53-inducible ribonucleotide reductase s	7.90 7.86
	437237	BE513073	1-0.5-12-02	gb:601171435F1 NIH_MGC_15 Homo sapiens c	7.86
	409582	R27430	Hs.271565	ESTs	7.84
50	419235	AW470411	Hs.288433	neurotrimin	7.83
50	439620	AA838727	Hs.124405	ESTs, Wealthy similar to A46010 X-finked	7.82
	441690 417735	R81733 AA188175	Hs.33106	ESTs	7.80
	441795	N58115	Hs.82506 Hs.21137	KIAA1254 protein AD024 protein	7.80
	442992	AI914699	Hs.13297	ESTs	7.80 7.80
55	422554	AA312219	Hs.296338	ESTs	7.80
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	7.80
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	7.80
	429228 429399	AI553633	Hs.337139	ESTs	7.80
60	438396	AA452244 AI683487	Hs.16727	ESTs	7.80
	455510	AA422029	Hs.152213 Hs.143640	wingless-type MMTV integration site fami ESTs, Wealdy similar to hyperpolarizatio	7.77 7.76
	429396	AW954598	Hs.201526	Homo sapiens clone 25015 mRNA sequence	7.76 7.76
	453439	A1572438	Hs.32976	guanine nucleotide binding protein 4	7.75
65	410561	8E540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	7.71
03	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	7.71
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	7.70
	413374 404996	NM_001034	Hs.75319	ribonucleolide reductase M2 polypeptide NA	7.70
	418947	W52990	Hs.22860	ESTs	7.70 7.70
70	427401	U20582	Hs.2149	actin like protein	7.70
	410748	BE383816	Hs. 12532	chromosome 1 open reading frame 21	7.70
	426262	A1792141	Hs.196270	folate transporter/carrier	7.70
	446955	AW613138	Hs.156747	ESTs	7.70
75	449199 443212	AI990122 AW269515	Hs.196988		7.70
	446155	AVV269515 AI553695	Hs.102500 Hs.159422		7.70
	427164	AB037721	Hs.173871		7.70 7.70
	452627	AJ122843	Hs.184319		7.70
٥٨	452588	AA889120	Hs.110637	homeo box A10	7.70
80	451838	AW005866	Hs.193969		7.67
	422956	BE545072	Hs.122579		7.66
	451227 450701	R84429 H39960	Hs.151944		7.66
	70101	.~.,,,,,,,	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	7.65

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	432695	D63480	Hs.278634	KIAAD146 protein	7.63
	447476	BE293466	Hs.20880	ESTs, Weakly similar to 138022 hypotheti	7.60
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	7.60
5	447505 423065	AL049266 R96158	Hs.18724 Hs.267130	Homo sapiens mRNA; cDNA DKFZp564F093 (tr Homo sapiens, clone MGC:5406, mRNA, como	7.60
_	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	7.60 7.60
	450628	AW382884	Hs.204715	EST8	7.60
	418995	H39599	Hs.294008	ESTs	7.60
10	416402 405545	NM_000715	Hs_1012	complement component 4-binding protein, NA	7.60
••	440866	A1703103	Hs.271360	hypothetical protein MGC16275	7.60 7.60
	421281	Al299139	Hs.17517	ESTs .	7.60
	424534 421041	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	7.60
15	453311	N36914 AW104911	Hs.14691 Hs.126707	ESTs, Moderately similar to I38022 hypot hypothetical protein FLJ11457	7.60
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	7.54 7.50
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.50
	417531 444099	NM_003157 D87432	Hs.1087	serine/threonine kinase 2	7.50
20	407853	AA336797	Hs.10315 Hs.40499	solute carrier family 7 (cationic amino dickkopf (Xenopus laevis) homolog 1	7.50 7.50
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	7.50 7.50
	447806	W03616	Hs.10432	ESTs, Weakly similar to I38022 hypotheti	7.48
	424748 421089	AA346257 AB037771	Hs.134933 Hs.101799	ESTs KIAA1350 protein	7.48
25	444856	AI888057	Hs.12097	ESTs	7.45 7.42
	447425	A1963747	Hs.18573	acylphosphalase 1, erythrocyte (common)	7.41
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	7.40
	434539 437036	AW748078 AI571514	Hs.214410 Hs.133022	ESTs, Weakly similar to MUC2_HUMAN MUCIN ESTs	7.40
30	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.40 7.40
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.40
	433577 453652	AW007080 AW009640	Hs.8817 Hs.28368	ESTs Medicalet elegants officer at the	7.40
~-	422665	AJ011812	Hs.119018	ESTs, Moderately similar to S65657 alpha transcription factor NRF	7.40 7.40
35	424188	AW954552	Hs.142634	zinc finger protein	7.40
	407300 431494	AA102616 AA991355	Hs.298312	gb:zn43e07.s1 Stratagene HeLa cell s3 93 hypothetical protein DKFZp434A1315	7.40
	452958	AA883929	Hs.40527	ESTs	7.40 7.40
40	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.40
40	428279 449670	AA425310 F07693	Hs.155766 Hs.23869	ESTs, Weakly similar to A47582 B-cell gr	7.40
	449601	AA461509	Hs.293565	Homo sapiens mRNA; cDNA DKF2p434K2172 (f ESTs, Wealdy similar to putative p150 [H	7.40 7.40
	438490	AW593272	Hs.301299	ESTs	7.40
45	410044 429509	BE566742 AW614420	Hs.58169 Hs.204354	highly expressed in cancer, rich in leuc	7.40
	433393	AF038564	Hs.98074	ras homolog gene family, member B itchy (mouse homolog) E3 ubiquitin prote	7.38 7.38
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	7.37
	425773 422755	N21279 T25365	Hs.237749 Hs.119687	EST8	7.36
50	410566	AA373210	Hs.43047	RAN binding protein 8 Homo sapiens cDNA FLJ13585 fis, clone PL	7.36 7.35
	412851	AJ826502	Hs.106149	ESTs	7.35
	418661 436246	NM_001949 AW450963	Hs.1189 Hs.119991	E2F transcription factor 3 ESTs	7.35
	433159	AB035898	Hs.150587	kinesin-like protein 2	7.34 7.33
55	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	7.32
	453878 414696	AW964440 AF002020	Hs.19025 Hs.76918	DC32	7.31
	402250	AV655272	Hs.20252	Niemann-Pick disease, type C1 novel Ras family protein	7.31 7.31
60	439039	A1656707	Hs.48713	ESTs	7.30
60	41 <b>7</b> 976 419436	BE565892 AA991639	Hs.83077 Hs.242413	interleukin 18 (Interferon-gamma-Inducin	7.30
	417008	AW673606	Hs.80758	hypothetical protein DKFZp434K1421 aspartyl-tRNA synthetase	7.30 7.30
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	7.30
65	425889 442969	M57414 AI025499	Hs.161305	tachylinin receptor 2	7.29
••	446360	N42553	Hs.132238 Hs.267914	ESTs homolog of mouse transient receptor pote	7.26 7.25
	438022	AW517524	Hs.135201	NOD2 protein	7.25
	407183 429882	AA358015 AA278898	Hs.225979	gb:EST66864 Fetal lung (II Homo sapiens	7.24
70	420120	AL049610	Hs.95243	hypothetical protein similar to small G transcription elongation factor A (SII)-	7.24 7.22
	400212	NA		NA .	7.20
	431812 419481	AA515902 AI879195	Hs.130650 Hs.90606	ESTs	7.20
	447078	AW885727	Hs.301570	15 kDa selenoprotein ESTs	7.20 7.20
75	413200	AA127395	Hs.222414	ESTs	7.20
	411750 439901	BE562298 N73885	Hs.71827	KIAA0112 protein; homolog of yeast ribos	7.20
	411815	AA156679	Hs.124169 Hs.125790	ESTs leucine-rich repeat-containing 2	7.20 7.20
80	459279	AW814996		gb:MR1-ST0206-170400-024-h09 ST0206 Homo	7.20 7.20
οU	445263 413801	H57646 M62246	Hs.42586	KIAA 1560 protein	7.20
	418407	AL044818	Hs.35406 Hs.84928	ESTs. Highly similar to unnamed protein nuclear transcription factor Y, beta	7.20 7.20
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.20
				490	
				430	

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	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	7.20
	403764			NA	7.20
	416896	AJ752862	Hs.5638	KIAA1572 protein	7.20
5	416636 428071	N32536 AF212848	Hs.42645 Hs.182339	ESTs ets homologous factor	7.20
•	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (barna	7.20 7.18
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	7,17
	409759	N40285	Hs.81182	histamine N-methyttransferase	7.16
10	452448 427951	AW182440 AI826125	Hs.61389 Hs.43546	ESTs, Wealthy similar to unnamed protein ESTs	7.16 7.16
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	7.15 7.15
	419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	7.12
	411769	AI694575	Hs.27207	KIAA0982 protein	7.11
15	430355 419511	NM_006219 AA429750	Hs.239818 Hs.75113	phospholnositide-3-kinase, catalytic, be general transcription factor IIIA	7.10 7.10
•••	409032	AW301807	Hs.297260	ESTs	7.10
	424539	L02911	Hs.150402	activin A receptor, type I	7.10
	439221 430719	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	7.10
20	408020	AA488988 AA127940	Hs.293796 Hs.62781	ESTs ESTs	7.10 7.10
	420218	AW958037	Hs.286	ribosomal protein L4	7.10 7.10
	443487	AI073491	Hs.269887	ESTs, Highly similar to KPBB_HUMAN PHOSP	7.10
	414865	AA157155	Hs.274414	hypothetical protein FU14457	7.10
25	428724 413293	AL390128 AL047483	Hs.191268 Hs.302498	KIAA1530 protein GTP-binding protein homologous to Saccha	7.10 7.10
	419126	AJB10144	Hs.135276	ESTs	7.09
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	7.09
	433730 417381	AK002135 AF164142	Hs.3542 Hs.82042	hypothetical protein FLJ11273	7.07
30	457019	AA421844	Hs.12830	solute carrier family 23 (nucleobase tra hypothetical protein	7.07 7.07
	409697	AB018348	Hs.55947	KIAA0805 protein	7.06
	400977	NA		NA	7.06
	436668 451684	AA831857 AF216751	Hs.209071 Hs.26813	E\$Ts	7.03
35	404029	AF210/31	HS.40013	CDA14 NA	7.03 7.02
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	7.02
	445577	N40696	Hs.137084	cytoplasmic polyadenylation element bind	7.00
	419647 442075	AA348947 AW135928	Hs.91816	hypothetical protein	7.00
40	429598	AA811257	Hs.269710	gb:UI-H-BI1-adp-d-08-0-UI.s1 NCI_CGAP_Su ESTs	7.00 7.00
. •	450832	AW970602	Hs.105421	ESTs	7.00
	421389	AA531291	Hs.101064	Homo sapiens cDNA FLJ12777 fis, clone NT	7.00
	453931 432343	AL121278 NM_002960	Hs.25144 Hs.2961	ESTs S100 calcium-binding protein A3	7.00
45	452979	AW167599	Hs.232282	ESTs	7.00 7.00
	431696	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	7.00
	413583	AL120806	Hs.5888	ESTs	7.00
	436758 455944	AW977167 BE160643	Hs.155272	ESTs gb:PM1-HT0422-291299-002-f03 HT0422 Homo	7.00 6.98
50	430302	AL137502	Hs.238679	Rag D protein	6.96
	437613	R19892	Hs.10267	MIL1 protein	6.96
	440524 451047	R71264	Hs.16798	ESTs	6.95
	450377	AB022317 AB033091	Hs.25887 Hs.74313	sema domain, immunoglobulin domain (lg), KIAA1265 protein	6.93 6.93
55	457396	Z20964	Hs.323817	OKFZP547E1010 protein	6.93
	417393	R10484	Hs.82071	Cbp/p300-interacting transactivator, wit	6.92
	414417 412246	BE299433 AI160873	Hs.68533 Hs.69233	KIAA1679 protein zinc finger protein	6.92
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	6.90 6.90
60	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.90
	405696	NA AA300000		NA .	6.90
	431689 414429	AA305688 R51494	Hs.267695 Hs.71818	UDP-Gal:betaGlcNAc beta 1,3-galactosyttr ESTs	6.90 6,90
	424841	AB001106	Hs.151413	gia maturation factor, beta	6.90
65	418895	AA894638	Hs.14600	ESTs	6.90
	445900 446006	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.90
	432038	NM_004403 AA524746	Hs.13530 Hs.162110	deafness, autosomal dominant 5 ESTs	6.90 6.87
<b>~</b>	446610	AV659433	Hs.282984		6.86
70	451286	AW139789	Hs.16370	Homo sapiens cDNA FLJ11652 fis, clone HE	6.86
	408915 418934	NM_016651 TB3845	Hs.48950	heptacellular carcinoma novel gene-3 pro	6.85
	435143	R12375	Hs.191116 Hs.194600		6.82 6.82
75	442660	AW138174	Hs.130651	ESTs .	6.82
75	432729	AK000292	Hs.278732		6.81
	435990 449062	AI015862 AJ272268	Hs.131793 Hs.22958		6.80
	453688	AW381270	Hs.194110	calcium channel, voltage-dependent, atph hypothetical protein PRO2730	6.80 6.80
٥٨	421476	AW953805	Hs.21887	EST\$	6.80
80	430510	AW162916	Hs.241576		6.80
	409045 410298	AA635062 A1693821	Hs.50094 Hs.182185	Homo sepiens mRNA; cDNA DKFZp43400515 (I ESTs	6.80 6.80
	420560	AW207748	Hs.59115	ESTs	6.80

	427752	AA470687	Hs.104772	ESTs	6.80
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	6.80
	422420 416913	U03398 AW934714	Hs.1524	tumor necrosis factor (ligand) superlami	6.80
5	426890	AA393167	Hs.41294	gb:RC1-DT0001-031299-011-a11 DT0001 Homo ESTs	6.80
-	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	6.60 6.80
	413328	Y15723	Hs.75295	guanyiate cyclase 1, soluble, alpha 3	6.79
	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	6.79
10	434267	AI206589	Hs.116243	ESTs	6.79
10	419358	T78763	Hs.90063	neurocalcin delta	6.79
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	6.78
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	6.77
	443184 444484	A/538728 AK002126	Hs.131973 Hs.11260	ESTs	6.77
15	429483	AA974832	Hs.128708	hypothetical protein FLJ11264 ESTs	6.77
	425605	BE544300	Hs.7076	KIAA1705 protein	6.78 6.76
	425045	AW953186	Hs.92400	ESTs	6.76
	438776	AW245243	Hs.334368	hypothetical protein MGC11257	6.75
20	458174	AA781530	Hs.127236	hypothetical protein FLJ12879	6.74
20	445129	R39878	Hs.21394	ESTs .	6.74
	435532	AW291488	Hs.117305	Homo sapiens, clone tMAGE:3682908, mRNA	6.73
	444442 431240	A1149234 AA496790	Hs.298423	ESTs, Moderately similar to I54374 gene	6.73
	422109	S73265	Hs.179481 Hs.1473	ESTs	6.72
25	416655	AW968613	Hs.79428	gastrin-releasing peptide BCL2/adenovirus E1B 19kD-interacting pro	6.70 6.70
	423811	AW299598	Hs.50895	homeo box C4	6.70
	443695	AW204099	Hs.337720	ESTs, Wealdy similar to AF126780 1 retin	6.70
	420686	A1950339	Hs.40782	ESTs	6.70
30	419574	AK001989	Hs.91165	hypothetical protein	6.70
30	418269 434164	AA806113 AW207019	Hs.189025	EST8	6.70
	408660	AA525775	Hs.148135 Hs.292523	serine/threonine kinase 33	6.70
	453370	AJ470523	Hs.139336	ESTs, Moderately similar to PC4259 femi	6.70
	409506	NM. 006153	Hs.54589	ATP-binding cassette, sub-family C (CFTR NCK adaptor protein 1	6.70 6.70
35	454029	W05150	Hs.37034	homeo box A5	6.70
	413365	AW205188	Hs.124304	Homo sapiens cDNA FLJ14635 fts, clone NT	6.70
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	6.70
	426566	AF131836	Hs.170453	tropomodulin	6.70
40	446261	AA313893	Hs.306219	hypothetical protein FLJ12615 similar to	6.70
70	408547 430458	AA574291 AA479300	Hs.57837 Hs.225706	ESTS	6.70
	413627	BE182082	Hs.246973	ESTs, Wealdy similar to 138022 hypotheti ESTs	6.70
	410498	AA355749	110.240373	gb:EST64459 Jurkat T-cells VI Homo saple	6.70 6.70
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	6.70
45	453691	H12235	Hs.226505	ESTs	6.68
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.68
	415885	D79983	Hs.78894	KIAA0161 gene product	6.68
	405529	AW410458	Hs.5258	chromosome 11 open reading frame2	6.68
50	438242 442643	AW241910 U82756	Hs.122254 Hs.8551	ESTs, Wealdy similar to JX0369 collagen	6.68
•	424802	X79201	Hs.153221	PRP4/STK/WD splicing factor synovial sarcoma, translocated to X chro	6.67
	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	6.67 6.67
	458714	R20916	Hs.202501	ESTs	6.66
66	414591	AJB88490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.65
55	433260	AB040966	Hs.83575	KIAA1533 protein	6.65
	400268	NA NASSAS		NA	6.63
	453180 403973	N46243 NA	Hs.110373	ESTs, Highly similar to T42626 secreted	6.62
	436862	AJ821940	Hs.264622	NA ESTs, Moderately similar to ALUS_HUMAN A	6.60
60	428046	AW812795	Hs.155381	ESTs, Moderately similar to (38022 hypot	6.60 6.60
	453387	A1990741	Hs.252809	ESTs	6.60
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	6.60
	418444	Al902899	Hs.85155	butyrate response factor 1 (EGF-response	6.60
65	448172	N75276	Hs.135904	ESTs	6.60
05	409571 423025	AA504249	Hs.187585 Hs.12244	ESTs .	6.60
	423025 430701	AA831267 A1760833	Hs.12244 Hs.293971	hypothetical protein FLJ20097	6.60
	450373	AI915790	Hs.337282	ESTs ESTs	6.60
	419384	AA490866	Hs.39429	ESTS	6.60 6.60
70	429828	AB019494	Hs.225767	IDN3 protein	6.60
	441761	AJ222880		gb:qp40c06.x1 NCI_CGAP_Co8 Homo sapiens	6.60
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	6.60
	421111	BE299047	Hs.43532	ESTs. Weakly similar to T20177 hypotheti	6.60
75	407424	AF120493		gb:Homo sapiens elastase 1 precursor (EL	6.59
, ,	412396 416209	AW947895 AA236776	Hs.79078	gb:PM1-MT0010-200300-001-f10 MT0010 Homo	6.57
	406674	AA332152	Hs.288036	MAD2 (mitotic arrest deficient, yeast, h tRNA isopentenylpyrophosphate transferas	6.57
	400860			NA	6.57 6.56
00	457893	AA744292		gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sepiens	6.55
80	426108	AA622037	Hs. 166468	programmed cell death 5	6.54
	422133	AW612779	Hs.333159	Homo sapiens laryngeal carcinoma related	6.54
	421044 414135	AF061871	Hs.311736		6.54
	414130	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	6.53

	400351	AF060169	Hs.272369	Homo sepiens AS11 protein mRNA, partial	6.52
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	6.52
	410416 419852	BE410072 AW503756	Hs.63304	protein phosphatase methylesterase-1	6.50
5	419677	N77342	Hs.286184 Hs.21851	hypothetical protein dJ55102.5	6.50
-	431806	AF186114	Hs.270737	Homo sapiens cDNA FLJ12900 fis, clone NT turnor necrosis factor (figand) superfami	6.50 6.50
	429774	AI522215	Hs.50883	KIAA1804 protein	6.50
	428228	AA424352	Hs.210586	ESTs	6.50
	418134	AA397769	Hs.86617	ESTs	6.50
10	403859	NA		NA	6.50
	422704	AA972147	Hs.132275	ESTs	6.50
	416737	AF154335	Hs.79691	LIM domain protein	6.50
	429854	R55508	Hs.99472	ESTs	6.50
15	422672	X12784	Hs.119129	collagen, type IV, alpha 1	6.49
13	453600	BE245211	Hs.119120	E3 ubiquitin ligase SMURF1	6.48
	454835 434603	AW833763 AF147384		gb:QV4-TT0008-130100-077-d10 TT0008 Homo	6.48
	408243	Y00787	Hs.624	gb:Homo sapiens full length insert cDNA	6.48
	429317	AAB31552	Hs.268016	Interleukin 8 Homo sapiens cDNA: FLJ21243 fis, clone C	6.48
20	451316	AI770011	Hs.208310	ESTs	6.47 6.46
	448339	AL035920	Hs.20938	RNA binding motif, single strended inter	6.46
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	6.44
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	6.44
0.5	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.42
25	440526	AI832243	Hs.211471	ESTs	6.42
	432727	AA305233	Hs.278712	eukaryotic translation initiation factor	6.41
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	6.40
	435782	N49433	Hs.285737	Homo sapiens cDNA: FLJ20895 fis, clone A	6.40
30	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone Pt.	6.40
20	407162	N63855	Hs.142634	zinc finger protein	6.40
	446152 422828	AI292036 AL133396	Hs.150028	ESTs	6.40
	418866	T65754	Hs.121281	prion protein 2 (dublet) gb:yc11c07.s1 Stratagene lung (937210) H	6.40
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.40 6.40
35	429039	AI524793	Hs.301897	ESTs	6.40
	447254	NM 004153	Hs.17908	origin recognition complex, subunit 1 (y	6.40
	435159	AA668879	Hs.116649	ESTS	6.40
	429625	AA455568	Hs.193814	ESTs	6.40
40	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	6.40
40	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	6.40
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	6.40
	449911	AJ262106	Hs.12653	ESTs	6.40
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	6.40
45	440395 429500	AA884412 X78565	Hs.216342	ESTS	6.37
7.5	417771	AA804698	Hs.289114 Hs.82547	hexabrachion (tenascin C, cytotactin)	6.37
	417092	H97508	Hs. 181165	retinoic acid receptor responder (tazaro eukaryotic translation elongation factor	6.36 6.36
	412227	AW902282	715.101100	gb:QV3-NN1023-260400-169-g10 NN1023 Homo	6.36
	400845			NA	6.36
50	403546	NA		NA	6.36
	412345	AW938386		gb:PM4-DT0057-201299-002-G10 DT0057 Homo	6.35
	422186	AW962364	Hs. 129051	ESTs	6.34
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6.34
55	417687	AI828596	Hs.250691	ESTs	6.33
22	426223	AW977812	Hs.130391	ESTs	6.32
	417588	Z44510		gb:HSC220091 normalized infant brain cDN	6.32
	432829	AW860548	Hs.280658	ESTs	6.31
	440495 407771	AA887212 AL138272	Hs.14161	hypothetical protein DKFZp434I1930	6.31
60	417517	AF001176	Hs.62713 Hs.82238	ESTS	6.31
••	431041	AA490967	Hs.197955	POP4 (processing of precursor , S. cerev KIAA0704 protein	6.30 6.30
	445571	Al378000	Hs.158489	ESTs, Wealthy similar to 2184_HUMAN ZINC	6.30
	433309	AA807060	Hs.126558	ESTs	6.30
	415659	W27214	Hs.78547	zinc finger protein (clone 647)	6.30
65	420271	A1954365	Hs.42892	ESTs	6.30
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.30
	400950	NA		NA .	6.30
	429692	N48422	Hs:9977	ESTs, Wealdy similar to 834087 hypotheti	6.30
70	439813	AA846321	Hs.124501	ESTs	6.30
70	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.30
	453596 446847	AA441838 T51454	Hs.62905	hypothetical protein FLJ14834	6.30
	435820	T51454 AA700580	Hs.82845	Homo sapiens cDNA: FLJ21930 ffs, clone H	6.30
	452576	AB023177	Hs.189000		6.30
75	448924	ABU23177 AW450569	Hs.29900 Hs.188399	KIAA0960 protein ESTs	6.30
. •	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.30 6.30
	412591	BE217736	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	6.30 6.30
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.30
00	419088	AI538323	Hs.52620	integrin, beta 8	6.30
80	401424			NA	6.30
	412189	R60982	Hs.22581	ESTs	6.30
	435501	AW051819	Hs.129908	KIAA0591 protein	6.30
	408221	AA912183	Hs.47447	ESTs	6.28

	413943 416845	AW294416	Hs.144687	Homo saplens cDNA FLJ12981 fis, clone NT	6.28
	402732	H95279 NA		gb:yu20h02.s1 Soares fetal fiver spleen NA	6.27
_	413224	AI732470	Hs.191157	ESTs, Wealdy similar to ALU7_HUMAN ALU S	6.26 6.24
5	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	6.24
	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	6.24
	419548 453880	AW978142 AI803166	Hs.326248 Hs.28462	Homo sapiens cDNA: FLJ22071 fis, clone H	6.23
	422675	BE018517	Hs.119140	ESTs, Weakly similar to 138022 hypotheti eukaryotic translation initiation factor	6.22 6.22
10	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.21
	445584	AF217518	Hs.8360	PTD012 protein	6.21
	451065	AW295132	Hs.222231	ESTs, Wealthy similar to granule cell mar	6.21
	420807 421155	AA280627 H87879	Hs.57846 Hs.102267	ESTs hysyl oxidase	6.20
15	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	6.20 6.20
	440209	H05049	Hs.22269	neurexin 3	6.20
	408170	AW204516	Hs.31835	ESTs	6.20
	433590 442008	N98410 AI457814	Hs.48364	Homo sapiens regulator of G-protein sign	6.20
20	420617	AK001652	Hs.270272 Hs.99423	ESTs ATP-dependent RNA helicase	6.20 6.20
	402343		1.0.00 120	NA NA	6.20
	432682	AJ376400	Hs.159588	ESTs	6.20
	452109 429954	AI525873	Hs.61164	hypothetical protein FLJ14909	6.20
25	417256	A1918130 U94332	Hs.21374 Hs.81791	ESTs tumor necrosis factor receptor superfami	6.20 6.20
	435525	AI831297	Hs.123310	ESTs	6.20
	413604	R51767		gb:yg73g11.r1 Soares infant brain 1NIB H	6.20
	425305 443285	AA363025	Hs.155572	Human clone 23801 mRNA sequence	6.20
30	446565	Al301918 D13757	Hs.334264 Hs.311	ESTs phosphoribosyl pyrophosphate amidotransf	6.20 6.20
	451027	AW519204	Hs.40808	ESTs	6.20
	452243	AL355715	Hs.28555	programmed cell death 9	6.19
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	6.17
35	424060 432494	X92108 AA551060	Hs.138629	H.sapiens mRNA for subtelomeric repeat s gb:rik74f02.s1 NCI_CGAP_Sch1 Homo sapiens	6.17 6.16
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	6.14
	419638	N46504	Hs.91747	profilin 2	6.13
	445595 433036	W25950 AA574091	Hs.14512	DIPB protein	6.13
40	457155	AL110243	Hs.105964 Hs.187991	ESTs DKFZP564A122 protein	6.13 6.13
	443715	AI583187	Hs.9700	cyclin E1	6.13
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.12
	453286 424897	AA034319 D63216	Hs.29041 Hs.153684	Homo sapiens cDNA FLJ14177 fls, clone NT frizzled-related protein	6.11
45	429188	AB011171	Hs.198037	KIAA0599 protein	6.11 6.11
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	6.10
	413339 453685	A1818080 AL110309	Hs.194290	ESTs	6.10
	421195	BE464560	Hs.133017	gb:DKFZp564L0278_r1 564 (synonym: hfbr2) ESTs	6.10 6.10
50	453296	AA034413	Hs.62560	ESTs	6.10
	444985	AI677737	Hs.28329	hypothetical protein FLJ14005	6.10
	423492 419841	AF020761 BE005848	Hs.129683 Hs.7326	ubiquitin-conjugating enzyme E2D 1 (homo	6.10
	429190	H18650	Hs.92602	ESTS ESTS	6.10 6.10
55	426116	AA868729	Hs.144694	ESTs	6.10
	451441	AA017601	Hs.84529	ESTs, Wealdy similar to Z202_HUMAN ZINC	6.10
	401740 441953	H11695	Hs.322901	NA dispushes of oliversine 10	6.10
	401464	AF039241	Hs.9028	disrupter of sitencing 10 histone deacetylase 5	6.10 6.10
60	405033			NA .	6.10
	410743	AA089474	Hs.272153	ESTs	6.10
	454758 417728	AW845266 AW138437	Hs.24790	gb:IL2-CT0031-160999-003-808 CT0031 Homo	6.10
	418553	T88964	113.24730	KIAA1573 protein gb:yd97a07.r1 Soares fetal liver spleen	6.10 6.09
65	431617	AK000738	Hs.264636	hypothetical protein FLJ20731	6.08
	455608	BE011437		gb:CM4-BN0220-080500-170-03 BN0220 Homo	6.08
	450755 455217	AA010984 AW867534	Hs.159464	ESTs	6.07
	437179	AA393508	Hs.300642	gb:MR0-SN0037-160400-004-e05 SN0037 Homo serotogically defined coton cancer antig	6.07 6.06
70	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	6.06
	415308	F05251		gb:HSC04H101 normalized infant brain cDN	6.06
	428417 426501	AK001699 AW043782	Hs.184227 Hs.293616	F-box only protein 21	6.05
	431077	A1669133	Hs.115660		6.03 6.03
75	403040			NA	6.02
	445704	AJ493742	Hs.165210		6.02
	415637 427925	R25517 N51323	Hs.255935	gb:yg44f01.r1 Soares infant brain 1NIB H	6.02
	404702	NA NA	. 10.23333	Homo sapiens, clone IMAGE:3448993, mRNA NA	6.02 6.02
80	433183	AF231338	Hs.222024	transcription factor BMAL2	6.01
	437762 443833	T78028 AI654108	Hs.154679		6.01
	422263	AA307639	Hs.135125 Hs.129908		6.01 6.00
					0.00

	420909	AJ640551	Hs.88878	Homo sapiens cDNA: FLJ23536 fs, clone L	6.00
	407612	U26403	Hs.37142	ephrin-A5	- 6.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	6.00
5	453853	AL040600	Hs.188083	ESTs	6.00
J	444188	Al393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	422505	AL120862	Hs.124165	ESTs	6.00
	420734	AW972872	Hs.293736	ESTs	6.00
10	455082 -	BE148180	44000	gb:RCO-HT0232-211099-011-e04 HT0232 Homo	6.00
10	444200	AA327113	Hs.149057	ESTs	6.00
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate finked moi	6,00
	419752 428412	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN 2	6.00
	407790	AA428240	Hs.126083	ESTs	6.00
15	428945	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	6.00
13	431878	AW192803	Hs.98974	ESTs, Wealdy similar to S65824 reverse t	6.00
	425282	AA521207	Hs.270202	ESTs, Wealdy similar to ALU4_HUMAN ALU S	6.00
	401093	AW163518	Hs.155485	huntingtin interacting protein 2	6.00
	411861	AW867875		NA	6,00
20	411800	N39342	Hs.103042	gb:MR0-SN0040-050500-003-f11 SN0040 Homo	6.00
	446925	AW974605	Hs.176669	microtubule-associated protein 18 ESTs	5.99
	401708	NA NA	rts.170003	NA	5.98
	449894	AK001578	Hs.24129	CLLL7 protein	5.98
	403278	NA NA	140.24123	NA NA	5.97
25	455212	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	5.96
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	5.96 5.96
	441271	AA927290	Hs.130462	ESTs	5.95
	404072			NA .	
	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) hornolog A	5.95
30	421622	AB037748	Hs.106204	KIAA1327 protein	5.94 5.93
	441300	R35063	Hs.181536	ESTs	5.92
	445517	AF208855	Hs.12830	hypothetical protein	5.91
	429559	AI985345	Hs.26425	ESTs	5.91
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	5.91
35	440510	H08427	Hs.309165	ESTs, Wealthy similar to ISHUSS protein d	5.90
	414727	BE466904		gb:hz28f03.x1 NCI_CGAP_GC6 Horno sapiens	5.90
	451686	AA059246	Hs.110293	ESTs	5.90
	438032	BE045624	Hs.152992	ESTs	5.90
	450470	Z75330	Hs.286148	stromal antigen 1	5.90
40	430533	AA480895	Hs.201552	ESTs. Weakly similar to T17288 hypotheti	5.90
	432662	AL049314	Hs.280700	ESTs	5.90
	451742	T77609	Hs.117970	ankyrin 2, neuronal	5.90
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	5.90
4.5	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	5.90
45	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	5.90
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	5.90
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.90
	433865	N29862	Hs.44104	ESTs	5.90
50	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	5.90
50	448743	AB032962	Hs.21898	KIAA1138 protein	5.90
	447153	AA805202	Hs.315562	ESTs .	5.90
	425793	AA363946	Hs.20969	ESTs	5.90
	404632			NA	5.90
55	446364	AB006624	Hs.14912	KIAA0286 protein	5.90
"	452240	AI591147	Hs.61232	EST6	5.90
	410424	AA084984		gb:zn11a08.r1 Stratagene hNT neuron (937	5.90
	404170 458390	A1702505	N- 400000	NA	5.89
	408296	A1792585 AL117452	Hs.133272 Hs.44155	ESTs, Wealthy similar to ALUC_HUMAN !!!!	5.89
60	444406	AL117452 AL147237		DKFZP586G1517 protein	5.88
~	413894	BE177983	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.87
	453922	AF053306	Hs.36708	gb:RC3-HT0600-230300-021-g10 HT0600 Homo	5.87
	446700	AW206257	Hs.156326	budding uninhibited by benzimidazoles 1 Human DNA sequence from clone RP11-145L2	5.86
	443377	AJ792547	Hs.133292	ESTs	5.86
65	419162	AA234591	Hs.304123	ESTS	5.86
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	5.85
	428650	AI560456	Hs.107319	ESTs	5.84
	437410	AW023340	Hs.14880	ESTs	5.84
	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	5.84
70	401004			NA	5.84 5.83
	414504	AW0691B1	Hs.115175	sterile-alpha motif and leucine zipper c	
	410979	BE151480		gb:RC0-HT0295-071199-011-801 HT0295 Homo	5.83 5.82
	424576	BE154142	Hs.96833	ESTs	5.82 5.82
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	
75	423057	AW961597	Hs.130816	ESTs. Moderately similar to 138022 hypot	5.81 5.80
	429250	H56585	Hs.198308		5.80
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.80 5.80
	451367	AA923729	Hs.26322	cell cycle related kinase	5.80
00	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	5.80
80	421589	AW954177	Hs.82919	cultin 2	5.80
	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	5.80
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.60
	436096	H55931	Hs.269582	ESTs	5.80



	443353	At052659	Hs.133255	ESTs	5.80
	457244 407746	AA581385 AKD01962	Hs.162473	ESTs, Weakly similar to 138022 hypotheti	5.80
	440688	AW404591	Hs.38114 Hs.147440	hypothetical protein FLJ11100 ESTs, Wealdy similar to Z192_HUMAN ZINC	5.60 5.80
5	445745	AB007924	Hs.13245	KIAA0455 gene product	5.80
	405637	NA	·	NA .	5.80
	415293 440404	R49462 AI015881	Hs.106541	ESTs	5.80
	442227	AW771958	Hs.324527 Hs.175437	mitochondrial ribosomal protein S5 ESTs, Moderately similar to PC4259 ferri	5.80 5.80
10	423395	AA326613	10.110107	gb:EST29922 Cerebellum II Homo sapiens c	5.80
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.80
	416000	R82342	Hs.79856	ESTs. Weakly similar to S65657 alpha-1C-	5.80
	422108 430818	AA297914 AI311928	Hs.111749	postmetotic segregation increased (S. ce gb:qo89h04.x1 NCI_CGAP_Kid5 Homo septens	5.80
15	444749	AI190672	Hs.65926	ESTs	5.80 5.80
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	5.79
	456192	D84109	Hs.80248	RNA-binding protein gene with multiple s	5.78
	411253 417219	AW833897 AW973473	Hs.220938	gb:QV0-TT0009-111199-055-b07 TT0009 Homo ESTs	5.78 5.78
20	409450	AW628650	Hs.61260	hypothetical protein FLJ13164	5.76
	412013	AA400753	Hs.43761	ESTs, Weakly similar to A46010 X-linked	5.76
	425566	AW162943	Hs.250618	UL16 binding protein 2	5.75
	417877 437114	AI025829 AA836641	Hs.86320 Hs.163085	ESTA ESTs	5.75
25	421238	AB033101	Hs.102796	Homo sapiens cDNA FLI10708 fis, clone NT	5.75 5.74
	428959	AF100779	Hs.194680	WNT1 inducible signating pathway protein	5.73
	415209	F00183	Hs.172004	66n	5.73
	429922 420022	Z97630 AA256253	Hs.226117 Hs.120817	H1 histone family, member 0 ESTs	5.72
30	431485	BE621320	Hs.257486	hypothetical protein FLJ20062	5.71 5.71
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	5.71
	434276	AF123659	Hs.93605	leucine zipper, putative turnor suppresso	5.71
	438085 444379	R52518 N99035	Hs.7967 Hs.222657	ESTs ESTs	5.70
35	401348	NA	113.222037	NA	5.70 5.70
	428878	AA436884	Hs.48926	ESTa	5.70
	422564	AI148006	Hs.222120	ESTs	5.70
	452560 408384	BE077084 BE144344	Hs.336432 Hs.7589	ESTs ESTs, Weakly similar to A46010 X-linked	5.70
40	409948	AA078643	115.7303	gb:7P08801 Chromosome 7 Ptacental cDNA L	5.70 5.70
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	5.70
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	5.70
	439203 442029	AA448930 AW956698	Hs.8453 Hs.14456	KIAA1587 protein	5.70
45	451922	BE463995	Hs.211033	neural precursor cell expressed, develop ESTs	5.70 5.70
	407808	AA663559	Hs.279789	histone deacetytase 3	5.70
	428161	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi	5.70
	413430 428223	R22479 AA424313	Hs.167073 Hs.98402	Homo sapiens cDNA FLJ13047 ffs, clone NT ESTs	5.70
50	427972	AA864870	Hs.181304		5.70 5.70
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	5.70
	416319	AI815601	Hs.79197	CD83 antigen (activated 8 lymphocytes, i	5.70
	458044 432911	AW979114 AW807634	Hs.326135 Hs.279799	ESTs putative zinc finger protein NY-REN-34 a	5.70 5.70
55	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	5.70 5.70
	408867	AA437199	Hs.656	cell division cycle 25C	5.70
	428679 428822	AA431765	U- 2024¢	gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.70
	420022 409570	W28418 AW418720	Hs.30715 Hs.167583	potassium voltage-gated channel, isk-ret ESTs	5.70 5.70
60	457441	BE467737	Hs.146125		5.70 5.70
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	5.70
	420192 423582	AA256281	Hs.105040		5.69
	454511	BE000831 AW948146	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE gb:RC0-MT0013-280300-031-e02 MT0013 Homo	5.69 5.68
65	419586	AI088485	Hs.144759	ESTs, Weakly similar to (38022 hypotheti	5.67
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	5.67
	435849	BE305242	Hs.16098	claudin 2	5.67
	457892 450191	AA744389 AW137243	Hs.222446	gb:ny51e10.s1 NCt_CGAP_Pr18 Homo sapiens ESTs	5.66
70	438653	AW188099	Hs.131813		5.66 5.66
	422910	AI269508	Hs.121591	Human DNA sequence from PAC 257A7 on chr	5.66
	453694	AW504918	Hs.258208	Homo sapiens, clone MGC: 15606, mRNA, com	5.66
	445302 446080	AK001537 Al221741	Hs.12488 Hs.117777	hypothetical protein FLJ10675 ESTs	5.66
75	425474	Z48054	Hs.117777 Hs.158084		5.65 5.55
-	432542	AW083920	Hs.16098	claudin 2	5.65
	446983	AA157484	Hs.97199	complement component C1q receptor	5.65
	420898 401372	A8002379	Hs.100113		5.65
80	428541	AJ862570	Hs.299214	NA Homo sapiens, clone IMAGE:2822295, mRNA	5.64 6.63
	426249	F05422	Hs.168352		5.63 5.63
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	5.63
	451883	AL120634	Hs.305923	ATPase, Ca++ transporting, plasma membra	5.62



	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transf	5.62
	401183 426029	AW294138	Hs.255277	NA ESTs	5.62
	443462	AI064690	Hs.171176	ESTs	5.61 5.61
5	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	5.60
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	5.60
	444577	AI207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.60
	423605 413447	AF047826 AW969388	Hs.129887	cadherin 19, type 2	5.60
10	442957	AI949952	Hs.10450 Hs.49397	Homo sapiens cDNA; FLJ22063 fis, clone H ESTs	5.60 5.60
	424296	AJ631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	5.60
	430679	R44428	Hs.22801	ESTs	5.60
	449358	AA001229	Hs.131436	ESTs	5.60
15	418348 433133	AI537167 AB027249	Hs.96322	hypothetical protein FL123560	5.60
	444059	R69743	Hs.104741 Hs.116774	PDZ-binding kinase; T-cell originated pr Integrin, alpha 1	5.60 5.60
	438157	AW137011	Hs.49576	ESTs	5.60
	428233	Al358831	Hs.20578	ESTs	5.60
20	434265	AAB46811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	5.60
20	451652 422762	AA018968 AL031320	Hs.133536 Hs.119976	ESTs	5.59
	447591	AI675417	Hs.282855	Human DNA sequence from clone RP1-20N2 o ESTs	5.59 5.58
	417958	AA767382	Hs.193417	ESTs	5.57
25	438146	Z36842	Hs.57548	ESTS	5.57
25	413595	AW235215	Hs.16145	ESTs .	5.57
	422406 420529	AF025441 D25259	Hs.116206 Hs.319844	Opa-interacting protein 5	5.56
	439582	W79161	Hs.118327	ESTs, Moderately similar to 154374 gene Homo sepiens cDNA FLJ11522 fis, clone HE	5.56 5.56
20	408744	AW806177		gb:MR1-UM0108-130400-003-d04 UM0108 Homo	5.56
30	447230	AW972147	Hs.101395	hypothetical protein MGC11352	5.54
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	5.54
	446813 451424	AA971436 AI862026	Hs.16218 Hs.302810	KIAA0903 protein Novel human gene mapping to chomosome 20	5.53
	410516	BE537917	Hs.90034	hypothetical protein FLJ21916	5.53 5.53
35	453994	BE180964	Hs.165590	ribosomal protein 613	5.53
	435583	AA767714	Hs.291627	ESTs	5.52
	431585 408912	BE242803 AB011084	Hs.262823	hypothetical protein FLJ10326	5.51
	427966	R97130	Hs.48924 Hs.189699	KIAA0512 gene product; ALEX2 ESTs	5.51
40	433611	AW327692	Hs.3446	mitogen-activated protein kinase kinase	5.51 5.51
	401244			NA .	5.50
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	5.50
	434006 425650	AF113688 NM_001944	U- 102E	gb:Homo sapiens clone FLB4630	5.50
45	427507	AF240467	Hs.1925 Hs.179152	desmoglein 3 (pemphigus vulgaris entigen toll-like receptor 7	5.50 5.50
	423268	BE386898	Hs.131162	ESTs. Weakly similar to ALU5_HUMAN ALU S	5.50 5.50
	405065	NA		NA .	5.50
	444302 418183	A1140115 NM_001772	Hs.225130 Hs.83731	ESTs	5.50
50	435586	AI279137	Hs.151498	CD33 antigen (gp67) ESTs	5.50 5.50
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	5.50 5.50
	427189	HB2453	Hs.5635	ESTs	5.50
	415263	AA948033	Hs.130853	ESTs	5.50
55	441818 407834	AI630451 AW084991	Hs.7976 Hs.26100	KIAA0332 protein ESTs	5.50
	404012	NA NA	115.20100	NA NA	5.50 5.50
	449932	A1675444	Hs.263024	ESTs	5.50
	423760	AA775891	Hs.191980	ESTs	5.50
60	431576 423172	M76665 R15652	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	5.50
•	422295	AF051151	Hs.114408	gb:HH503-F Adult heart, Clontech Homo sa toll-like receptor 5	\$.50 5.50
	429044	AJ261490	Hs.145527	ESTs	5.50 5.50
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 ffs, clone MA	5.50
65	414323	NM_014759	Hs.334688	KIAA0273 gene product	5.50
UJ	405511 444665	NA BE613126	Hs.47783	NA B aggressive lymphoma gene	5.49
	434434	AA633516	Hs.157201	ESTs	5.49 5.48
	421997	R66740	Hs.110613	KIAA0220 protein	5.47
70	410276	AI554545	Hs.68301	ESTs	5.47
70	435867 453837	AA954229 AL138387	Hs.114052	ESTs	5.47
	409617	BE003760	Hs.256126 Hs.55209	baculoviral IAP repeat-containing 7 (liv Homo sapiens mRNA; cDNA DKFZp434K0514 (f	5.47 5.47
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.47 5.47
75	401629	NA		NA	5.46
75	433071	BE150229	Hs.281564	retinal outer segment membrane protein 1	5.46
	458247 418049	R14439 AA211467	Hs.209194	ESTS	5.46
	418247	R55174	Hs.190488	Homo sapiens, Similar to nuclear localiz gb:yg87h04.r1 Soares infant brain 1NIB H	5.45 5.45
00	453716	AA037675	Hs.152675	ESTs	5.44
80	431157	AI823969	Hs.132578	EST8	5.44
	426873 437092	Al190540 AA744292	Hs.131092	ESTS	5.43
	445782	AW407872	Hs.315367	gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens Homo sapiens, Similar to hypothetical pr	5.42 6.42
			110001	rond seprens, column to hypothetical pr	5.42

	447393	Al377458	Hs.158831	EST	5.42
	425283	AA354338	Hs.131100	ESTs	5.42
	401208	NA		NA	5.42
5	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	5.42
,	405523			NA .	5.42
	409012 429803	AL117435 W81489	Hs.49725 Hs.223025	DKFZP434I216 protein	5.41
	436982	AB018305	Hs.5378	RAB31, member RAS oncogene family spondin 1, (Fspondin) extracellular mat	5.41 5.40
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	5.40
10	456027	BE327387	Hs.13913	KIAA1577 protein	5.40
• •	411897	AW875066	Hs.326876	Homo saplens SOX8 mRNA, complete cds	5.40
	449689	AF228421	Hs.23889	DKFZP564A032 protein	5.40
	432865	AJ753709	Hs.152484	ESTs, Wealty similar to 138022 hypotheti	5.40
	408248	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.40
15	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.40
	423289	N77774		gb:yz83e01.r1 Soares_multiple_sclerosis_	5.40
	453365	AA035211	Hs.17404	ESTs	5.40
	406465	4144777770	14- 435555	NA SOT-	5.40
20	441858 432507	AW173339	Hs.135665 Hs.324667	ESTs	5.40
20	440570	BE391093 Al205712	Hs.125998	ESTs ESTs	5.40
	445062	Al339915	Hs.44324	ESTS	5.40 5.40
	421639	NM_012082	Hs. 106309	Friend of GATA2	5.40
	410406	AI969703	Hs.1466	glycerol kinase	5.40
25	418939	AW630803	Hs.89497	lamin B1	5.40
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.40
	400250	NA		NA .	5.40
	424650	AW576156	Hs.250824	Homo sapiens cONA: FLJ23435 ffs, clone H	5.40
20	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (tectin	5.39
30	433384	AI021992	Hs.124244	ESTs	5.38
	428781	AF164799	Hs.193384	putatative 28 kDa protein	5.38
	438150 400639	AA037534	Hs.79059	transforming growth factor, beta recepto	5.38
	426485	NM_006207	Hs.170040	NA stated desired arouth faster successes	5.38
35	424205	AA336825	113.170040	platelet-derived growth factor receptor- gb:EST41732 Endometrial turnor Homo saple	5.37 5.36
	459596	H29554	Hs.113871	ESTs	5.36
	408234	AW993356	Hs.285814	sprouty (Drosophila) homotog 4	5.36
	414547	T47770	Hs.191463	ESTs	5.35
	419851	AA287987	Hs.13477	ESTs, Wealthy similar to 1207289A reverse	5.35
40	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	5.34
	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.34
	405352			NA	5.33
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	5.32
45	424284	BE541008	Hs.6193	hypothetical protein FLJ14590	5.32
73	427741 426021	AW753185	Hs.180628	dynamin 1-like	5.31
	442186	AW770897 AA984083	Hs.34392 Hs.269746	ESTs, Wealth similar to I38022 hypotheti	5.31
	437319	BE410958	Hs.56406	ESTs, Wealthy similar to T03306 PSD-95/SA Homo sapiens cDNA FLJ13549 fis, clone PL	5.30 5.30
	405287	NA NA	16.50400	NA	5.30 5.30
50	427032	AF012023	Hs.173274	Integrin cytoplasmic domain-associated p	5.30
	415371	R15239		gb:yf89b02.r1 Soares infant brain 1NIB H	5.30
	420024	AA252905	Hs.194477	E3 ubiquitin tigase SMURF2	5.30
	434408	AI031771	Hs.132586	ESTs	5.30
55	434739	AAB04487	Hs.144130	ESTs	5.30
22	421327	AAB37295	Hs. 188802	ESTs	5.30
	453058	AW612293	Hs.288684		5.30
	448776 417845	BE302464 AL117461	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.30
	430264	AA470519	Hs.82719	Homo sepiens mRNA; cDNA OKFZp586F1822 (f	5.30
60	411402	BE297855	Hs.69855	gb:nc71f10.s1 NCI_CGAP_Pr1 Homo saplens NRAS-related gene	5.30 5.30
••	419220	AA811938	Hs.291759	ESTs	5.30 5.30
	407995	AI094748	Hs.100134		5.30
	459256	AW967468	Hs.99821	hypothetical protein FLJ14547	5.30
~	452449	AW068658	Hs.20943	ESTs	5.30
65	430366	AI057368	Hs.105575	ESTs	5.30
	434360	AW015415	Hs.127780		5.30
	422560	F11469	Hs.118281		5.29
	441704	AI458766	Hs.201988		5.29
70	443635	AI080230	Hs.134214		5.29
, 0	434342 423409	AI791138 NM_006466	Hs.116768 Hs.128207		5.29
	449000	U69560			5.29
	452381	H23329	Hs.3826 Hs.290880	keich-like protein C3IP1 FSTs Wealth similar to ALLIA HUMAN ALUS	5.29 6.20
_	409068	AW236991	Hs.102495		5.29 5.29
75	434860	AA932386	Hs.292667		5.28
_	408096	BE250162	Hs.83765	dihydrofolate reductase	5.28
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	5.28
	435443	AJ248674	Hs.14295	ESTs	5.26
00	414269	AA298489	Hs.303171		5.26
80	408371	AF161545	Hs.279883	hypothetical protein	5.26
	401205	NA DOZANO		NA	5.26
	450904	R07118	Hs.189924		5.26
	416351	H49704	Hs.173522	! ESTs	5.26

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	426524	AA380611	Hs.163841	ESTs .	5.25
	412901 452487	AJ127359 AW207659	Hs.289088 Hs.6630	heat shock 90kD protein 1, alpha	5.25
	444825	AW167613	Hs.248	Homo sapiens cDNA FLJ13329 fis, clone OV mitogen-activated protein kinase kinase	5.24 5.24
5	412953	Z45794	Hs.238809	ESTs	5.24
	404117	NA		NA	5.22
	427956	AL046175	Hs.108169	Homo sapiens mRNA; cDNA DKFZp586C1619 (I	5.22
	421787 437255	AA227068 R58970	Hs.108301	nuclear receptor subfamily 2, group C, m	5.22
10	424697	AL136169	Hs.9887 Hs.250708	ESTs CAAX box 1	5.22 5.20
- •	449771	A1668702	Hs.54976	ESTs	5.20 5.20
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.20
	438885	AI886558	Ha.184987	ESTs	5.20
15	407182	AA312551	Hs.230157	EST ₈	5.20
13	452150 419680	W42490 AA249720	Hs.260844 Hs.59335	ESTs ESTs	5.20 5.20
	438940	AF075045	Hs.271609	ESTs	5.20
	405362	NA		NA .	5.20
20	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.20
20	442353 409331	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.20
	415397	M36634 H10818	Hs.53973	vasoactive intestinal peptide gb:ym04f10.r1 Soares infant brain 1NIB H	5.20 5.20
	406735	AA603092		gb:rp37a01.s1 NCI_CGAP_Lu1 Homo sapiens	5.20
25	418489	U76421	Hs.85302	adenosine dearninase, RNA-specific, 81 (h	5.20
25	431480	AA837274	Hs.257005	hypothetical protein FLJ20837	5.20
	425523 425673	AB007948 R70318	Hs.158244	KIAA0479 protein	5.20
	439267	AA287747	Hs.339730 Hs.173012	ESTs ESTs, Weakly similar to A46010 X-Enked	5.20 5.20
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	5.20
30	424638	AI472106	Hs.49303	Homo sepiens cDNA FLJ11663 fis, clone HE	5.20
	454434	AA083558	Hs.261286	ESTs	5.20
	448336 429534	R53848 AW976987	Hs.44976	ESTs	5.20
	434803	AW974640	Hs.163327 Hs.303413	ESTs, Weakly similar to 2109260A B cell ESTs	5.20 5.20
35	403199	NA	. 13.000713	NA NA	5.20 5.20
	435225	AI021912	Hs.187983	ESTs	5.20
	451664	AA889081	Hs.153952	5 nucleotidase (CD73)	5.20
	440385 432328	AA884283 A1572739	Hs.192136 Hs.195471	ESTS	5.20
40	400484	MJ/2/35	F13. 19347 I	6-phosphofructo-2-kinase/fructose-2,6-bi NA	5.20 5.20
-	425757	AA363171		gb:EST72986 Ovary II Homo sapiens cDNA 5	5.19
	449841	AJ671502	Hs.199602	ESTS	5.19
	420303	AA258282	Hs.278436	KIAA1474 protein	5.19
45	429687 453345	A1675749 AA302862	Hs.211608 Hs.90063	nucleoporin 153kD	5.19
15	447499	AW262580	Hs.147674	neurocalcin delta protocadherin beta 16	5.18 5.18
	404913			NA	5.18
	405114	NA		NA	5.18
50	431117 411995	AF003522 W49701	Hs.250500	delta (Orosophila)-Eke 1	5.18
50	401738	NA NA	Hs.29667	ESTs NA	5.17 5.17
	425250	AA353496	Hs.269762	ESTs, Weakly similar to A47582 B-cell gr	5.16
	454388	AA630905	Hs.333300	hypothetical protein FLJ14026	5.16
55	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	5.16
33	443646 436032	AI085198 AA150797	Hs.154226 Hs.109276	ESTs latexin protein	5.15
	456896	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	5.15 5.15
	433672	BE281165	Hs.288038	TLS-essociated serine-arginine protein 1	5.15
60	432826	X75363	Hs.250770	ACO for serine protesse homologue	5.14
oo	439441 400205	W67993	Hs.323135	ESTs	5.14
	430854	NA AW440369	Hs.47026	NA ESTs	5.14 5.14
	408771	AW732573	Hs.47584	potassium voltaga-gated channel, delayed	5.14 5.14
"	456804	Al421645	Hs.139851	caveolin 2	5.14
65	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	5.13
	449210 419013	AI635363 T90378	Hs.197636	ESTS	5.12
	425843	BE313280	Hs.14463 Hs.159627	ESTs death associated protein 3	5.12 5.12
	422545	X02761	Hs.287820		5.12
70	424785	R23519	Hs.6126	hypothetical protein dJ1141E15.2	5.11
	442833	AA328153	Hs.88201	ESTs, Wealdy similar to A Chain A, Cryst	5.10
	422411 457565	AW749443 BE294029	Hs.22511 Hs.279903	ESTs Post homolog accident in busin 3	5.10
	437722	AW292947	Hs.122872		5.10 5.10
75	446893	A1610818	Hs.7110	ESTs	5.10 5.10
	401581			NA .	5.10
	417511	AL049176	Hs.82223	chordin-like	5.10
	422336 437662	A1761322 AA765387	Hs.115285		5.10
80	429526	AA454182	Hs.145095 Hs.99360	ESTs ESTs	5.10 5.10
-	447332	AW445012	Hs.160918		5.10 5.10
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	5.10
	428155	H17012	Hs.14633	ESTs	5.10

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	420185	AL044056	Hs.158047 Hs.279575	ESTs Homo sapiens G-protein coupled receptor	5.10 5.10	
	445657 440913	AW612141 Al267491	Hs.160593	ESTs	5.10	
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	5.10	
5	428603	BE241619	Hs.24641	cytoskeleton associated protein 2	5.10	
	436577	W84774	Hs.17643	ESTs	5.10	
	400241	NA	11- 070242	NA Homo sapiens mRNA; cDNA DKFZp564D2071 (f	5.10 5.10	
	437205 423654	AL110232 AI674253	Hs.279243 Hs.35828	ESTs	5.10	
10	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	5.10	
	430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.10	
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	5.10	
	440381	AA917808	Hs.190495	ESTS	5.10 5.10	
15	441033 450229	BE562555 R18717	Hs.8929	gb:601335867F1 NIH_MGC_44 Homo sapiens c hypothetical protein FLJ11362	5.10	
13	447197	R36075	115.0323	gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.10	
	442150	AJ368158	Hs.70983	PTPL1-associated RhoGAP 1	5.10	
	415651	AJ207162	Hs.3815	stathmin-like-protein RB3	5.10	
20	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	5.09 5.09	
20	434442	AA737415	Hs.152826 Hs.201441	ESTs Horno sapiens cDNA FLJ11079 fis, clone PL	5.09	
	429389 435419	AA454779 AI281068	Hs.152835	ESTs	5.09	
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	5.09	
0.0	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	5.08	
25	424071	R71340	Hs.12876	ESTs	5.08 5.08	
	428227 426400	AA321649 M78361	Hs.2248 Hs.169743	small inducible cytokine subfamily B (Cy Homo sapiens clone 25121 neuronal offact	5.08	
	429026	AA443385	Hs.221993	ESTs	5.08	
	455847	BE146775		gb:QV4-HT0222-181099-013-e04 HT0222 Homo	5.08	
30	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	5.08	
	436854	AA749167	Hs.173911	ESTs	5.08 5.08	
	421799 452154	AW972292	Hs.292998 Hs.302746	ESTs MSTP028 protein	5.06	
	444946	AW953265 AW139205	Hs.156457	hypothetical protein FLJ22408	5.06	
35	445950	AI267957	Hs.145706	ESTs	5.06	
-	443124	A1033500	Hs.132895	ESTs	5.06	
	440698	AI348455	Hs.147492	Homo sapiens cDNA FLJ11777 fis, clone HE	5.06 5.06	
	444713	AW812074	Hs.28631 Hs.20136	Homo sapiens cDNA: FLJ22141 fis, clone H chromosome X open reading frame 6	5.06	
40	447970 419307	AW086109 AW953190	Hs.23180	ESTs	5.06	
	421954	AA410245	Hs.40323	BUB3 (budding uninhibited by benzimidazo	5.06	
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	5.05	
	421782	AB029290	Hs.108258	actin binding protein; macrophin (microf	5.05 5.05	
45	407976 400869	AI633875	Hs.77823	hypothetical protein FLJ21343 NA	5.04	
43	416153	R13894		gb:yf62a06.r1 Soares infant brain 1NIB H	5.04	
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	5.04	
	406038	Y14443	Hs.88219	zinc finger protein 200	5.03	
50	440659	AF134160	Hs.7327 Hs.155071	claudin 1 hypothetical protein FLJ11190	5.03 5.02	
50	425188 446051	AK002052 BE048061	Hs.37054	ephrin-A3	5.02	
	443387	BE139135	Hs.254629		5.02	
	414407	AA147026	Hs.76704	ESTs	5.02	
55	408349	BE546947	Hs.44276	horneo box C10	5.01 5.01	
23	452510	Z33566 AK001713	Hs.301491 Hs.17860	ESTs hypothetical protein FLJ10851	5.00	
	447245 413472	BE242870	Hs.75379	solute carrier family 1 (gliat high affi	5.00	
	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	5.00	
<b>60</b>	423648	AK000456	Hs.130546		5.00	
60	412997	BE046600	U= 40340	gb:hn41d08.x1 NCI_CGAP_RDF2 Homo sapiens	5.00 5.00	
	408964 411636	AF201468 AW855001	Hs.49349	beta-site APP-cleaving enzyme gb:PM3-CT0263-091299-007-f05 CT0263 Homo	5.00	
	418111	R42003	Hs.106513		5.00	
	402709	NA.		NA	5.00	
65	408677	A1279892	Hs.46801	sorting nexin 14	5.00	
	411350		U= £007	gb:QV2-PT0010-250300-096-b05 PT0010 Homo hypothetical protein FLJ13078	5.00 5.00	
	453382 458090		Hs.5997 Hs.56213		5.00	
	408512				5.00	
70	453240		Hs.16625		5.00	
	440491		Hs.24944		5.00 5.00	
	423896		Hs.13058 Hs.18793		5.00	
	429091 410968		Hs.67397		5.00	
75	436859				5.00	
	452198	A1097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	5.00	
	424511				5.00 5.00	
	414631		) Hs.65406	6 ESTs NA	3.00	5.00
80	405481 431118		Hs.25050		5.00	2.30
	421373	AA808229	Hs.16777	71 ESTs	5.00	
	424916	AW86744			5.00	
	433106	6 AB002443	Hs.1844		5.00	
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5.00
5.00
5.00
5.00
5.00
                                             Hs.337717 ESTs
            427386
                           AW836261
                                                              ESTs, Weakly similar to ALU1_HUMAN ALU S
            441998
                           A1733236
                                             Hs.128312
            420161
430899
                           A1683069
                                             Hs.175319
                                                              ESTs
                                                              hypothetical protein FLJ 14906
                           BE018217
                                             Hs.183528
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            415188
                           BE007531
AW293291
                                             Hs.258791
Hs.255180
                                                              ESTs
                                                                                                                                          5.00
5.00
                                                              ESTs
            420429
                                              Hs.8366
Hs.304802
             439038
                           AV655045
                                                              ESTs
                                                                                                                                          5.00
5.00
                                                              ESTs. Weakly similar to KIAA0944 protein
             457031
                           A1497955
              430865
                                              Hs.5232
                                                              HSPC125 protein
                           A1073424
10
             420583
432229
                           H77859
AW290976
                                              Hs 65450
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                                                                                                                                          5.00
5.00
                                              Hs.143587
                                                               ESTs
                                                               gb:RC3-HT0622-130400-022-a02 HT0622 Homo
             455208
                           BE180276
                                                                                                                                          5.00
5.00
                                              H$.89832
             419263
                           AW583874
                                                               insulin
                                                               hypothetical protein FLJ13164
                           AA286844
AA464362
                                              Hs.61260
Hs.6748
              452279
15
                                                               hypothetical protein PP1665
             419100
438585
                            AA811371
                                               Hs.123362
                                                               ESTs
                                                                                                                                          5.00
                                                                                                                                          5.00
5.00
                                                               Homo sapiens cDNA FLJ13097 fis, clone NT
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                            AW959074
                                              Hs.23648
             428775
                            AA434579
                                              Hs.143691
                                                               ESTs
                                                               ESTs, Weakly similar to I38022 hypotheti
              422471
                            AA311027
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CAT number:
                                       Gene cluster number
25
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                             116139 1
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W73484 AW748569 AW748532 AW748585
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AA332680 AA332831 AW962684
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AW136928 AI685655 BE218584 BE455078 N68963 AA975338 BE147199 N76377
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10	455212	1260678_1	AW866330 A	W866410 AW866332 AW866411 AW866327 AW866326 AW866335 AW866334 AW866331 AW866333 AW866328 AW866329
10	455217	1261522_1	AW867534 A	W867539
	455608	1337389_1	BE011437 BI	E011402 BE011395 BE011428 BE011407 BE011421 BE011406
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1.5	455944	1385569_1	BE160643 B	E160585
15	457892	432926_1	AA744389 A	A74427D AA744284 AA744299 AA745380 AA744337 AA846905 AA847698 A745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923
	457893	432938_1		A/455// AW/465// AW/46564 AW/465// AW/465/5 AW/46565 AW/465/
	459279	975649_1	A11014330 A	Edition to Automatic
	TABLE 460	<b>:</b>		
20	Pkey:	Ideia	pue number con	responding to an Eos probeset
- •	Ref:	Sen	Jence SOUTCE.	The 7 digit numbers in this column are Gentrank Identifier (GI) numbers. "Dunham, et al." reters to the publication entities." The DIAA
		sequ	ence of human	chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:		ates UNA strar	ud from which exons were predicted. a positions of predicted exons.
25	Nt_position	i: indi	cates nucleooue	positions of previous activity.
23	Pkey	Ref	Strand	NL position
	400484	8569067	Minus	52725-52912
	400570	9884797	Minus	156787-156862,178082-178208,186819-186957
	400639	9887597	Plus	23150-23580
30	400845	9188605	Ptus	34428-34612
	400860	9757499	Minus	151830-152104,152649-152744
	400869	9838306	Plus	29152-30102 157920-158564
	400950 400977	7658481 8072510	Minus Plus	73950-74364
35	401004	7229982	Plus	62580-62772
	401093	8516137	Minus	22335-23166
	401183	7670214	Minus	39921-40601
	401205	9743388	Ptus	167373-167433,167936-168031
40	401208	7712287	Plus	163145-163281
40	401244	4827300	Minus	\$5359-\$6376 0366 0400
	401348 401372	9930791 9944181	Minus Plus	9365-9490 127056-127196
	401424	8176894	Plus	24223-24428
	401581	9502454	Plus	9440-10165
45	401629	8575965	Minus	169336-169788
	401708	2951946	Ptus	154511-155298
	401736	3219338	Plus	1771-1894
	401740	2982169	Plus	148357-148484,148591-148590 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-
50	401747	9789672	Minus	131932 132451-132575,133580-134011
50	401961	4581193	Minus	124054-124209
	402343	8099256	Plus	4677-6084
	402363	9454515	Plus	25693-25991
	402408	9796239	Minus	110326-110491
55	402524	9798518	Minus	20529-21096
	402709 402732	8901246 9211639	Minus Minus	56847-57055 147904-148107
	403040	3133144	Minus	91632-91788 97918-98115
_	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
60	403199	9958183	Minus	58895-59036,66618-66789
	403278	8072597	Plus	146823-146986
	403546	8078400	Plus	94703-94849
	403764 403776	7717105 7770511	Minus Minus	118692-118853 1414-1513,1624-1756
65	403859	7708954	Plus	113738-113858
0.5	403973	8575876	Plus	93873-94384
	404012	8655948	Plus	551356-552233
	404029	7671252	Ptus	108716-111112
70	404072	9931705	Plus	49546-50498
70	404117	9796029 9930793	Plus Plus	149723-149920 168836-169248
	404170 404335		Minus	21030-21145,26504-26692
	404440		Phrs	80430-81581
	404632		Plus	45096-45229
75	404702	7630798	Plus	78043-78890
	404913		Ptus	97717-97976
	404996		Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405033		Minus Minus	142358-142546 13855-14027
80	405065 405114		Minus	97013-97560
00	405287		Plus	89802-89999
	405352	2822162	Minus	97253-97742
	405362		Minus	105008-105142,105980-106091,140445-140556,142519-142641

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	405481	3688109	Plus 5718-	5837,8719-8818	
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,	405545 405637	1054740 6289229		52-189978	
	405696	4309923		-2013,2124-2231	
	405770	2735037	Ptus 6105	7-62075	FART AREARA ARTROS ARTAST ARREST ARROND
10	406465	9795550	Plus 9450	2-94706,96776-96914,98795-98928,102423-102576,10	508/-105191,10/023-10/12/,106632-106332
10					
	TABLE 47A	: ABOUT 370	GENES SIGNIFICAN	ITLY DOWN-REGULATED IN STOMACH CANCER CO	IMPARED TO NORMAL STOMACH
	Table 47A	ists about 370 g	enes significantly do	nwn-regulated in stomach cancer compared to normal str	ornach. These were selected as for Table 46A, except that the numerator and
15	denominate Pkey:		i and the ratio was e e Eos probeset iden	qual to or less than 0.33.	
	ExAcon:			ber, Genbank accession number	
	UnigenelD:		ne number		
	Unigene Ti		ne gene tite	ad Serve	
20	R1:	Rauo	of turnor to normal b	ody ussue	
	Pkey	ExAcon	UnigenelD	Unigene Title	RI
	412859	NM_000705	Hs.813	ATPase, H+/K+ exchanging, beta polypepti	0.02 0.02
	423371	AU076819 U09860	Hs.1650 Hs.158333	solute carrier family 26, member 3 protease, serine, 7 (enterokinase)	0.04
25	425607 429050	X81333	Hs.194777	meprin A, beta	0.04
	421996	AW583807	Hs.1460	glucagon	0.05
	441212	AW242447	Hs.146182	cytosofic beta-glucosidase	0.05
	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	0.06 0.07
30	403697 402760	NA NA		NA NA	0.08
50	428285	AW340797	Hs.98434	ESTs	0.08
	419279	AA235900	Hs.87500	ESTs	0.08
	422459	K02100	Hs.117050	omithine carbamoyltranslerase	0.09 0.09
35	422992 430867	AF016833 M16404	Hs.122785 Hs.248099	mattase-glucoamytase (alpha-glucosidase) cholinergic receptor, muscarinic 2	0.09
55	453989	M63962	Hs.36992	ATPase, H+/K+ exchanging, alpha polypept	0.10
	443022	AL046485	Hs.207604	ESTs	0.10
	413382	BE090689		gb:RC1-8T0720-280300-011-f08 BT0720 Homo	0.10 0.10
40	450769 428070	AA057418 T63918	Hs.33654 Hs.182313	ESTs retinol-binding protein 2, cellular	0.10
70	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	0.11
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.11
	431716	089053	Hs.268012	tatty-acid-Coenzyme A tigase, long-chain	0.12 0.12
45	416889 405650	AW250318 NA	Hs.80395	mal, T-cell differentiation protein NA	0.12
-1.5	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.12
	401623	NA		NA	0.12
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto nb:MR0-HT0165-140200-009-d04 HT0165 Homo	0.13 0.13
50	455826 414949	BE144228 C15314	Hs.323349	ESTs	0.13
50	407486	569741	113.02.00 13	gb:hSCG-3=stomach cancer gene-3 (oncogen	0.13
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	0.13
	401015	NA AU076646	Hs.171683	NA nuclear receptor subfamily 1, group H, m	0.13 0.14
55	426651 450926	A1744361	Hs.205591	ESTs, Weakly similar to T46608 zinc fing	0.14
	443564	Al921685	Hs.199713	ESTs	0.14
	457955	AI208986	Hs.143945	ESTs	0.14 0.14
	457345 417118	A1699933 U38654	Hs.192175 Hs.50477	ESTs RAB27A, member RAS oncogene family	0.14
60	408518	BE162203	Hs.314758	ESTs	0.14
•	444938	AW470690	Hs.148814	ESTs	0.15
	403670	NA		NA	0.15 0.15
	432440 428492	X63597 AW662740	Hs.2996 Hs.259391	sucrase-isomaltase ESTs	0.15
65	443607	AM52512	Hs.134069	ESTs	0.15
	446914	BE044496	Hs.166994	FAT tumor suppressor (Drosophila) homolo	0.15
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	0.15 0.16
	430350 431094	BE169639 AW972276	Hs.116195	gb:PM1-HT0527-280200-005-a05 HT0527 Homo ESTs	0.16
70	401683	NA NA	13.110133	NA	0.16
	419278	AU076799	Hs.1247	apolipoprotein A-IV	0.16
	455071	BE145826		gb:MR0-HT0208-101299-202-e12 HT0208 Homo	0.16 0.16
	454282	AW296422 NM_00023	) Hs.194236	gb:UI-H-BW0-aio-h-05-0-UI.s1 NCI_CGAP_Su leptin (murine obesity homolog)	0.16
75	428848 451729	AW160725		ESTs	0.16
	451103	R52804	Hs.25956	DKFZP564D206 protein	0.16
	428502	AL137479	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (f	0.16 Q.17
	437157	BE048860 AL138411	Hs.120655	ESTs gb:DKFZp434A1229_r1 434 (synonym: htes3)	0.17
80	422731 402015	NA NA		NA	0.17
	414758	H82022	Hs.282847	pregnancy specific beta-1-glycoprotein 3	0.17
	412793			gb:RC1-8N0056-230200-021-e11 BN0056 Homo	0.17 0.17
	438152	AW292520	Hs.122082	ESTs	wiff
				503	

	101000	144			
	401685 441519	NA AA972740	Hs.127092	NA ESTs	0.17 0.17
	438327	H87407	Hs.172944	chorionic gonadotropin, beta polypeptide	0.17
_	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e	0.17
5	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	0.18
	414507	AW102637	Hs.13349	Homo sapiens cDNA FLJ14647 fis, clone NT	0.18
	413808 401132	J00287 NA	Hs.182183	Homo sapiens mRNA for caldesmon, 3' UTR NA	0.18 0.18
	412374	X01388	Hs.73849	apolipoprotein C-III	0.18
10	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	0.18
	447677	AI419235		gb:t/21d02.x1 NCI_CGAP_Brn23 Homo sapien	0.18
	448828	AI580296	Hs. 174782	ESTs, Weakly similar to KIAA1437 protein	0.18
	424122	AA335593	Hs.116147	ESTs	0.18
15	417332 434597	AW972717 AW974668	Hs.288462	hypothetical protein FLJ21511 gb:EST386757 MAGE resequences, MAGM Homo	0.18 0.19
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	0.19
	410280	AA083558	Hs.261286	ESTs	0.19
	409382	AA071244		gb:zm73g03.r1 Stratagene neuroepithelium	0.19
20	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	0.19
20	426069 430135	H10807 NM_000035	Hs.281434 Hs.234234	Homo sapiens cDNA FLJ14028 fis, clone HE aldolase B, fructose-bisphosphate	0.19 0.19
	414802	AI793107	Hs.27018	Ris	0.19
	457432	NM_005136	Hs.268538	polassium vollage-gated channel, lsk-rel	0.19
25	446909	AA004895	Hs.30082	ESTs	0.19
25	435447	AI872932	40.400	gb:wm72e03.x1 NCI_CGAP_Ut2 Homo sapiens	0.20
	408611 423577	NM_004367 AW810107	Hs.46468 Hs.58633	chemokine (C-C motif) receptor 6	0.20 0.20
	439328	W07411	Hs.118212	Homo sapiens cDNA: FLJ22145 fis, clone H ESTs, Moderately similar to ALU3_HUMAN A	0.20
	436741	AA860163	Hs.291319	ESTs	0.20
30	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.20
	418277	AW135221	Hs.130812	ESTs	0.20
	448871 459370	BE616709 AA889982	Hs.159265	kruppel-related zinc finger protein hcKr	0.20
	427469	AA403084	Hs.271826 Hs.269347	ESTs, Weakly similar to I38022 hypotheti ESTs, Weakly similar to 2109260A B cell	0.21 0.21
35	432887	AI926047	Hs. 162859	ESTs	0.21
	421296	NM_002666	Hs.103253	perilipin	0.21
	449216	AW295417	Hs.224616	ESTs	0.21
	414835	AA156720	Hs.185342	ESTs	0.21
40	459233 439756	Al939966 Al359651	Hs.283852	gb:MR0-CT0015-160799-002-b06 CT0015 Homo Homo sapiens mRNA full length insert cDN	0.21 0.21
	427167	AJ239607	Hs.99196	hypothetical protein MGC11324	0.21
	400410	AF154915	Hs.283958	homeo box D12	0.21
	409828	AW501137		gb:UI-HF-BP0p-ail-e-12-0-U1.r1 NIH_MGC_5	0.22
45	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.22
77	455968 404145	8E168828 NA		gb:QV1-HT0517-020400-145-f04 HT0517 Hamo NA	0.22 0.22
	454011	M31008	Hs.37009	alkaline phosphatase, intestinal	0.22
	430588	AI741461	Hs.161904	ESTs	0.22
50	403652	NA		NA	0.22
50	440410	AW204436	Hs.128715	ESTs	0.22
	453871 458567	BE300380 AI222075	Hs.69476 Hs.147831	Homo sapiens cDNA FLJ12758 fis, clone NT ESTs	0.22 0.22
	436004	AA703332	Hs.196270	folate transporter/carrier	0.22
	417408	F17211	Hs.86092	Horno sapiens skeletal myosin light chain	0.22
55	448643	A/557531		gb:pt2,1-06.D06.r tumor2 Horno sapiens cD	0.22
	404401	NA AA 424420	11- 140010	NA FOT	0.22
	428088 427074	AA421130 AA527435	Hs.112640 Hs.178589	EST hepatocellular carcinoma antigen gene 52	0.22 0.22
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	0.22
60	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.22
	441155	AW161008	Hs.7719	GABA(A) receptor-associated protein	0.22
	402750	NA	11- 400004	NA SOT	0.22
	438587 404848	AA811450 NA	Hs.136984	ESTs NA	0.22 0.22
65	427833	AA416615	Hs.98242	ESTs	0.23
	439907	AA853978	Hs.124577	ESTs	0.23
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	0.23
	446817	AI700684	Hs.134166	ESTs	0.23
70	437333 404097	AA748898 NA		gb:ny76h10.s1 NCI_CGAP_GCB1 Homo sapiens NA	0.23 0.23
	446393	AW014174	Hs.301956	zinc finger protein	0.23
	456328	T41368		gb:ph1d1_19/1TV Outward Alu-primed hncDN	0.23
	401042	NA		NA	0.23
75	458441	AW842283	Hs.79933	cyclin I	0.23
13	435547	AW117431 AW139155	Hs.191906	ESTs	0.23
	429060 425158	AW954631	Hs.194995 Hs.266940	hypothetical protein DKFZp43400320 1-complex-associated-lestis-expressed 1-	0.23 0.23
	448758	AB018311	Hs.21917	KIAA0768 protein	0.23
0Λ	441240	AA923749	Hs.132442	ESTs	0.23
80	436562	H71937	Hs.322904	ESTs, Weakly similar to 138022 hypotheti	0.23
	424104 447452	AA669515 BE618258	Hs.144950 Hs.102480	ESTs Homo sapiens, clone IMAGE:3869590, mRNA,	0.23 0.23
	444515	AW204908	Hs. 102480 Hs. 169979	ESTs Cone IMAGE:386959U, mRNA,	0.23

	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.24
	406560	NA	14.202.00	NA	0.24
	432408	N39127	Hs.332557	ESTs, Wealdy similar to A46010 X-linked	0.24
5	455699	8E068121	U- 70000	gb:CM1-8T0368-061299-060-a02 BT0368 Homo alcohol dehydrogenase 6 (class V)	0.24 0.24
,	453979 439657	M68895 W93589	Hs.76800	gb:zd95g05.s1 Soares_fetal_heart_NbHH19W	0.24
	407512	X15674		gb:Human pTRS mRNA for repetitive sequen	0.24
	440875	AW138036	Hs.201788	ESTs	0.24 0.24
10	404753 411119	NA M60627	Hs.753	NA formyl peptide receptor 1	0.24
10	418692	AK000268	Hs.87383	hypothetical protein	0.24
	415327	H22769		gb:ym54c02r1 Soares infant brain 1NIB H	0.24
	429446	AI547111		gb:PN2.1_A01_G12.r mynorm Homo sapiens c	0.24 0.25
15	455391 422818	BE156230 AA404290	Hs.97848	gb:QVQ-HT0367-310100-102-c11 HT0367 Homo ESTs	0.25
13	435338	AA578071	Hs.194300	ESTs, Weakly similar to 138022 hypotheti	0.25
	414203	BE262170	Hs.78629	ATPase, Na+/K+ transporting, beta 1 poly	0.25
	403941	NA NA		NA qb:601157981F1 NIH_MGC_21 Homo sapiens c	0.25 0.25
20	414383 412008	BE279406 NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	0.25
20	424985	A1907236	Hs.279935	Homo sapiens cDNA FLJ11780 fis, clone HE	0.25
	450736	AW970060		gb:EST382140 MAGE resequences, MAGK Horno	0.25
	431185	H02767	Hs.28944	ESTs gb:RC4-NN0027-060400-011-a09 NN0027 Homo	0.25 0.25
25	455308 435464	AW893949 BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	0.25
	418525	AW450369	Hs.86937	ESTs	0.25
	402790			NA FOT-	0.25 0.25
	411869 400332	W20027 S66407	Hs.23439 Hs.248032	ESTs FLT4	0.25
30	424884	AW299437	Hs.225717	ESTs	0.25
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	0.25
	439780	AL109688	U= 40117	gb:Homo sapiens mRNA full length insert Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.25 0.25
	408947 404900	AL080093 NA	Hs.49117	NA	0.25
35	441918	A1733373	Hs.128119	ESTs	0.25
	441639	A1133287	Hs.303953	ESTs	0.25 0.25
	459396 452755	AJ907536 AW138937	Hs.103869 Hs.213436	ESTs ESTs. Weakly similar to A34087 hypotheti	0.25
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	0.25
40	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	0.26
	429450	AA824451	Hs.94292	hypothetical protein FLJ23311	0.26 0.26
	455615 454633	BE045344 AW811380	Hs.274923	ESTs, Moderately similar to unnamed prol gb:IL3-ST0143-290999-019-D05 ST0143 Homo	0.26
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	0.26
45	455802	BE141491		gb:MR0-HT0080-011099-002-h06 HT0080 Homo	0.26
	414003	AA134472	Hs.124434	gb:zo13c01.s1 Stratagene colon (937204) ESTs	0.26 0.26
	436363 456074	AA843926 BE409525	Hs.902	neurofibrornin 2 (bilateral acoustic neur	0.26
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	0.26
50	445635	A1769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.26 0.26
	405953 411021	NA F00055	Hs.172004	NA titin	0.26
	428443	BE618106	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	0.26
55	434345	AF127772		gb:Homo sapiens cell-line E8CASS clone E	0.26 0.26
55	455743 451138	BE073754 W92287	Hs.40268	gb:RC0-8T0561-210100-032-d07 BT0561 Homo ESTs	0.26
	449528	H63337	Hs.38178	hypothetical protein FLJ23468	0.26
	441040	AW449782	Hs.178803	ESTs	0.26
60	458830	AW501248	Hs.250824 Hs.269365	Homo sapiens cDNA: FLJ23435 fis, clone H ESTs, Weakly similar to ALU8_HUMAN ALU S	0.26 0.26
00	428861 435469	AW352234 AW388237	Hs. 191204	ESTs Asserbly similar in Acco-Lowert Acc 2	0.27
	427562	R56424	Hs.26534	ESTs	0.27
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	0.27 0.27
65	423528 406589	AB011137	Hs.300938	KIAA0565 gene product NA	0.27
0.5	450059	BE220223	Hs.279626	ESTs	0.27
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	0.27
	454007	AW015870	Hs.232081	ESTs	0.27 0.27
70	426062 441665	N57014 Al301355	Hs.75874 Hs.151285	pregnancy-associated plasma protein A ESTs	0.27
	405037	NA		NA	0.27
	446820	AW295037	Hs.254986	ESTs	0.27 0.27
	448487 447567	AJ523720 AW474513	Hs.172567 Hs.224397	ESTs ESTs, Wealdy similar to I38931 Wiskotl-A	0.27
75	408540		Hs.639	calbindin 3, (vitamin D-dependent calciu	0.27
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.27
	432501		Hs.25682	Homo sapiens mRNA for KIAA1863 protein, NA	0.27 0.27
	401350 417569		Hs.144651	ESTs	0.27
80	443542	AI927065	Hs.146040	ESTs	0.27
	437105		Hs.222127	ESTs Homo sapiens clone 24762 mRNA sequence	0.27 0.27
	432119 419056		Hs.302041 Hs.89575	CD79B antigen (immunoglobulin-associated	0.28
	713030			505	

	427812	AA770424	Hs.98162	ESTs	0.28
	423557	AB011176	Hs.129801	KIAA0604 gene product	0.28
	445311	AW027556	Hs.156286	ESTs	0.28
5	402758	NA .		NA	0.28
,	448240 401333	AJ478345 NA	Hs.191034	ESTs NA	0.28 0.28
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.28
	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.28
10	442896	R37725	Hs.261108	ESTs	0.28
10	447949 435625	A1446820 H50654	Hs.165839 Hs.113999	EST ESTs	0.28 0.28
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	0.28
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	0.28
15	442967	A1025460	Hs.220977	ESTs	0.28
15	448062 425860	AW295923 L29339	Hs.255472 Hs.1964	KIAA1843 protein	0.28 0.28
	451839	AI820516	Hs.16857	solute carrier family 5 (sodium/glucose ESTs	0.28
	446000	AV656052	Hs.1504	hemopéxin	0.28
20	443506	H10661	Hs.192124	ESTs, Weakly similar to 138022 hypotheti	0.28
20	418345 445481	AJ001696 AW661846	Hs.241407 Hs.148836	serine (or cysteine) proteinase inhibito	0.28 0.28
	409337	H71289	Hs.220535	ESTs ESTs	0.28
	411414	AW897236	1.0.02000	gb:CMO-NN0057-150400-335-c06 NN0057 Homo	0.28
25	427642	R40761	Hs.9834	ESTs .	0.28
25	456392	W28766	U- 42504	gb:51d3 Human retina cDNA randomly prime	0.28
	409920 410285	BE169746 AA083609	Hs.12504	likely ortholog of mouse Arkadia gb:zm63d05.r1 Stratagene fibroblast (937	0.28 0.28
	442496	R55073	Hs.124130	ESTs	0.28
20	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	0.28
30	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	0.29
	458716 423235	N99013 AW410698	Hs.16762 Hs.169917	Homo sapiens mRNA; cDNA DKFZp564B2062 (f neurabin fi	0.29 0.29
	431087	H12723	Hs.290791	ESTs	0.29
2.5	459106	AW589793	Hs.224713	ESTs	0.29
35	414870	N72264	Hs.300670	KIAA1204 protein	0.29
-	402243 432628	R02394	Hs.269436	NA ESTs, Moderately similar to PC4259 ferri	0.29 0.29
	404364	NA NA	16.203-130	NA	0.29
40	400480			NA	0.29
40	456083	U46922	Hs.77252	fragile histidine triad gene	0.29
	446598 422201	AW250546 NM_001505	Hs.113207	gb:2821774.5prime NIH_MGC_7 Homo sapiens	0.29 0.29
	443919	AI091284	Hs.135224	G protein-coupled receptor 30 ESTs, Wealdy similar to A47582 B-cell gr	0.29
	453948	AI970797	Hs.64859	ESTs	0.29
45	403792	NA		NA	0.29
	418957 457960	AI792615 AA771881	Hs.188712 Hs.298149	ESTs ESTs	0.29 0.29
	404269	AATTIOOT	rs.230143	NA .	0.29
	439309	AF090097	Hs.6524	Homo sapiens clone IMAGE 25997	0.29
50	458239	BE439877	Hs.283389	ESTs	0.30
•	414941 404954	C14865	Hs.332341	ESTs NA	0.30 0.30
	441609	AA946764	Hs.133460	ESTs	0.30
	426895	AA416880	Hs.225738	ESTs	0.30
<b>5</b> 5	403182	NA		NA .	0.30
	402319 429699	Al383469	Hs.159300	NA ESTs	0.30 0.30
	405669	NA NA	ns.133300	NA	0.30
	459312	AF107457	Hs.37035	homeo box HB9	0.30
60	431853	AA521034	Hs.70834	ESTs	0.30
	449768	AI972746 AV650231	Hs.102945	ESTs, Wealdy similar to 178885 serine/th ESTs, Highly similar to A Chain A, Human	0.30
	443609 454293	H49739	Hs.282941 Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	0.30 0.30
	447569	Al393202	Hs.147554	hypothetical protein FLJ23392	0.30
65	400128	NA		NA	0.30
	423208	AA323191	Hs.137064	cytoplasmic polyadenylation element bind	0.30
	434227 424208	AF119893 AW583123	Hs.63382 Hs.143113	hypothetical protein PRO2714 pancreatic lipase-related protein 2	0.30 0.30
	401165	NA	1.5.1.101.15	NA	0.30
70	415394	R19249	Hs.22654	sodium channel, voltage-gated, type I, a	0.30
	443110	AW352243	Hs.132665	ESTs	0.30
	426724 416035	AA383623 H42314	Hs.293616	ESTs gb:yo09e02.s1 Soares adult brain N2b5HB5	0.30 0.30
	409753	AA234847		gb:zs37b10.r1 Soares_NhHMPu_S1 Homo sapi	0.31
75	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	0.31
	408895	AA058730	Hs.191464	ESTs	0.31
	405110	NA AW079984	He 353400	NA ESTE Weathy similar to DINI 196 cations	0.31
	432430 426442	AA378656	Hs.262480 Hs.106510	ESTs, Weakly similar to PIHUB6 sativary ESTs, Moderately similar to ALU2_HUMAN A	0.31 0.31
80	411765	H43346	10.100210	gb:yp09a04.r1 Soares breast 3NbHBst Homo	0.31
	431854	AA383550	Hs.271699	polymerase (DNA directed) iota	0.31
	457553	A1861896	Hs.304505	ESTs	0.31
	412301	AW936328		gb:QV4-DT0021-281299-070-f07 DT0021 Homo	0.31

	418626	AW299508	Hs.135230	ESTs	0.31
	416156	Z41922		gb:HSC03B101 normalized infant brain cDN	0.31
	416275	H42823	Hs.155742	głyoxylate reductase/hydroxypyruvate red	0.31
-	419091	T85332	Hs.178294	ESTs	0.31
5	42011B	AW295297	Hs.182585	KIAA1276 protein	0.31
	451094	A1949825	Hs.260395	ESTs	0.31 0.31
	403214	NA ummara	LL 224770	NA ESTs	0.31
	412717 428782	W00973 X12830	Hs.334728 Hs.193400	interleukin 6 receptor	0.31
10	449202	AW295154	Hs.255396	ESTs	0.31
10	433138	AB029496	Hs.59729	semaphorin sem2	0.31
	436602	AJ793222	Hs.166817	ESTs	0.31
	424844	D61524		gb:HUM413E078 Clontech human fetal brain	0.32
	435253	W91884		gb:zh47f08.s1 Soares_fetal_fiver_spleen_	0.32
15	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	0.32
	416320	H47867	Hs.34024	ESTS	0.32
	406333			NA .	0.32
	443652	A1080692	Hs.134229	ESTs, Wealtly similar to IS4401 hypertens	0.32
20	457103	AJ421187	Hs.189192	ESTs, Weakly similar to T COMPLEX TESTIS	0.32
20	423593	AA328144		gb:EST31752 Embryo, 12 week I Homo sapie	0.32
	453242	T98327	Hs.18343	ESTs	0.32
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.32
	403847	NA		NA COT-	0.32 0.32
25	458711	AL036877	Hs.282878	ESTs	0.32
23	406242	NA AAEO401E	Un 455007	NA ESTs	0.32
	433493	AA594915	Hs.155087	gb:lt.3-CT0214-161299-045-B06 CT0214 Homo	0.32
	458147 437403	AW752597 AI208149	Hs.121196	ESTs	0.32
	407823	D44744	Hs.247447	ESTs	0.32
30	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	0.32
50	436089	AA804957	Hs.119840	ESTs	0.32
	457463	AW877031	Hs.272321	hypothetical protein FLJ12571	0.32
	433370	AI084343	Hs.122310	ESTs	0.32
	436298	AW293496	Hs.180138	ESTS	0.32
35	419768	T72104	Hs.93194	apolipoprotein A-I	0.33
	449428	AI651280	Hs.195685	ESTs	0.33
	406291	NA		NA .	0.33
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	0.33
	418162	T11958		gb:A802R Heart Horno sapiens cDNA clone A	0.33
40	408316	AW807771		gb:MR4-ST0098-090300-003-c05 ST0098 Homo	0.33
	404187	NA.		NA	0.33
	452992	AI792376	Hs.31290	Homo sapiens clone 23832 mRNA sequence	0.33
	448355	Al493734	Hs.329374	ESTs	0.33
4.5	442423	BE326264	Hs.246842	ESTs	0.33
45	439474	AI824060	Hs.211501	ESTs	0.33
	457149	AA429575	Hs.297493	ESTs	0.33 0.33
	448623	BE613468	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti	0.33
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo gb:S1h3 Human retina cDNA randomly prime	0.33
50	419372 406293	W28781 NA		NA	0.33
50	422933	AF073931	Hs.122359	calcium channel, voltage-dependent, alph	0.33
	451818	AI819018	Hs.339668	ESTs	0.33
	441912	AA971484	Hs.159938	ESTs	0.33
	429013	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	0.33
55	422304	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.33
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	0.33
	406597			NA	0.33
	451636	AW173270	Hs.140444	ESTs	0.33
-	424226	N94153	Hs.19155	ESTs	0.33
60					
	TABLE			a de la	
	Pkey:		ique Eos probeset i	denumer number	
	CAT nu		ene cluster number		
65	Accessi	on: Ge	enbank accession n	impers	
05	Die	CAT Numb	er Accession	Č	
	Pkey 408316		CI ACCESSIOI AWR/17771 AW	179260 AWR07851 AW179240 AWR45961 AWR07693	BE141176 AW807594 AW807772 AW846003 AW845963 AW179239
	409382			771477	
	409699			154785 AW458343 BE154816 BE154667	
70	409753				
	409828			/501295 AW501212	
	410285			083790 AA112048	
	411414				
	411765			3302 AA095182	
75	412301				
	412793	1327636	1 AW997986	•	
	413382	1365954_1	BE090689 BE	090685 BE090697 BE090680 BE090691 BE090696 BE0	19U698 BEUSU686
	414003	140888_1	AA134472 R7	5288 AW750262	
00	414383				
80	415327			82 Z43545 F05783 N92089 H71928	
	416035			90 H45217 H15384	
	416156				
	418162	1725383_1	11175	6 T11816 T20135 T19729 R45874	

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W28781 W26588 W26377
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                          220507_1
                                           AL138411 AL138412 AA315860
AA328144 AW962385 N30457
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            423593
424844
429446
430350
                          229955_1
244291_1
                                           D61524 AA347654 AW961758
  5
                          304683_1
316401_1
                                           AI547111 AW973749 AA558007
BE169639 AA476976
                                           AF127772 AF062358 AF060217 AA652270 F23288
AW974668 AA661959 AA649572 AA640401 AA640402
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                          389383_1
403478_1
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             435253
                                            W91884 W95119 AA676941
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437333
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                          436167_1
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47673_1
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AL109688 R23665 R26578
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732252_1
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AV419235 AW055016 BE007490 BE550241
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                                            AI557531
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AW296422 H72616 H63825
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             454633
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1232449_1
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BE072139 BE157977 BE157974 AW857974 AW817778
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BE145826 BE145815 BE145822 AW854707 BE145912
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             455071
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AW893946 AW893966 M983966 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
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BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105
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                                            BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
T41368 T41369 T41294
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1789791_1
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AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
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             458147
                           488021 1
                           944881_1
                                             AI939966 AI939988 AI939951 AI939981 AI939976 AI939959
              459233
 35
              TABLE 47C:
             Pkey:
Ref:
                                    Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                     sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.
 40
              Strand:
              Nt_position:
                                      Indicates nucleotide positions of predicted exons.
                                                            Nt_position
110553-111119
              400480
                           8439796
                                             Minus
 45
              401015
                           8117441
                                             Ptus
                                                             151364-151606
              401042
                           8117611
                                             Plus
              401132
                           8705350
                                                            85679-85795
                                             Minus
              401165
401333
                           9438376
9884881
                                             Minus
                                                            168244-168423
13852-14861
                                             Plus
 50
              401350
                           9931226
                                                             14471-14623
                                                             163249-163623
              401623
                           8575907
                                             Plus
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7689961
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8038-8319
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                                             Minus
                                                             48791-49043,50038-50205,51530-51672,54448-54565,55933-56073
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  55
              402243
                            7690137
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                                                             196521-196721
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7210067
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69466-69678,71139-71284,71572-71865
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Plus
              402750
               402758
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147744-147861
              402760
402790
                           9213869
4835258
                                             Plus
Minus
  60
                            9838273
7630945
                                                             102163-102345,102545-102725
76723-77027,79317-79484
               403182
                                              Plus
               403214
                                              Minus
                            8705848
7259739
                                                             49991-50129
88377-88537
               403652
                                              Minus
               403670
                                              Minus
  65
                                                              102965-103174
149707-149873
                                              Minus
                            7230192
               403792
                                              Minus
                            7708844
7454203
                                              Plus
                                                              317240-317391,317913-318032
               403941
                                              Plus
Plus
                                                              114876-115342
                                                              55512-55781
                             7770701
  70
                            9863643
4481839
                                                              30607-31266
7644-7991
               404145
                                              Plus
               404187
                                              Ptus
               404269
404364
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9964977
                                                              70261-70404,72944-73063
32986-33202
                                              Minus
                404401
                             7259738
7637341
                                                              71066-71326
14770-14931
                                              Ptus
   75
               404753
                                              Plus
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                                                              23955-24034,25143-25264
                404848
                                              Minus
                             7331453
                                                              22032-22219
131720-132042
               404900
                                              Plus
               404954
                             7387327
                                              Plus
                             7543748
8096888
                                                              127374-127578
118940-119100
                405037
   80
               405110
                                              Minus
               405650
                             4926905
                                              Minus
                                                              71743-72291
                             4508140
                                                              14130-14270
               405669
                                              Plus
                             7960374
                                                              65101-65574
                                              Minus
```

. . . .

300

	405242	7417725	Minus	36736-36951
	406291	5686274	Plus	9562-9867
	406293	5686274	Minus	17646-17953
_	406333	9213235	Plus	64689-64798
5	406560	7711569	Minus	35162-35292
	406589	8224211	Plus	38806-38989
	406597	8248613	Minus	132738-132985,134266-134425,135034-135192,135471-135608,137345-137478,138768-138912

10

TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES
Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Placy:

Unique Eos probeset identifier number
ExAcon:

Exemplar Accession number, Genbank accession number
UniquenelD:

Uniquene gene title

Uniquene gene title

Rt:

Mean of metanoma Als divided by the mean of normal fissue Als, where the minimum value for the numerator and denominator was set to 1.0

15

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene title
Mean of melanoma Als divided by the mean of normal tissue Als, where the minimum value for the numerator and denominator was set to 1.0

20	Pkey	ExAcon	UnigenetD	Unigene Title	RI
	426555	NM 000372	Hs.2053	tyrosinase (oculocutaneous afbinism IA)	376.61
	428655	H05769	Hs.188757	Homo sapiens, ctone MGC:5564, mRNA, comp	324.36
	430377 453344	NM 001922 8E349075	Hs.301865 Hs.44571	dopachrome tautomerase (dopachrome delta	231.30
25	425289	AW139342	Hs.155530	ESTs	180.67 107.36
23	417166	AA431323	Hs.42146	interferon, gamma-inducible protein 16 ESTs	97.76
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	96.76
	434826	AF155661	Hs.22265	pyruvata dehydrogenase phosphatase	94.52
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	90.88
30	438209	AL120659	Hs.6111	anyl-hydrocarbon receptor nuclear transi	87.91
	443983	H04482	Hs.163724	ESTs	85.55
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	85.03
	419956	AL137939	Hs.40096	cadherin 19, type 2	84.27
2.5	423605	AF047826	Hs. 129887	cadherin 19, type 2	80.88
35	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	80.64
	415975	NM 004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	79.09
	421633	AF121860	Hs.106260	sorting nexin 10	71.52
	442064	AI422B67	Hs.88594	ESTs	69.88
40	418310	AA814100	Hs.86693	ESTs	67.94
40	423799	AW026300	Hs.132906	19A24 protein	67.64
	432886 456508	BE159028 AA502764	Hs.279704 Hs.123469	chromatin accessibility complex 1	63.24
	432882	NM 013257	Hs.279696	ESTs, Weakly similar to AF208855 1 BM-01 serum/glucocorticoid regulated kinase-li	63.18 62.33
	454088	AW062425	113.273030	gb:CM0-CT0042-090899-018-f01 CT0042 Homo	61.62
45	430838	N46664	Hs.169395	hypothetical protein FLJ12015	60.52
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	59.73
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	59.33
	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	59.00
	441224	AU076964	Hs.7753	catumenin	58.27
50	408418	AW963897	Hs.44743	KIAA1435 protein	56.79
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	56.45
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	56.29
	420674	NM 000055	Hs.1327	butyrytchofinesterase	56.15
55	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	55.82
"	420552	AK000492	Hs.98806	hypothetical protein	55.39
	442355 429747	AA456539 M87507	Hs.8262 Hs.2490	lysosomal-associated membrane prolein 2	54.97 52.85
	410174	AA306007	Hs.59461	caspase 1, apoptosis-related cysteine pr DKFZP434C245 protein	52.00
	437396	BE140396	Hs.21621	hypothetical protein OKFZp7620076	51.97
60	409557	BE182896	Hs.3686	ESTs	51.64
•	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	51.42
	414403	AW969551	Hs.76064	ribosomal protein L27a	50.58
	452958	AA883929	Hs.40527	ESTs	50.21
	458997	AW937420		ESTs	49.97
65	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	49.85
	435905	AW997484	Hs.5003	KIAA0456 protein	48.76
	424800	AL035588	Hs.153203	MyoD family inhibitor	48.33
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	47.91
70	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	47.45
70	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	46.52
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	45.79
	451134 430066	AA318315 AI929659	Hs.25999 Hs.237825	hypothetical protein FLJ22195	45.52 45.45
	417427	M90391	Hs.82127	signal recognition particle 72kD	44.58
75	450447	AF212223	Hs.25010	interleukin 16 (lymphocyte chemoattracta hypothetical protein P15-2	43.35
, ,	446019	AI362520	113.23010	histone deacetylase 3	43.03
	430015	AW768399		ESTs	42.45
	446880	AJ811807	Hs.108646		42.36
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	42.30
80	425390	AI092634	Hs.156114		41.42
	411088	BE247593	Hs.145053		41.21
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	40.94
	441590	A1623207	Hs.190537	ESTs	40.66
				500	,

	457465	AW301344	Hs.122908	DNA replication factor	39.91
	430280 410700	AA361258 AA352335	Hs.237868 Hs.65641	interleukin 7 receptor hypothetical protein FLJ20073	38.91 38.70
	421282	AA286914	Hs.40782	ESTs	38.55
5	448275	BE514434	Hs.20830	kinesin-like 2	38.00
	453912	AL121031		SWI/SNF related, matrix associated, acti	37.94 37.88
	414844 421305	AA296874 BE397354	Hs.77494 Hs.324830	deoxyguanosine kinase diptheria toxin resistance protein requi	37.70
	439352	BE614347	Hs. 169615	hypothetical protein FLJ20989	37.64
10	409078	AW327515		ESTs	37.30
	449845	AW971183	Hs.6019	DnaJ (Hsp40) hornolog, subtamily C, membe	37.27 37.21
	444184 445819	T87841 AI767472	Hs.282990 Hs.146290	Human DNA sequence from clone RP1-28H20 ESTs, Wealdy similar to putative p150 [H	37.21
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	37.00
15	433226	AW503733	Hs.9414	KIAA1488 protein	36.88
	445784	AI253155	Hs.146065	ESTs	35.36 33.09
	454117 407756	BE410100 AA116021	Hs.40368 Hs.38260	adaptor-related protein complex 1, sigma ubiquifin specific protease 18	32.05
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	31.00
20	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	30.76
	429083	Y09397	Hs.227817	BCL2-related protein A1	30.73 28.45
	444570 446839	H58373 BE091926	Hs.332938 Hs.16244	hypothetical protein MGC5370 mitotic spindle coiled-coil related prot	27.62
	433576	BE080715	Hs.161091	ESTs .	27.42
25	422173	BE385828	Hs.250619	phorbalin-like protein MDS019 (CEM15)	27.36
	408962	BE386436	Hs.44317 Hs.28345	SRY (sex determining region Y)-box 10	26.66 25.94
	442757 414646	A1739528 AA353776	ns.20343 Hs.901	ESTs CD48 antigen (B-cell membrane protein)	25.39
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	24.55
30	438461	AW075485	Hs.286049	phosphoserine aminotransferase	22.48
	427581	NM 014788	Hs.179703	KIAA0129 gene product	22.15 20.61
	435256 409988	AF193766 N27687	Hs.13872 Hs.334334	cytokine-like protein C17 transcription factor AP-2 alpha (activat	19.79
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	19.73
35	417404	NM 007350	Hs.82101	pleckstrin homology-like domain, family	19.27
	458098	BE550224	15- 00007	metallothionein 1E (functional)	18.09 16.95
	417018 446054	M16038 AB014537	Hs.80887 Hs.13604	v-yes-1 Yamaguchi sarcoma viral related KIAA0637 gene product	15.67
	432606	NM 002104	Hs.3066	granzyme K (serine protease, granzyme 3;	15.54
40	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	15.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	14.89 14.84
	414821 422486	M63835 BE514492	Hs.77424 Hs.117487	Fc fragment of IgG, high affinity Ia, re gene near HD on 4p16.3 with homology to	14.61
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	14.12
45	421334	BE297729		gb:601175625F1 NIH_MGC_17 Homo sapiens c	13.94
	422423	AF283777	Hs.116481	CD72 antigen	13.77 13.33
	408996 416406	AI979168 D86961	Hs.344096 Hs.79299	glycoprotein (transmembrane) nmb lipoma HMGIC fusion partner-like 2	12.76
	427536	BE277141	Hs.115803	gb:601178566F1 NIH_MGC_20 Homo sapiens c	12.76
50	423198	M81933	Hs.1634	cell division cycle 25A	12.66
	430770 407833	AA765694 AW955632	Hs.123296 Hs.66666	ESTs ESTs, Weakly similar to S19560 profine-r	12.58 12.09
	430822	AJ005371	Hs.248017		11.46
	424259	AK001776	Hs.143954		10.58
55	446950	AA305800	Hs.5672	hypothetical protein AF140225	10.04
	420956 448356	AA351584 AL120837	Hs.100543 Hs.20993	Homo sapiens clone 24505 mRNA sequence high-glucose-regulated protein 8	9.98 9.88
	428799	Al478619	Hs.104677		9.56
۷0	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	9.03
60	447769	AW873704	Hs.320831		9.01 8.99
	408393 407966	AW015318 AA295052	Hs.23165 Hs.38516	ESTs Homo sapiens, clone MGC:15887, mRNA, com	8.99
	450534	AI570189	Hs.25132	KIAA0470 gene product	8.91
65	410101	A1338045	Hs.203559		8.90
65	417129	AI381800	Hs.300684		8.86 8.68
	453507 442739	AF083217 NM 007274	Hs.33085 Hs.8679	WD repeat domain 3 cytosolic acyl coenzyme A thioester hydr	8.45
	456249	Al206144	Hs.82508	HRIHFB2206 protein	8.38
70	437786	BE142681	Hs.15557		8.35
70	448410	AK000227	Hs.21126		8.20 8.14
	442711 408405	AF151073 AK001332	Hs.8645 Hs.44672	hypothetical protein hypothetical protein FLJ 10470	7.96
	420208		Hs.95972		7.88
75	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	7.79
75	449217	AA278536	Hs.23262		7.66 7.50
	451239 442426		Hs.23127 Hs.33293		7.40
	447233				7.39
00	439574	A1469788		ESTs	7.13
80	431360				7.12 6.96
	412438 452882		Hs.11074 Hs.19627		6.87
	436581		Hs. 18021		6.64

					c c2
	431317	AA502682		gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	6.63 6.58
	443264 412490	BE221477 AW803564	Hs.132137 Hs.288850	ESTs, Moderately similar to A47582 B-cel Homo sapiens cDNA: FLJ22528 fis, clone H	6.53
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	6.52
5	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	6.50
	453878	AW964440	Hs.19025	DC32	6.48
	424148	BE242274	Hs.1741	integrin, beta 7	6.44 6.44
	407876	NM 004519 AW979187	Hs.40866 Hs.293591	potassium voltage-gated channel, KQT-lik melanoma differentiation associated prot	6.39
10	409512 427951	AI826125	Hs.43546	ESTs	6.32
••	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	6.03
	416640	BE262478	Hs.79404	neuron-specific protein	6.01
	446830	BE179030		Human DNA sequence from clone RPS-1174N9	5.98 5.93
15	452629	W02772	Hs.180178 Hs.268231	Homo sapiens, clone IMAGE:3947276, mRNA, Homo sapiens cDNA: FLJ23111 fis, clone L	5.73
13	427390 427853	AI432163 AI569798	Hs.98260	ESTs	5.55
	434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	5.54
	450256	AA285887	Hs.24724	MFH-amplified sequences with leucine-ric	5.54
20	428524	AA429772		ESTs	5.53
20	431797	8E169641	Hs.270134	hypothetical protein FLJ20280	5.50 5.50
	418403 411524	086978 AW850303	Hs.84790	KIAA0225 protein gb:IL3-CT0219-191199-030-F09 CT0219 Homo	5.47
	426158	NM 001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	5.40
	443086	AW977125		sine oculis homeobox (Drosophila) homolo	5.38
25	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	5.38
	406843	AW196933	Hs.119598	ribosomal protein L3	5.36 5.35
	430594 447674	AK000790 BE270640	Hs.246885 Hs.19192	hypothetical protein FLJ20783 cyclin-dependent kinase 2	5.23
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.23
30	420338	AA825595	Hs.88269	Homo sepiens, clone MGC:17339, mRNA, com	5.09
	409264	NM 014937	Hs.52463	KIAA0966 protein	5.03
	414734	AA151712	Hs.82572	ESTs	5.01 4.99
	426759 426793	A1590401 X89887	Hs.21213 Hs.172350	ESTs HIR (histone cell cycle regulation defec	4.98
35	428612	AA770001	113.172300	ESTs	4.97
	413550	W03011	Hs.306881	MSTP043 protein	4.92
	447349	AI375546		gb:tr23d04.x1 Soares_total_fetus_Nb2HF8_	4.86
	403328		11- 12484	Target Exon	4.85 4.83
40	452840 439310	AJ097393 AF086120	Hs.43481 Hs.102793	hypothetical protein DKFZp564K192 ESTs	4.82
40	451281	A1768965	Hs.292708	ESTs	4.82
	431183	NM 006855	Hs.250696	KDEL (Lys-Asp-Ghr-Leu) endoplasmic retic	4.81
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	4.74
45	435963	AF271212	Hs.322901	disrupter of silencing 10	4.67 4.66
43	418699 414770	BE539639 BE257224	Hs.173030	ESTs, Weakly similar to ALUS_HUMAN ALU S Homo sapiens, clone IMAGE:3873720, mRNA	4.66
	419628	H67546	Hs.49768	ESTs	4.64
	420258	AA477514	Hs.96247	translin-associated factor X	4.63
50	446341	AL040763	Hs.310735		4.58
50	420267	N37030	Hs.173337		4.57 4.55
	412228 432888	AW503785 T86823	Hs.73792	complement component (3d/Epstein Barr vi gb:yd81a08.s1 Soares fetal liver spleen	4.55
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	4.53
	418340	NM 013286	Hs.84162	chromosome 3p21.1 gene sequence	4.50
55	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.44 4.42
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697 sema domain, seven thrombospondin repeat	4.41
	452036 406903	NM 003966 K03121	Hs.27621	gb:Human glyceraldehyde-3-phosphate dehy	4.40
	405451	1		dihydropyrimidinase-like 3	4.34
60	434203	BE262677	Hs.283558		4.33
	450088	AW292933	Hs.254110		4.31 4.31
	421535	AB002359 H08859	Hs.105476 Hs.206469		4.30
	415912 451259	NM 006052			4.29
65	452548	AL050321	Hs.301532		4.28
	432195	AJ243669	Hs.8127	KIAA0144 gene product	4.24
	445101	175202	Hs.12314		4.22 4.19
	425913 423494	AA365799 AW504365	Hs.24143	SEC22, vesicle trafficking protein (S. c Wiskott-Aldrich syndrome protein interac	4.18
70	442092			hypothetical protein FLJ12439	4.16
• -	424954			tumor protein p53 (Li-Fraumeni syndrome)	4.05
	427719		Hs.13472		4.04
	415310		Un 7000F	gb:yf93h09.r1 Soares infant brain 1NIB H	4.04 4.03
75	416058 427828		Hs.78995 Hs.98232		3.93
,,	410079		Hs.58589		3.92
	420265		Hs.88087	ESTs	3.92
	426181	AA371422	Hs.33437		3.90
80	431639		Hs.26617		3.89 3.88
00	410275 422150		Hs.61796	calpastatin	3.87
	429238		9 Hs.19828		3.86
	418827		Hs.47166		3.84

	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	3.82
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.81
	410235	AA082977		gb:zn07h10.r1 Stratagene hNT neuron (937	3.79
	408535	BE294925	Hs.46680	CGI-12 protein	3.78 3.76
5	424524	AB032947 AA311919	Hs.151301 Hs.69851	Ca2+dependent activator protein for secr nucleotar protein family A, member 1 (H/	3.74
	411400 458215	AA928160	15.03631	gb:gn86i10.s1 Soares_NFL_T_GBC_S1 Homo s	3.73
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	3.72
	442643	U82756		PRP4/STK/WD splicing factor	3.70
10	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.70 3.67
	447644 422616	AW861622 BE300330	Hs.108646 Hs.118725	Homo sapiens cDNA FLJ14934 fis, clone PL selenophosphate synthetase 2	3.64
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.64
	418180	BE618087	Hs.83724	hypothetical protein MGC5466	3.62
15	423032	A1684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.62
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HE Homo sapiens mRNA; cDNA DKFZp434C2016 (f	3.62 3.61
	412156 417426	H29487 NM 002291	Hs.17110 Hs.82124	laminin, beta 1	3.61
	407188	AA457592	10.01.124	gb:aa92i11.s1 Stratagene fetal retina 93	3.61
20	426600	NM 003378	Hs.171014	VGF nerve growth factor inducible	3.61
	440760	AK001145	Hs.284216	hypothetical protein FLJ10283	3.60
	448481	W15284	Hs.74832	ESTs	3.59 3.59
	414111 437862	BE047679 AW978107	Hs.152982 Hs.5884	hypothetical protein FLJ13117 Homo sapiens mRNA; cDNA DKFZp586C0224 (I	3.59
25	409703	NM 006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	3.59
	406981	S71129		acetylcholinesterase (YT blood group)	3.59
	431586	AW971100	Hs.293189	ESTs	3.58 3.57
	415173	AW501735 AF182294	Hs.180059 Hs.241578	ESTs U6 snRNA-essociated Sm-like protein LSm8	3.57
30	430512 446126	AW085909	113.241370	pleckstrin homology domain interacting p	3.57
50	409305	AA070078		gb:zm60f05.r1 Stratagene fibroblast (937	3.57
	433867	AK000596	Hs.3618	hippocalcin-like 1	3.56
	459721	A1299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	3.56 3.55
35	441412 416114	AI393657 AI695549	Hs.159750 Hs.183868	ESTs glucuronidase, beta	3.55
33	454870	AW836081	15.10000	gb:PMO-LT0019-090300-002-e11 LT0019 Homo	3.54
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.53
	444680	AI186671	Hs.22670	ESTs	3.51 3.51
40	413949 437033	AA316077 AW248364	Hs.75639 Hs.5409	Human TB1 gene mRNA, 3 end RNA polymerase I subunit	3.50
40	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	3.49
	437158	AW090198		KIAA1150 protein	3.48
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	3.47 3.47
45	440634 445652	AA921767 AL117473	Hs.132447 Hs.13036	ESTs DKFZP727A071 protein	3.46
73	429500	X78565	Hs.289114		3.43
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.43
	426141	C05886	Hs.293972	ESTs lymphocyte-specific protein tyrosine kin	3.40 3.40
50	424321 449209	W74048 BE616830	Hs.1765 Hs.294145		3.39
50	408304	AW810279	110.201110	gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.37
	416561	D87328	Hs.79375	holocarboxylase synthetase (biotin-[prop	3.35
	422947	AA306782	Hs.122552 Hs.31803	G-2 and S-phase expressed 1 ESTs, Weakly similar to N-WASP [H.sapien	3.34 3.34
55	453005 409430	AW055308 R21945	Hs.346735		3.32
-	417386	AL037228	Hs.82043	D123 gene product	3.32
	440999	AI951562	Hs.126370		3.31
	407516 450065	X64974	Hs.24341	gb:H.sapiens mRNA HTPCRH02 for offactory transcriptional co-activator with PDZ-bi	3.31 3.31
60	416902	AL050107 AA375634	Hs.288974		3.28
v	432878	BE386490	Hs.279663		3.28
	443296	A1765286	Hs.313347		3.27
	429954	AJ918130	Hs.21374 Hs.30140		3.25 3.25
65	428044 425317	AA093322 AW205118			3.25
05	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.25
	432917	NM 014125	Hs.24151	7 PRO0327 protein	3.24
	447871		Hs.23905		3.24 3.24
70	414829 426996		Hs.77436 Hs.17310		3.23
,,	416188				3.22
	429530	AA454191	Hs.99362	Human DNA sequence from clone RP11-530N1	3.21
	445174				3.19
75	459227		) Hs.48713	ESTs ESTs	3.19 3.15
15	439039 418803		Hs.88556		3.15
	420005				3.15
	422511	AU076442			3.14
80	452480		Hs.13131	gb:RC-BT031-090199-053 BT031 Homo sapien lymphocyte adaptor protein	3.14 3.14
OU	445701 410678				3.14
	458664	Al300427		gb:qo18h07.x1 NCI_CGAP_Lu5 Homo sapiens	3.13
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.13

	430441	BE398091		desmoplakin (DPI, DPII)	3.12
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	3.12 3.11
	425606 432978	U52112 AF126743	Hs.158331 Hs.279884	renin-binding protein DNAJ domain-containing	311
5	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.10
	446627	AJ973016	Hs.15725	hypothetical protein SBB148	3.10
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.09 3.08
	417211 448140	T97617 AF146761	Hs.269092 Hs.20450	ESTs BCM-like membrane protein precursor	3.08
10	448752	AA593867	Hs.300842	KIAA1608 protein	3.07
	416355	H49875	Hs.268906	ESTs	3.07
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	3.07
	410321 411395	Y12860 AA889673	Hs.62245 Hs.7542	solute carrier family 25 (mitochondrial KIAA1802 protein	3.07 3.07
15	416065	BE267931	Hs.78996	profiferating cell nuclear antigen	3.06
	432343	NM 002960	Hs.2961	S100 calcium-binding protein A3	3.06
	457991	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	3.05
	433201 416178	AB040896 A1808527	Hs.21104 Hs.192822	KIAA1463 protein serologically defined breast cancer anti	3.03 3.02
20	411975	Al916058	Hs.144583	ESTs	3.01
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	3.00
	419870	AW403911	Hs. 266175	phosphoprotein associated with GEMs	3.00
	409601	AF237621 AW957684	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	2.94 2.93
25	415668 453256	AV957004 AI565587	Hs.306814 Hs.32556	hypothetical protein FLJ21889 KIAA0379 protein	- 2.81
	436856	A1469355	Hs.127310	ESTs	2.75
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.60
	408209	NM 004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.59 2.55
30	440457 415314	BE387593 N88802	Hs.21321 Hs.5422	Homo sapiens clone FLB9213 PRO2474 mRNA, glycoprotein M6B	2.51
•	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.50
	424085	NM 002914	Hs.139226	replication factor C (activator 1) 2 (40	2.48
	410600	AW575742	11- 400000	ESTs, Moderately similar to S65657 alpha	2.48 2.43
35	439180 444809	AI393742 BE207568	Hs.199067 Hs.208219	v-erb-b2 avlan erythroblastic leukernia v oculospanin	2.39
-	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	2.39
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.37
	411358	R47479	Hs.94761	KIAA1691 protein	2.35 2.34
40	427550 426312	BE242818 AF026939	Hs.311609 Hs.181874	nuclear RNA helicase, DECD variant of DE interferon-induced protein with tetratri	2.34
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.27
	418661	NM 001949	Hs.1189	E2F transcription factor 3	2.24
	459373	BE408266	Hs.301406	hypothetical protein PP3501	2.21 2.21
45	417437 436700	U52682 Al693690	Hs.82132 Hs.301406	interferon regulatory factor 4 hypothetical protein PP3501	2.18
	450690	AA296696	Hs.333418	FXYO domain-containing ion transport reg	2.15
	432800	BE391046	Hs.278962	AIM-1 protein	2.15
	421773	W69233	Hs.112457	ESTS	2.09 2.03
50	409415 433364	AA579258 AI075407	Hs.6083 Hs.296083	Homo sapiens cDNA; FLJ21028 fis, clone C ESTs, Moderately similar to I54374 gene	2.02
-	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.01
	443950	NM 001425	Hs.9999	epithelial membrane protein 3	2.01
	451537	R56631	Hs.26550	retinoid X receptor, gamma	2.00 1.96
55	427080 413190	AW068287 AA151802	Hs.301175 Hs.40368	ras-related C3 botulinum toxin substrate adaptor-related protein complex 1, sigma	1.94
••	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.91
	453779	N35187	Hs.43388	28kD interferon responsive protein	1.86
	453107 430637	NM 016113	Hs.279746 Hs.256290		1.86 1.86
60	408561	BE 160081 AI308037	Hs.84120	S100 calcium-binding protein A11 (calgiz hypothetical protein MGC13016	1.84
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	1.83
	406016			Target Exon	1.82
	446644	NM 003272 AF 178532	Hs.15791 Hs.271411	transmembrane 7 superfamily member 1 (up beta-site APP-cleaving enzyme 2	1.81 1.77
65	431836 439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	1.77
•	447604	AW089933	Hs.301342		1.76
	438866	U44385	Hs.325495		1.74
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.70 1.69
70	416091 446291	AF295370 BE397753	Hs.283082 Hs.14623	defensin, beta 3 interferon, gamma-inducible protein 30	1.67
. •	422532	AL008726	Hs.118126		1.67
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	1.67
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.67
75	448258 414945	BE386983 BE076358	Hs.343214 Hs.77667		1.66 1.66
, ,	425262	D87119	Hs.155418		1.65
	439237	AW408158	Hs.31889	3 ESTs, Weakly similar to A47582 B-cell gr	1.64
	427923	AW274357	Hs.301400	6 hypothetical protein PP3501	1.63
80	424825	AF207069 AW194364	Hs.15335		1.62 1.60
00	441859 445982	AW194364 BE410233	Hs.94814 Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.58
	412939	AW411491	Hs.75069		1.58
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.56



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	412856	BE386745	Hs.74631	basigin (OK blood group)	1.56
	447200	BE543145	Hs.281434	Homo sapiens cONA FLJ14028 fis, clone HE	1.54 1.53
	409614 450663	BE297412 H43540	Hs.55189 Hs.25292	hypothetical protein ribonuclease HI, large subunit	1.53
5	423397	NM 001838	Hs.1652	chemokine (C-C motif) receptor 7	1.49
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.48
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	1.46 1.46
	446755 454429	AW451473 BE273437	Hs.16134 Hs.301406	serine/threonine kinase 10 hypothetical protein PP3501	1.46
10	425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.45
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.44
	452203	X57522	11-00011	transporter 1, ATP-binding cassette, sub	1.43 1.42
	436378 424218	AJ227874 AF031824	Hs.99244 Hs.143212	ESTs cystatin F (leukocystatin)	1.42
15	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.42
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.42
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.42 1.40
	427634 403409	AL399745	Hs.18449	hypothetical protein MGC10820 NM_005929:Homo sapiens antigen p97 (mela	1.40
20	434262	AF121858	Hs.12169	sorting nexin 8	1.34
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.32
	427730	AW250549	Hs.180577	granulin	1.32
	411742 450395	AW247593 BE048545	Hs.71819 Hs.161757	eukaryotic translation initiation factor ESTs	1.31 1.30
25	413291	NM 006278	Hs.75268	sialyttransferase 4C (beta-galactosidase	1.26
	442609	AL020996	Hs.8518	selenoprotein N	1.24
	416929	N20535		melastatin 1	1.21
	421975	AW961017 AW805749	Hs.6459	hypothetical protein FLJ11856 superoxide dismutase 2, mitochondrial	1.21 1.20
30	454478 437723	A1672731	Hs.13256	ESTs	1.18
-	416350	AF188625	Hs.189507		1.08
		_			
	TABLE 4		Fan amba	set identifier number	
35	Pkey: CAT num		e cluster num		
-	Accession		bank accessio		
	Pkey 430540	CAT Number 713_2	Accession	DC012106 NIA 007126 AE100752 AI 137377 7707	68 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
40	430340	113_2	BM045810	AU120387 BG770238 BG686740 BG913323 B1759	9980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
			AI770171	RE196861 RE856897 AA463876 AI375927 AA64881	10 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
			Al365196	AW337984 AW026150 BE466591 BE674599 AI818	438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903667
			BE732715	BM043200 BE900263 BE900706 BE731097 BE394	0023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
45			RE208100	AW245422 AI423847 AI914618 HR0534 BE301004	I AL 531791 AI435581 BF793112 AL 577303 AA 373265 BE746965 BF743630 BE879290
			AI359493	BM018598 AI689260 AW072450 F20201 AW15140	5 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953
			BG340524	W52648 AA113434 BE785431 BIO41981 BG83238	35 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
			W58732 V	V85690 BG958989 ALZOSZOG H19721 V17031 V477 ALZOA ALZOSEZER DC180077 REZAGASS AAR12018 /	AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114
50			A1243844	AAR09493 AA481029 AA825718 AI347866 AI43167	70 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103
			AW00818	8 R07703 AA989120 AA746235 AW028983 AA7891	102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BIB00809
				BG746251 BE962912 BM454584 AL134894 BF10	4082 H80591 .
	454088	1007145_1	AW06242	5 AW062411 4 AA760703 DE218602 AI3/00/6 AW166131 RE51!	5854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396
55	458997	11847_4		4 AW937420 AA 137082 AA013374 BG619478 BG4	
	446019	658727_1	AI362520	D25917 AI670784 AI742347 AW269789 AI270700	AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
			AW36222	5 AW362228 AL119827	700 DA1474000 DC7E4000 ALM94370 DC7E7303 DC7E4430 DC775038 BC834418
	430015	713_2	8C01717	1 BC012195 NM_00/126 AF100/52 AL13/3// Z/V n ALISO0397 BC770238 BC686740 BC913323 BL75	768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 9980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
60	•		AI770171	BF196861 BE856897 AA463876 AI375927 AA6488	910 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
-			Al365196	AW337984 AW026150 BE466591 BE674599 AI818	8438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
			BE73271	5 BM043200 BE900263 BE900706 BE731097 BE39	90023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
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			DC000022 A A000040 A1620444 A1740276 A1920420 DC007676 A1473422 A11158860 RF300655 AW170777 AA586920 AL5/1889 AL500850 AL5/1999
60	•		AL CONORD DISCOLA DES ASSES DE DESTEDRA A RELACED A ASESTES ATOMINA PER 16577 AT 577636 ATAY SM 2013// AUTO-3433 AVV33 12/ PAV3444
			ALSEZBU BIO-3034 BF 34201 B-05 1379 ALSESSA 1429904 AA279809 AISS2549 AWS12517 BG056280 AA521222 BE271141 AL581932 AL541575 BIB19184 AVG60190 AL556475 AIG20020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AW33367 T78652 AL554988 AA36688 AL582615
			DENTALON DEDUCED ALETALED DIMACENO MICECAL MESSON MATSERS ABSANTIN ABRIGINA ARAK/DJ/ ARUJIR94 ARDJDZZI RVV/094200
			ANDS1447 RETRREAS AIGRORGO AARONGRO AAREONEG AAREONEG AMDON154 AA135727 HU5927 HZ3433 K42244 N79997 AVV300000 AVV3000001
65			AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 BC017849 BC005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535
	416929 454478		
	75770	42/0_10	AW 321 AW
70	TABLE		
70	Pkey: Ref:		Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	MG.		sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
	Strand		Indicates DNA strand from which exons were predicted.
75	Nt_pos	ition:	Indicates nucleotide positions of predicted exons.
,,	Pkey	Ref	Strand Ni_position
	40332	8469088	Minus 120428-120703
	40545 40601		
80	40340		

PCT/US02/29560 WO 03/025138

Table 49A lists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body issues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genectip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (A), a normalized value reflecting the retative level of mRNA expression.

Pkey:

Unique Eos probeset identifier number

ExAcor:
Exemplar Accession number, Genbank accession number

UnigenelD:
Unigene Tite:
Unique gene title

R1:
Stit percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of normal tissue Als

90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of heart, liver, lung, and kidney Als

10

	Pkey	ExAcon	1 biograph	Italiana Yu-			
	452838	U65011	UnigenelD	Unigene Title	R1	R2	R3
15	426555	NM_000372	Hs.30743 Hs.2053	preferentially expressed antigen in meta	14.05	11.83	14.05
13	430377			tyrosinase (oculocutaneous albinism IA)	13.15	13.27	13,15
		NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	11,77	7.43	11.77
	420208	BE276055	Hs.95972	silver (mouse homolog) like	10.53	19.95	10.27
	431360	NM_000427	Hs.251680	toricrin	9.78	7.09	0.89
20	430822	AJ005371	Hs.248017	glyceratdehyde-3-phosphate dehydrogenase	9.40	7.20	8.84
20	422158	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	8.03	10.27	12,84
	419628	H67546	Hs.49768	ESTs	7.56	8.92	6.49
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	7.52	5.47	15,47
	430686	NM_001942	Hs.2633	desmoglein 1	6.06	4.13	3.31
25	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	5.86	9.22	0.77
25	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.84	3.46	5.84
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.82	3.94	5.82
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.81	3.33	6.79
	453344	BE349075	Hs.44571	ESTs	5.78	3.07	5.98
	425088	AA663372	Hs. 169395	hypothetical protein FLJ12015	5.60	3.92	
30	402075			ENSP00000251056*:Plasma membrane calcium	5.60 5.12		- 5.60
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp		4.22	5.12
	420602	AF060877	Hs.99236		5.09	3.33	4.14
	426600	NM_003378	Hs.171014	regulator of G-protein signalling 20	5.06	5.78	5.06
	430838	N46664	Hs.169395	VGF nerve growth factor inducible	5.04	6.77	9.42
35	417542	J04129	Hs.82269	hypothetical protein FLJ12015	5.03	3.06	5.03
	425234	AW152225		progestagen-associated endometrial prote	4.93	8.13	5.41
	408962	BE386436	Hs.165909	ESTs, Wealty similar to I38022 hypotheti	4.78	2.93	4.78
	410361		Hs.44317	SRY (sex determining region Y)-box 10	4.75	3.28	5.30
		BE391804	Hs.62661	guarrylate binding protein 1, interferon-	4.70	3.11	4.70
40	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	2.27	4.68
70	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.65	3.21	3.31
	417166	AA431323	Hs.42146	ESTs	4.56	5.23	4.56
	421773	W69233	Hs.112457	ESTs	4.52	11.11	0.96
	442711	AF151073	Hs.8645	hypothetical protein	4.37	3.70	4.30
15	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.37	3.08	6.75
45	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	4.32	2.61	4.32
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.31	3.13	4.31
	4510 <del>99</del>	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.28	2.89	2.17
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.18	2.68	5.92
	420301	AA767526	Hs.22030	paired box gene 5 (8-cell lineage specif	4.16	2.57	
50	433447	U29195	Hs.3281	neuronal pentraxin (I	4.15	2.26	4.16
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A			6.46
	408380	AF123050	Hs.44532	diabiquitin	4.10	4.04	4.64
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.02	2.46	5.33
	421633	AF121860	Hs.106260	sorting nextin 10	4.02	3.48	3.19
55	454117	BE410100	Hs.40368		4.01	2.61	3.36
	417355	D13168	Hs.82002	adaptor-related protein complex 1, sigma	3.96	2.68	3.96
	420267	N37030		endothelin receptor type B	3.95	2.46	3.66
	412228	AW503785	Hs.173337 Hs.73792	ESTs	3.88	3.87	3.88
	427528			complement component (3d/Epstein Barr vi	3.61	3.04	7.94
60	405451	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.79	2.23	3.79
00	449078	41/004000	11- 20020	dihydropyrimidinase-like 3	3.78	3.74	4.06
		AK001256	Hs.22975	KIAA1576 protein	3.76	2.83	3.76
	423799	AW026300	Hs.132906	19A24 protein	3.75	2.36	3.75
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.73	2.59	6.97
65	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	3.72	2.15	3.92
03	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.69	4.17	1.18
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.64	2.08	3.64
	422423	AF283777	Hs.116481	CO72 antigen	3.64	2.94	3.64
	419956	AL137939	Hs.40096	cadherin 19, type 2	3.56	2.22	4.68
70	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	3.55	2.96	4.70
70	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.54	1.96	3.54
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.53	2.18	3.27
	444381	BE387335	Hs.283713	ESTs. Weakly similar to S64054 hypotheti	3.48	2.83	11.00
	449722	BE280074	Hs.23960	cyclin 81	3.48	2.10	
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.47	3.90	4.64
75	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (Ir	3.45	2.38	4.98
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas			3.45
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	3.44	3.83	2.09
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.43	2.39	3.43
	423605	AF047826	Hs.129887	cadherin 19, type 2	3,41	4.33	5.41
80	421508	NM_004833	Hs.105115	absent in melanoma 2	3,40	1.97	4.06
-	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.38	2.77	5.46
	430770	AA765694	Hs.123296	ESTs Moderately stimilar to Transforming	3.36	2.41	3.36
	445784	AI253155	Hs.146065	ESTS .	3.36	2.08	3.83
	******	. 4200 103	113.140003	E313 ·	3.32	2.02	3.80

	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.32	1,87	3.76
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.31	2.10	3.31
	441224	AU076964	Hs.7753	catumenin	3.28	2.04	3.28
-	428242	H55709	Hs.2250	teukemia inhibitory factor (cholinergic	3.26	2.43	3.56
5	413385	M34455	Hs.840	indoleamine-pyrrote 2,3 dioxygenase	3.24	2.94	2.85
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	3.23	1.84	3.87 3.13
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889 ESTs	3.22 3.22	3.10 3.41	1.45
	442757 426317	A1739528 AA312350	Hs.28345 Hs.169294	transcription factor 7 (T-cell specific,	3.18	2.50	3.18
10	432874	W94322	Hs.279651	melanoma inhibitory activity	3.18	5.31	4.55
10	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.17	3.09	4.28
	443983	H04482	Hs.163724	ESTs	3.16	2.21	3.16
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.14	1.74	3.25
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.14	2.07	3.33
15	422424	Al185431	Hs.296638	prostate differentiation factor	3.10	3.20	215
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.10	2.23	3.10
	401747			Homo sapiens keratin 17 (KRT17)	3.10	2.10	3.02
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.08	3.08	4.00 3.07
20	419870	AW403911 BE386490	Hs.266175	phosphoprotein associated with GEMs Pirin	3.07 3.06	3.16 2.92	4.20
20	432878 401454	BE380490	Hs.279663	NM_014226*:Homo sapiens renal tumor anti	3.05	1.96	3.05
	410079	U94362	Hs.58589	glycogenin 2	3.01	2.26	3.27
	426501	AW043782	Hs.293616	ESTs	3.01	2.00	3.68
	418310	AA814100	Hs.86693	ESTs	3.00	2.35	6.76
25	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.96	2.31	3.78
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	2.96	2.49	4.74
	408418	AW963897	Hs.44743	KIAA1435 protein	2.94	1.80	2.94
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.93	1.74	2.93
20	416640	BE262478	Hs.79404	neuron-specific protein	2.93	2.78	3.09
30	443264	BE221477	Hs.132137	ESTs, Moderately similar to A47582 B-cel	2.92	2.35	4.27
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.91 2.90	2.83 2.44	3.84 2.90
	405545 451537	R56631	Hs.26550	Target Exon retinoid X receptor, gamma	2.90 2.90	4.09	3.40
	431337	AW014875	Hs.137007	ESTs	290	2.43	2.90
35	406673	M34996	Hs.198253	major histocompatibility complex, class	2.89	3.22	1.44
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.89	3.90	2.89
	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.69	4.40	3.05
	442739	NM_007274	Hs.8679	cytosofic acyl coenzyme A thioester hydr	2.88	2.36	4.54
40	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	2.86	3.23	1.95
40	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.84	1.84	2.84
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	2.84	1.80	2.92
	424153	AA451737	Hs.141496	MAGE-like 2	2.84	2.26	2.84
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.81	2.91	0.83
45	431317	AA502682	11- 153303	gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	2.81 2.80	2.17 2.06	2.96 4.10
73	424800 448111	AL035588 AA053486	Hs.153203 Hs.20315	MyoD family inhibitor interferon-induced protein with tetratri	2.79	1.85	2.42
	431183	NM_006855		KDEL (Lys-Asp-Gtu-Leu) endoplasmic retic	2.78	2.34	6.53
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	2.78	3.75	4.01
	427951	AI826125	Hs.43546	ESTs	2.78	1.99	2.70
50	453912	AL121031		SWI/SNF related, matrix associated, acti	2.77	2.28	2.77
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.75	1.98	2.75
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.74	3.18	3.60
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.72	2.24	2.72
55	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.72	2.31	3.59
23	420552 409103	AK000492 AF251237	Hs.98806 Hs.112208	hypothetical protein XAGE-1 protein	2.72 2.72	1.85 2.18	2.72 2.72
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.71	2.20	4.48
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.71	5.74	2.62
	436700	A1693690	Hs.301406	hypothetical protein PP3501	2.71	3.37	3.32
60	419098	AA234041	Hs.87271	ESTs	2.70	3.53	1.35
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.69	2.48	2.69
	418067	AJ127958	Hs.83393	cystatin E/M	2.68	3.04	0.56
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.67	2.35	3.16
65	437723	AI672731	Hs.13256	ESTs	2.66	2.16	2.66
03	411252	AB018549	Hs.69328	MD-2 protein	2.66	1.81	2.66
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.66	2.43	3.92
	453837	AL138387	Hs.256126 Hs.22265	bacutoviral IAP repeat-containing 7 (liv pyruvate dehydrogenase phosphatase	2.65 2.64	3.71 1.85	2.80 4.72
	434826 414696	AF155661 AF002020	Hs.76918	Niemann-Pick disease, type C1	2.64	2.07	2.64
70	444371	BE540274	Hs.239	forkhead box M1	2.64	2.82	4.46
, 0	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.63	1.81	2.95
	439310	AF086120	Hs.102793	ESTs	2.62	2.38	10.12
	420218	AW958037		ribosomal protein L4	2.62	2.80	2.62
~-	438746	AI885B15	Hs.184727	Human melanoma-associated antigen p97 (m	2.60	3.27	2.12
75	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.60	2.67	3.03
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.59	3.22	2.59
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.58	1.69	2.05
	444809	BE207568	Hs.208219	oculospanin	2.58	2.77	2.88
80	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.58	1.83	2.58
80	434276	AF123659 R07566	Hs.93605	leucine zipper, putative tumor suppresso small inducible cytokine A3 (homologous	2.55 2.55	3.70 2.14	3.28 1.62
	412326 410174		Hs.73817 Hs.59461	OKFZP434C245 protein	2.55 2.55	2.07	2.55
	447735		Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	2.54 2.54	2.17	4.01
					2.0		****

	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	2.53	1.68	3.16
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.53	2.74	3.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.52	1.62	3.17
_	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.51	2.67	1.88
5	442426	AI373062	Hs.332938	hypothetical protein MGC5370	2.51	2.68	4.57
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.51	1.74	2.68
	427581	NM_014788	Hs.179703	KIAAD129 gene product	2.51	1.67	2.24
	432800	8E391046	Hs.278962	AIM-1 protein	2.51	5.55	2.42
10	408996 410326	Al979168 Al368909	Hs.344096	glycoprotein (transmembrane) nmb	2.50	1.95	241
10	452833	RE559681	Hs.47650 Hs.30736	ESTs	2.50	2.85	2.63 3.07
	410016	AA297977	Hs.57907	KIAA0124 protein	2.50 2.49	3.14 3.38	2.91
	429083	Y09397	Hs.227817	small inducible cytokine subfamily A (Cy BCL2-related protein A1	2.48	1.85	2.70
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.48	2.33	2.99
15	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.47	1.88	4.14
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.45	2.00	0.98
	401780			NM_005557*:Homo sapiens keratin 16 (foca	244	2.30	1.39
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.44	1.57	0.88
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.42	1.91	2.56
20	417880	8E241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.42	2.31	4.27
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.41	2.73	241
	415752	BE314524	Hs.78776	putative transmembrane protein	2.41	2.07	3.41
	409703	NM_006187	Hs.56009	2-5-ofigoadenylate synthetase 3 (100 k	2.41	2.34	3.26
25	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.40	1.65	2.40
25	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.40	2.18	8.13
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.40	2.88	2.46
	403328	D40044	11. 00070	Target Exon	2.39	2.00	1.95
	427540	R12014	Hs.20976	ESTs	2.39	1.73	3.24
30	449523 433848	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.39	1.96	2.39
50	438501	AF095719 Z44110	Hs.93764 Hs.86149	carboxypeptidase A4	2.38 2.38	2.45 1.85	2.65 2.38
	430066	A1929659	Hs.237825	phosphoinositol 3-phosphate-binding prot signal recognition particle 72kD	2.38	1.60	2.79
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.37	1.99	6.23
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.37	1.72	3.24
35	458997	AW937420	1.0.25516	ESTs	2.37	1.57	3.27
-	451446	AI826288	Hs.171637	hypothetical protein MGC2628	2.35	1.90	2.39
	408838	AI669535	Hs.40369	ESTs	2.35	1.59	2.71
	448275	BE514434	Hs.20830	kinesin-fike 2	2.35	2.19	2.35
40	424148	BE242274	Hs.1741	integrin, beta 7	2.35	1.89	3.07
40	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.35	1.65	2.35
	409105	AW467539	Hs.255877	ESTs	2.35	2.50	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	2.34	2.12	2.90
	425606	U52112	Hs.158331	renin-binding protein	2.34	2.69	1.69
45	433576	BE080715	Hs.161091	ESTs	2.34	3.74	2.34
47	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	2.34	2.08	4.48
	431620 436614	AA126109 AW104388	Hs.264981	2-5-oligoadenylate synthetase 2 (69-71	2.33	2.43	2.66
	425289	AW139342	Hs.149091 Hs.155530	ESTs interferon, gamma-inducible protein 16	2.33 2.33	3.37 1.67	2.33 4.28
	426827	AW067805	Hs.172665	methylenetetrahydrotolate dehydrogenase	2.33	1.58	0.40
50	430015	AW768399	715.772.500	ESTs	2.33	1.76	2.33
	421282	AA286914	Hs.40782	ESTs	2.32	1.65	2.49
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	2.32	2.16	1.48
	432540	AI821517	Hs.105866	ESTs	2.32	1.58	2.35
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	2.32	2.46	9.99
55	414829	AA321568	Hs.77436	pleckstrin	2.32	1.91	2.32
	425390	AJ092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.31	1.63	2.31
	448569	8E382657	Hs.21486	signal transducer and activator of trans	2.31	2.79	2.41
	428819	AL135623	Hs.193914	KIAA0575 gene product	2.30	1.60	2.95
60	409512 425231	AW979187 AA527161	Hs.293591	metanoma differentiation associated prot	2.30	1.95	3.66
UU	416091	AF295370	Hs.283082	ESTs defensin, beta 3	2.28 2.28	1.96 2.76	2.36 2.18
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.27	2.76	2.46
	427719	AI393122	Hs.134726	ESTs	2.27	1.88	2.29
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	2.27	2.16	4.09
65	457465	AW301344	Hs.122908	DNA replication factor	2.26	2.23	2.26
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.26	2.13	3.16
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.26	1.75	2.84
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.26	3.38	2.56
70	449317	AW293413	Hs.132906	19A24 protein	2.26	2.04	2.73
70	429922	Z97630	Hs.226117	H1 histone family, member 0	2.26	1.59	2.38
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.25	1.86	3.07
	425388	AA329384	Hs.156110	immunoglobulin kappa constant	2.25	1.91	2.25
	417282	AA195203		RAB5C, member RAS oncogene family	2.25	2.23	3.20
75	406687	M31126	Ltn C004	matrix metalloproteinase 11 (stromelysin	2.24	2.69	2.78
13	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (I	2.23	2.20	2.51
	408015 442503	AW136771 AF147078	Hs.244349 Hs.150853	epidermal differentiation complex protei p53-responsive gene 5	2.23	4.59	2.47
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine or	2.23 2.22	3.62 1.60	0.85 1.69
_	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.22	5.53	2.46
80	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	2.21	2.40	4.37
	422947	AA306782	Hs. 122552	G-2 and S-phase expressed 1	2.21	2.06	2.32
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA sequence	2.20	2.69	2.91
	417366	BE185289	Hs.1076	small profine-rich protein 1B (comifin)	2.20	2.26	3.79
				, ,			

	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	2.20	1.96	2.44
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.20	3.28	2.99
	427051	BE178110	Hs.173374	Homo sapiens cDNA FU10500 fis, clone NT	2.20	1.98	3.40
5	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.20	1.44	2.31
,	409354	N68188	Hs.159472	Homo sapiens cDNA: FL/22224 fis, clone H	2.18	244	2.70
	418941 424723	AA452970 BE409813	Hs.239527 Hs.152337	E1B-55kDa-associated protein 5	2.18 2.18	1.75 1.55	2.70 2.44
	430132	AA204686	Hs.234149	protein arginine N-methyltransferase 3(h hypothetical protein FLJ20647	2.18	1.43	2.37
	452194	AI694413	113.207173	Ubiquitin-like protein FAT 10777 - diubiq	2.17	3.07	1.76
10	417933	X02308	Hs.82962	Drymidylate synthetase	2.17	1.86	4.15
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.17	2.38	2.91
	425317	AW205118	Hs.210546	interleukin 21 receptor	2.17	2.02	2.22
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.16	1.87	2.49
1.5	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.16	1.55	2.26
15	452958	AA883929	Hs.40527	ESTs	2.15	1.56	2.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	2.15	1.76	2.97
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.15	1,85	2.74
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	2.14	1.88	4.99
20	451952 450534	AL120173 AI570189	Hs.301663	ESTs	213	2.08	213
20	449217	AA278536	Hs.25132 Hs.23262	KIAA0470 gene product ribonuclease, RNase A family, k6	2.12 2.12	1.67 1.75	3.41 2.27
	432734	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.12	2.14	2.49
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.12	2.46	2.67
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	2.12	2.16	2.82
25	429624	AA458648	Hs.99476	ESTs, Weakly similar to 13131848 alpha1	2.11	2,01	0.68
	447178	AW594641	Hs.192417	ESTs	2.10	2.52	2.10
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	2.10	1.52	4.01
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	2.10	1.53	2.10
30	436797	AA731491	Hs.334477	hypothetical protein MGC14879	2.10	1.55	. 2.41
30	453256	AI565587	Hs.32556	KIAA0379 protein	2.09	213	2.89
	405547	BE262677	U- 202550	NM_018833*:Homo sapiens transporter 2, A	2.09	2.61	2.09
	434203 412609	248804	Hs.283558 Hs.74124	hypothetical protein PRO1855 ocular albinism 1 (Nettleship-Falls)	2.09 2.09	1.76 3.91	4.10 2.38
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.09	1.62	1.28
35	417576	AA339449	Hs.82285	phosphoribosytglycinamide formytransfer	2.08	1.86	2.08
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	2.08	2.83	2.08
	423198	M81933	Hs.1634	cell division cycle 25A	2.08	1.66	2.23
	433068	NM_006456	Hs.288215	sialytransferase	2.08	1.94	2.60
40	409038	T97490	Hs.50002	small inducible cytokine subtamily A (Cy	2.07	1.91	3.62
40	452392	L20815	Hs.507	comeodesmosin	2.07	3.96	0.97
	403532			NM_024638:Homo sapiens hypothetical prot	2.07	1.88	2.68
	439859	AW292872	Hs.124554	ESTs	2.07	1.72	2.22
	428484 442643	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.07	2.26	4.22
45	426312	U82756 AF026939	Hs.181874	PRP4/STK/WD splicing factor interferon-induced protein with tetratri	2.07 2.06	1.74 2.08	1.90 1.43
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.06	2.12	2.06
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.06	1.65	2.91
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.06	1.97	2.42
	414142	AW368397	Hs.334485	hemicentin (fibutin 6)	2.05	2.44	2.05
50	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.05	2.37	2.05
	450325	A1935962	Hs.91973	ESTs	2.05	1.67	1.82
	424090	X99699	Hs.139262	XIAP associated factor-1	2.05	1.56	1.99
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	2.04	1.52	2.07
55	413794	AF234532	Hs.61638	myosin X	2.04	2.02	2.11
"	414945 425580	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.04	4.57	1.64
	420052	L11144 AA418850	Hs.1907 Hs.44410	galanin ESTs	2.04 2.03	1.67 1.90	2.26 2.21
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	2.03	1.53	2.31
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.02	1.73	2.02
60	426759	AI590401	Hs.21213	ESTs	2.02	1.86	5.47
	432435	BE218886	Hs.282070	ESTs	2.02	1.39	1.67
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	2.02	1.57	2.02
	421574	AJ000152	Hs.105924	defensin, beta 2	2.02	2.22	2.15
65	411358	R47479	Hs.94761	KIAA1691 protein	2.01	2.55	1.75
05	408209	NM_004454		ets variant gene 5 (ets-related molecule	201	2.58	2.39
	409262 400750	AK000631	Hs.52256	hypothetical protein FLI20624	2.01	1.50	2.01
	439496	BE616501	Hs.32343	Target Exon Homo sapiens, Similar to RIKEN cDNA 1110	2.01 2.01	1.73	2.09
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.01	2.42 1.65	0.78 1,72
70	446839	BE091926	Hs.16244	mitotic spindle colled-coil related prot	2.01	1.61	1.03
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	200	2.11	2.33
	436200	R51386	Hs.124881	ESTs	2.00	1.89	2.24
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	1.99	1.50	1.99
~-	420005	AW271106	Hs.133294	ESTs	1.99	2.03	2.59
75	417848	AA206581	Hs.116586	ESTs, Weakly similar to JC5314 CDC28/odc	1.99	1.42	2.17
	435545	AA587415	Hs.28107	ESTs	1.99	1.89	1.99
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.99	2.23	3.44
	444342	NM_014398		similar to lysosome-associated membrane	1.99	2.05	0.32
80	453905	NM_002314		LIM domain kinase 1	1.98	2.48	2.79
δU	453884	AA355925	Hs.36232	KIAA0186 gene product	1.98	1.93	1.98
	459373	BE408266	Hs.301406	hypothetical protein PP3501	1.98	2.22	1.91
	422809 452840	AK001379 AI097393	Hs.121028 Hs.43481	hypothetical protein FLJ10549 hypothetical protein DKFZp564K192	1.98 1.98	1.68 1.67	1.98 2.18
	772070		113.73401	Hyponesia historii eut chasiu 135	1.30	1.01	4.10
				510			

	409178 420991		Hs.50915 Hs.287379	katūkrein 5 Homo sapiens mRNA for FLJ00111 protein,	1.98 1.98	3.76 1.90	1.37 2.63
	414020		Hs.75703	small inducible cytokine A4 (homologous	1.97	1.88	1.23
_	443105	X96753	Hs.9004	chondroitin suttate proteoglycan 4 (meta	1.97	1.95	5.55
5	413450	Z99716	Hs.75372	N-acelylgalactosaminidase, alpha-	1.97 1.97	1.77 1.73	1.97 3.89
	431574 408561	AW572659	Hs.261373 Hs.84120	hypothetical protein dJ434014.3 hypothetical protein MGC13016	1.97	2.89	2.08
	421866	AJ308037 M24470	Hs.1435	guanosine monophosphate reductase	1.97	1.95	2.65
	405506			Target Exon	1.96	1.72	2.27
10	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	1.96 1.95	1.74 2.09	2.35 2.77
	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr high-glucose-regulated protein 8	1.95	1.66	2.58
	448356 453931	AL120B37 AL121278	Hs.20993 Hs.25144	ESTs	1.95	2.38	1.95
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	1.95	1.63	2.82
15	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	1.94	2.02	1.35 2.21
	442064	Al422867	Hs.88594	ESTS ENCORMONO2002755-DDEDES emisio /Erromes	1.94 1.94	1.49 1.69	1.94
	400533 448752	AA593867	Hs.300842	ENSP0000209376*:PRED65 protein (Fragmen KIAA1608 protein	1.94	1.71	2.40
	408636	BE294925	Hs.46680	CGI-12 protein	1.94	1.69	2.93
20	439569	AW602166	Hs.222399	CEGP1 protein	1.93	1.62	3.21
	405779			NM_005367:Homo sapiens metanoma antigen,	1.93 1.93	1.83 1.97	1.99 1.93
	444570 446950	H58373 AA305800	Hs.332938 Hs.5672	hypothetical protein MGC5370 hypothetical protein AF140225	1.93	1.56	1.61
	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	1.93	2.12	2.63
25	409098	AA132672	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	1.92	2.12	2.51
	413916	N49813	Hs.75615	apolipoprotein C-II	1.92 1.92	1.98 1.65	0.22 6.39
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to NM_002463*:Homo sapiens myxovirus (influ	1.92	2.45	1.89
	402994 425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.92	2.69	2.30
30	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.92	2.10	2.93
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.91	1.57	1.91
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	1.91 1.90	1.44 1.52	1.68 1.14
	430280 426251	AA361258 M24283	Hs.237868 Hs.168383	interleukin 7 receptor intercetlular adhesion molecula 1 (CD54)	1.90	2.16	1.21
35	440773	AA352702	Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	1.90	1.84	2.07
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.90	4.26	1.70
	426470	AA528794	Hs.128644	ESTs	1.90 1.90	2.69 2.01	2.04 1.90
	409557 429714	BE182896 BE561801	Hs.3686 Hs.2484	ESTs T-cell leukemia/lymphoma 1A	1.90	2.49	2.52
40	428125	AA393071	Hs.182579	leucine aminopeptidase	1.89	1.89	1.49
	427634	Al399745	Hs.18449	hypothetical protein MGC10820	1.89	3.59	1.71
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	1.89 1.89	1.67 2.55	1.45 1.39
	418883 448243	BE387036 AW369771	Hs.1211	acid phosphatase 5, tartrate resistant integrin, beta 8	1,89	1.96	1.89
45	416114	A1695549	Hs.183868	glucuronidase, beta	1.89	1.70	1.10
,	425935	Z98200	Hs.163724	HSPC019 protein	1.88	1.86	2.04
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.88	4.16 2.70	1.78 0.75
	430171	AF086289 AF026942	Hs.234766 Hs.17518	skin-specific protein gb:Horno sapiens cig33 mRNA, partial sequ	1.87 1.87	2.25	1.87
50	407366 454294	AB000734	Hs.50640	JAK binding protein	1.87	1.98	1.46
•	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.87	2.73	1.71
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	1.87 1.87	1.79 1.88	2.72 1.16
	401781 440590	AI863446	Hs.266308	Target Exon mosaic serine protease	1.86	1.79	1.13
55	428450			KIAA0175 gene product	1.86	1.72	4.39
	433675	AW977653	Hs.75319	ribonucteotide reductase M2 polypeptide	1.86	1.81	1.86
	429323			apical protein, Xenopus lævis-like	1.86 1.85	1.57 1.71	1.86 5.82
	433001 453107		Hs.279905 3 Hs.279746	done HQ0310 PRO0310p1 vanilloid receptor-like protein 1	1.85	2.75	1.84
60	430441		113.273740	desmoplakin (DPI, DPII)	1.85	1.80	2.79
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	1.85	1.80	1.86
	423673		Hs.1695	matrix metalloproteinase 12 (macrophage	1.85 1.85	1.94 1.72	1.85 2.52
	431958 414737		Hs.2877 Hs.125087	cadherin 3, type 1, P-cadherin (placenta ESTs	1.84	1.90	1.84
65	439979			hypothetical protein FLJ 10430	1.84	1.57	1.84
	428311			tryptophan 2,3-dioxygenase	1.84	1.41	0.12
	412141		Hs.48938	hypothetical protein FLJ21802	1.84 1.84	1.70 1.66	3.15 1.84
	428515		Hs.286229	plexin C1 ESTs	1.84	2.32	2.17
70	427914 439352		Hs.20575 Hs.169615	hypothetical protein FLJ20989	1.84	1.55	1.84
. •	41327			interferon-stimulated protein, 15 kDa	1.83	3.20	1.75
	435080		Hs.155111	hypothetical protein FLJ14428	1.83	1.62	1.47
	40796			Homo sapiens, clone MGC:15887, mRNA, com phosphoribosylformylghycinamidine syntha	1.83 1.83	1.58 1.73	2.11 2.18
75	421535 433025			opsin 3 (encephalopsin)	1.83	1.96	1.83
,,	42615			v-erb-b2 avian erythroblastic leukernia v	1.83	1.61	2.46
	42689	0 AA393167	Hs.41294	ESTs	1.82	2.44	1.82
	41102			leukocyte immunoglobulin-like receptor,	1.82 1.82	2.24 2.72	2.01 2.16
80	44185			ESTs, Wealdy similar to FIG1 MOUSE FIG-1 hypothetical protein DKFZp762H1311	1.82	1.50	1.82
50	43743 44835		Hs.27027 Hs.108923	RAB38, member RAS oncogene family	1.82	2.52	1.76
	42067	4 NM_00005		butyrylcholinesterase	1.82	1.43	0.68
	43921	9 N33883	Hs.41322	ESTs	1.82	1.88	2.43

	432810	AA863400		ESTs	1.82	1.43	1.82
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	1.82	1.98	1.82
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	1.82	1.63	1.82
5	436456 418918	AW292677 X07871	Hs.248122 Hs.89476	G protein-coupled receptor 24 CD2 antigen (p50), sheep red blood cell	1.82 1.82	2.80 2.28	2.18 2.00
•	424755	AB033094	Hs.152925	KIAA1268 protein	1.82	1.85	1.62
	435315	BE390513	Hs.27935	hypothetical protein MGC4837	1.82	1.74	5.18
	420783	A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.81	1.87	0.80
10	417105	X60992	Hs.81226	CD6 antigen	1.81	1.88	2.03
10	423961 446019	D13666 Al362520	Hs.136348	periostin (OSF-2os) histone deacetylase 3	1.81 1.81	1.73 1.39	2.45 2.24
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.81	3.05	1.58
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	1.80	2.00	1.78
1.5	453684	AK001922	Hs.34578	alpha2,3-sialyltransferase	1.80	1.98	1.22
15	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.80	1.56	1,71
	453779 434706	N35187 AI656291	Hs.43388 Hs.116394	28kD interferon responsive protein ESTs	1.80 1.80	2.42 1.58	2.04 1.80
	416065	BE267931	Hs.78996	profilerating cell nuclear antigen	1.80	1.79	2.51
••	453331	AI240665		ESTs	1.79	1.43	2.33
20	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.79	1.46	4.46
	428784	Y12851	Hs.193470	purinergic receptor P2X, figand-gated to	1.79	2.30	1.79
	453507 452826	AF083217 BE245286	Hs.33085 Hs.301636	WD repeat domain 3 peroxisomal biogenesis factor 6	1.79 1.79	1.49 1.57	1.51 2.00
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.79	2.26	2.22
25	406672	M26041	Hs.198253	major histocompatibility complex, class	1.79	1.76	1.78
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	1.79	1.43	3.32
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	1.78	1.66	1.29
	424954 436378	NM_000546 AJ227874	Hs.1846 Hs.99244	tumor protein p53 (Li-Fraumeni syndrome) ESTs	1.78 1.78	1.73 1.84	2.35 . 1.78
30	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.78	1.66	3.67
	421948	L42583	Hs.334309	keratin 6A	1.78	1.74	3.00
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.77	2.27	2.13
	437317	AA748613	Hs.311977	ESTs, Highly similar to SWI/SNF related,	1.77	1.98	2.32
35	427318 418403	AF186081 D86978	Hs.175783 Hs.84790	zinc transporter KIAA0225 protein	1.77 1.76	1.61 1.49	0.92 2.24
-	421433	AI829192	Hs.22380	ESTs	1.76	1.49	2.52
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.76	1.74	1.76
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	1.76	1.43	1.76
40	427536	BE277141	Hs.115803	gb:601178666F1 NIH_MGC_20 Homo sapiens c	1.76	2.12	1.76
70	433364 401994	A1075407	Hs.296083	ESTs, Moderately similar to I54374 gene Target Exon	1.76 1.75	1.86 1.44	1.48 1.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	1.75	1.69	1.79
	408633	AW963372	Hs.46677	PRO2000 protein	1.75	1.46	1.68
15	429978	AA249027		ribosomal protein S6	1.75	1.60	1.92
45	450690	AA296696	Hs.333418	FXYD domain-containing ion transport reg	1.75	2.13	2.03
	456967 417866	AW004056 AW067903	Hs.168357 Hs.82772	T-box 2 collagen, type XI, atpha 1	1.74 1.74	1.95 2.64	1.42 2.01
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	1.74	2.82	2.31
50	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.74	1,51	1.62
50	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	1.73	1.54	3.15
	412851 453953	AI826502 AW408337	Hs.97269 Hs.36972	ESTs CD7 antigen (p41)	1.73 1.73	1.67 2.22	1.05 2.28
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	1.73	2.05	1.47
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	1.73	1.71	1.73
55	447217	BE465754	Hs.17778	neuropilin 2	1.73	1.62	4.70
	437673	AW665665	Hs.153034	ESTs	1.72	1.55	2.10
	437879 448410	BE262082 AK000227	Hs.5894 Hs.21126	hypothetical protein FLJ10305 hypothetical protein FLJ20220	1.72 1.72	2.50 1.48	1.80 3.98
	413313	NM_002047	Hs.283108	ghycyl-IRNA synthetase	1.72	2.19	1.62
60	452203	X57522		transporter 1, ATP-binding cassette, sub	1.72	2.68	1.68
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	1.71	2.17	2.24
	403969 450832	AW970602	Hs.105421	ENSP00000034663:Zinc finger protein 131	1.71 1.71	1.31 1.33	1.71 2.38
	453005	AW055308	Hs.31803	ESTs ESTs, Wealdy similar to N-WASP [H.sapien	1.71	1.67	1.95
65	439783	Al125760	Hs.24835	hypothetical protein FLJ14594	1.71	2.10	2.20
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.71	3.86	1.76
	432259	BE269103	Hs.274201	60S acidic ribosomal protein PO	1,71	1.85	1,94
	420340	NM_000734 M26301		CD32 antigen, zeta polypeptide (TIT3 com	1,71	2.12	1.98
70	428289 424006	AF054815	Hs.2253 Hs.137548	complement component 2 CD84 antigen (leukocyte antigen)	1,71 1,70	2.46 1.70	0.76 2.78
. •	440039	Z46188	Hs.6874	KIAA0472 protein	1.70	2.24	1.60
	406646	M33600	Hs.308026	major histocompatibility complex, class	1.70	2.27	1.33
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.70	2.77	2.07
75	420286	AI796395	Hs.111377	ESTs	1.70	1.50	3.21
, ,	430255 445247	AK000703 AW274290	Hs.323822 Hs.153997	Homo sapiens mRNA for KIAA1551 protein, ESTs	1.69 1.69	1.44 2.57	1.69 1.65
	436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	1.69	1.52	3.13
	410257	BE244044	Hs.61469	hypothetical protein	1.69	1.99	1.97
90	424663	NM_002351		SH2 domain protein 1A, Duncan's disease	1.69	1.76	1.69
80	427792 458098	M63928 BE550224	Hs.180841	tumor necrosis factor receptor superfami	1.69 1.68	1.98 1.83	2.48 1.68
	425397	J04088	Hs.156346	metallothionein 1E (functional) topoisomerase (DNA) II alpha (170kD)	1.68	1.57	4.09
	421485	AA243499	Hs.104800	hypothetical protein FL 10134	1.68	1.64	0.68

	421563	NM_006433	Hs.105806	granutysin	1.68	2.24	1.55
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	1.68	1.98	2.05
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	1.68	1.35	1.68
_	440457	8E387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	1.68	1.88	1.63
5	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.67	2.54	1.90
	401760	4 4 0 0 4 0	11. 440044	Target Exon	1.67	1.93 1.85	1.61 4.25
	422158 446644	L10343 NM_003272	Hs.112341 Hs.15791	protease inhibitor 3, skin-derived (SKAL transmembrane 7 superfamily member 1 (up	1.67 1.67	1.94	1.48
	415701	NM_003878	Hs.78619	gamma-glutarnyl hydrolase (conjugase, fol	1.67	1.65	0.90
10	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.67	1.54	1.95
	412856	BE386745	Hs.74531	basigin (OK blood group)	1.67	2.71	1.47
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.66	1.82	1.19
	424399	AI905687	LL- 4C340F	AI905687:IL-BT095-190199-019 BT095 Homo	1.66	3.65 1.98	0.44 1.45
15	432355 427239	AA534416 BE270447	Hs.162185	ESTs, Wealdy similar to S42799 garp prec ubiquitin carrier protein	1.66 1.66	2.94	1.92
13	425262	087119	Hs.155418	GS3955 protein	1.66	2.36	1.66
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.66	1.86	1.90
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.65	2.05	1.31
20	446217	A1651594	Hs.99709	ESTs	1.65	1.98	1.77
20	400222	414400156	11- 2003	NM_002082*:Homo sapiens G protein-couple	1.65 1.65	1,74 2.50	1.81 1.77
	432468 417237	AW402155 H86385	Hs.3003 Hs.81737	CD3E antigen, epsilon polypeptide (TiT3 palmitoyl-protein thioesterase 2	1.65	2.89	1.57
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, yeast) homo	1.64	2.76	1.26
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	1.64	1.96	1.24
25	433867	AK000596	Hs.3618	hippocatcin-like 1	1.64	1.47	1.00
	433671	AW138797	Hs.132906	19A24 protein	1.64	2.17	1.96
	418371 432336	M13560 NM_002759	Hs.84298 Hs.274382	CD74 antigen (invariant polypeptide of m protein kinase, interferon-inducible dou	1.64 1.64	2.18 1.47	1.43 1.64
	409264	NM_002733	Hs.52463	KIAA0966 protein	1.64	1.46	4.89
30	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.64	2.58	1.79
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	1.63	1.72	1.88
	418117	AI922013	Hs.83496	linker for activation of T cells	1.63	1.98	1.99
	448304	BE622768	Hs.290356	mesoderm development candidate 1	1.63 1.63	1.67 2.56	1.86 1.97
35	425535 453258	AB007937 AW293134	Hs.158287 Hs.32597	KIAAD468 gene product ring linger protein (C3H2C3 type) 6	1.63	1.46	2.43
,,	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	1.63	1.34	1.94
	447321	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.63	1.96	1.77
	422192	AA305159	Hs.113019	fls485	1.62	1.45	1.62
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	1.62	2.23	1.53
40	419381 424779	AB023420 AL046851	Hs.90093 Hs.153053	heat shock 70kD protein 4 CD37 antigen	1.62 1.62	1.57 1.92	2.38 2.10
	413283	R78669	Hs.23756	hypothetical prolein similar to swine ac	1.62	1.41	1.12
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.62	2.03	2.13
	414159	AW511414	Hs.257352	apolipoprotein L. 6	1.62	1.89	1.32
45	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	1.52	1.81	1.27
	428179	A1127772	Hs.279696	serum/glucocorticoid regulated kinase-li	1,62 1,61	1.50 1,71	2.13 2.02
	436251 451708	BE515065 Al306536	Hs.296585 Hs.60975	nucleolar protein (KKE/D repeat) ESTs	1.61	2.31	1.70
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.61	1.53	2.50
50	410600	AW575742		ESTs, Moderately similar to S65657 alpha	1.61	1.83	1.69
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	1.61	1.56	1.61
	440201	AL359588	Hs.7041	hypothetical protein DKFZp762B226	1.61	1.58	1.85
	414368 454429	W70171 BE273437	Hs.75939 Hs.301406	uridine monophosphate kinase hypothetical protein PP3501	1.61 1.61	1.59 3.54	2.75 1.52
55	422257	NM_001716		Burkitt lymphoma receptor 1, GTP-binding	1.61	2.15	1.54
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.60	2.01	1.36
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.60	2.00	1.60
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.60	1.38	2.23
60	429612 411263	AF062649 BE297802	Hs.252587 Hs.69360	pituitary tumor-transforming 1 kinesin-like 6 (mitotic centromere-assoc	1.60 1.60	1.78 1.78	2.59 2.07
oo	417324	AW265494	113.03000	ESTs	1.60	2.48	1.91
	430325	AF004562	Hs.239356	syntaxin binding protein 1	1.60	1.74	2.53
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	1.60	1.46	2.46
45	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.60	1.81	3.00
65	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.59 1.59	1.88 1.90	1.68 2.26
	417437 437949	U52682 U78519	Hs.82132 Hs.41654	ESTs, Weakly similar to A46010 X-linked	1.59	2.14	1.59
	401797	0.02.5	113.71007	Target Exon	1.59	1.82	1.78
	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	1.59	1.45	4.69
70	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	1.59	1.82	1.68
	415474	NM_014252		solute carrier family 25 (mitochondrial	1.58	1.51	0.30
	430017 422515	AA263172 AW500470	Hs.35 Hs.117950	protein tyrosine phosphatase, non-recept multifunctional polypeptide similar to S	1.58 1.58	1.72 1.85	2.46 1.94
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	1.58	1.25	2.09
75	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	1.58	1.72	1.80
	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.58	2.60	1.58
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	1.58	1.84	1.22
	401151	AICTTON	Un 100527	Target Exon	1.58 1.58	2.43 1.40	1.60 1.58
80	441590 418677	A1623207 S83308	Hs.190537 Hs.87224	ESTs SRY (sex determining region Y)-box 5	1.58	1.68	1.58
-	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.58	2.28	1.60
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	1.58	2.14	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	1.57	1.46	1.57

	427700	AA262294	Hs.180383	dual specificity phosphatase 6	1.57	1.42	0.88
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.57	1.49 1.46	2.6 <del>9</del> 1.36
	404872 408212	AA297567	Hs.43728	ENSP00000243173":DJ1109J22.1 (novel home hypothetical protein	1.57 1.57	1.55	2.73
5	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	1.57	1.36	1.57
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.57	1.70	1.13
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.57 1.57	1.75 2.26	1.57 2.10
	417929 431629	R27219 AU077025	Hs.74647 Hs.265827	Human T-cell receptor active alpha-chain interferon, alpha-inducible protein (clo	1.57	2.09	1.57
.10	402876			NM_022161*:Horno sapiens fivin inhibitor-	1.56	2.28	1.45
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.56	2.97	1.54
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyttransferase 1	1.56 1.56	1.75 2.76	1.88 1.67
	450663 425818	H43540 AB021225	Hs.25292 Hs.159581	ribonuclease HI, large subunit matrix metalloproteinase 17 (membrane-in	1.56	2.36	1.83
15	422765	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	1.56	1.78	2.06
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.56	1.32	2.70
	453613	F06838	11- 2050	ESTs	1.56 1.56	1.76	1.84 1.56
	428379 429500	X06026 X78565	Hs.2259 Hs.289114	CD3G antigen, gamma polypeptide (TiT3 co hexabrachion (tenascin C, cytotactin)	1.56	اده.1 1.47	3.15
20	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	1.56	2.01	1.56
	420842	A1083668	Hs.50601	hypothetical protein MGC10986	1.55	2.24	1.90
	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	1.55	1.24	3.07
	408901 437669	AK001330 Al358105	Hs.48855 Hs.123164	hypothetical protein FLJ10468 ESTs, Wealdy similar to match to ESTs AA	1.55 1.55	1.79 1.83	2.17 1.96
25	439437	AI207788	Hs.343628	sialytransferase 48 (beta-galactosidase	1.55	1.63	2.20
	418835	AL023694	Hs.88977	hypothetical protein dJ511E16.2	1.55	1.73	1.50
	448533	AA311426	Hs.21635	tubulin, gamma 1	1.54	2.02	1.67
	447763 430223	BE619911 NM_002514	Hs.115803 Hs.235935	hypothetical protein nephroblastoma overexpressed gene	1.54 1.54	2.52 1.54	1.52 · 3.03
30	448258	BE386983	Hs.343214	hypothetical protein FLJ20396	1.54	1.97	1.53
	440165	AW014718	Hs.7753	calumenin	1.54	1.53	2.55
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.54	1.34	1.69
	445982 419741	BE410233 NM_007019	Hs.13501 Hs.93002	pescadillo (zebrafish) homolog 1, contai ubiquitin carrier protein E2-C	1.54 1.54	2.21 2.50	1.54 1.94
35	416926	H03109	Hs.263395	HT018 protein	1.54	1.41	2.01
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.54	1.89	1.23
	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.54	1.93	1.79
	420421 406973	AF281133 M34996	Hs.343589 Hs.198253	exosome component Rrp41 major histocompatibility complex, class	1.53 1.53	2.47 1.62	1.61 1.19
40	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.53	1.74	1.37
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	1.53	2.49	1.59
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.53	2.72	1.54
	429837 412939	NM_003896 AW411491	Hs.225939 Hs.75069	sialytransferase 9 (CMP-NeuAc:lactosylc eukaryotic translation elongation factor	1.53 1.52	1.64 1.98	2.40 0.98
45	410678	BE540516	Hs.293732	hypothetical protein MGC3195	1.52	1.39	2.17
	431186	NM_012249	Hs.250697	ras-like protein	1.52	1.91	1.82
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.52	1.57	1.82
	422532 413063	AL008726 AL035737	Hs.118126 Hs.75184	protective protein for beta-galactosidas chitinase 3-like 1 (cartilage glycoprote	1.51 1.51	2.08 1.50	1.19 0.67
50	417308	H60720	Hs.81892	KIAA0101 gene product	1.51	1.42	7.41
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	1.51	2.75	1.51
	405204			NM_002086*:Homo sapiens growth factor re	1.51	1.44	1.53
	424481 422516	R19453 BE258862	Hs.1787 Hs.117950	proteolipid protein 1 (Pelizaeus-Merzbac multifunctional polypeptide similar to S	1.51 1.50	1.92 1.61	2.32 1.47
55	418827	BE327311	Hs.47166	HT021	1.50	1.35	3.53
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	1.50	1.55	2.09
	432992	BE270472	Hs.279900	HSPC015 protein	1.50	1.82	0.82
	442432 413566	BE093589 AW604451	Hs.38178 Hs.285814	hypothetical protein FLJ23468 sprouty (Drosophila) homolog 4	1.50 1.50	1.34 3.05	4.87 1.51
60	422615	8E300330	Hs.118725	selenophosphale synthetase 2	1.50	1.35	0.46
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	1.50	2.05	1.78
	421861	\$78798	Hs.108966	phosphatidylinositol-4-phosphate 5-kinas	1.49	1.52	2.62
	422684 452363	BE561617 Al582743	Hs.119192 Hs.94953	H2A histone famity, member Z Homo sapiens, Similar to complement comp	1,49 1,49	1.53 2.02	2.02 1.41
65	411825	AK000334	115,54555	hypothetical protein FLJ20327	1.49	2.55	1.38
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (he-	1.49	1.77	1.49
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.49	1.79	1.75
	427080 440676	AW068287 NM_004987	Hs.301175 Hs.112378	ras-related C3 botulinum toxin substrate LIM and senescent cell antigen-like doma	1.49 1.49	1.57 1.42	2.14 1.46
70	411296	BE207307	Hs.10114	growth suppressor 1	1.49	1.74	1.50
	442894	W02112	Hs.8836	parvin, beta	1.49	2.25	1.51
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	1.49	2.06	1.89
	424162 447131	AA336229 NM_004585	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S retinoic acid receptor responder (tazaro	1.49 1.49	1.59 2.00	1.65 1.22
75	427759		Hs.17466 Hs.2200	perforin 1 (pore forming protein)	1.49	2.12	1.41
. •	422846		Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.49	1.61	1.67
	417007	AF224741	Hs.80768	chloride channel 7	1.48	1.94	1.71
	421924		Hs.109606	coronin, actin-binding protein, 1A	1.48	1.68	1.67
80	422241 410741	Y00062 Z11695	Hs.170121 Hs.324473	protein tyrosine phosphatase, receptor t mitogen-activated protein kinase 1	1.48 1.48	1.43 1.37	2.25 3.17
-	447471		Hs.18676	sprouty (Drosophila) homolog 2	1.48	1.35	1.46
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.47	1.58	1.48
	442945	AI024849	Hs.131853	ESTs	1.47	1.73	1.38

	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.47	1.89	1.60
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	1.47	2.03	1.47
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.47	1.86	1.93
5	416350 458207	AF188625 T28472	Hs.189507 Hs.7655	phospholipase A2, group IID	1,47 1,47	2.92 1.61	1.49 1.73
,	447940	D86982	Hs.20060	U2 small nuclear ribonucleoprotein auxil KIAA0229 protein	1.47	1.93	1.72
	445106	AA377165	Hs.44833	ESTs	1,47	1.56	1.63
	425811	ALD39104	Hs.159557	karyopherin atpha 2 (RAG cohort 1, impor	1.47	1.78	1.84
10	432615	AA557191	Hs.55028	ESTs. Wealdy similar to 154374 gene NF2	1.47	2.04	1.47
10	435099 402294	AC004770	Hs.4756	flap structure-specific endonuclease 1 Target Exon	1.47 1.47	1.76 1.27	1.83 1.46
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	1.46	2.00	1.59
	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	1.46	1.58	2.15
1.5	400270			NM_000026":Homo sapiens adenylosuccinata	1.46	1.42	2.32
15	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.46	2.07	1.40
	419625 430594	U91616 AK000790	Hs.182885 Hs.246885	nuclear factor of kappa light polypeptid hypothetical protein FLJ20783	1.45 1.45	1.78 1.31	1.53 0.90
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.45	213	1.46
	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	1.45	200	1.39
20	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	1.45	1.37	3.17
	411619	AI418609	Hs.71040	hypothetical protein FLJ20425	1.45	1.39	3.01
	424218 450395	AF031824 BE048545	Hs.143212 Hs.161757	cystatin F (leukocystatin) ESTs	1.45 1.45	1.82 2.40	1.44 1.33
	438555	Al222089	Hs.143878	Horno sapiens mRNA for FLJ00024 protein,	1,45	1.91	1.65
25	422497	D29642	Hs.1528	KIAA0053 gene product	1.45	1.94	1.49
	400991			Target Exon	1.45	2.10	1.42
	431779 424618	AW971178 L29472	Hs.268571	apolipoprotein C-I major histocompatibility complex, class	1.45 1.44	1.53 1.96	0.42 1.86
	423032	A1684746	Hs.1802 Hs.119274	RAS p21 protein activator (GTPase activa	1,44	1.34	. 3.36
30	424232	AB015982	Hs.143460	protein kinase C, nu	1.44	1.28	2.94
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	1.44	1.63	1.45
	445745	AB007924	Hs.13245	KIAA0455 gene product	1.44	1.17	1.52
	449209 410129	BE616830 BE244074	Hs.294145 Hs.58831	ESTs	1.44 1.44	1.35 2.10	2.48 1.79
35	401284	00244074	ns.30031	regulator of Fas-induced apoptosis Target Exxon	1.44	1.71	1,44
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.44	1.68	1.45
	433020	Al375726	Hs.279918	hypothetical protein	1.44	1.37	2.02
	420042	AW015140	Hs.161723	ESTs	1.44	2.02	1.29
40	453878 427268	AW964440 X78520	Hs.19025 Hs.174139	DC32 chloride channel 3	1.44 1.44	1.69 1.45	1.44 1.96
40	417386	AL037228	Hs.82043	D123 gene product	1.43	1.32	2.81
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	1.43	1.80	1.17
	411009	W37572	Hs.285864	ESTs	1.43	1.57	1.72
45	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.43	1.36	1.49
7.7	416084 407826	L16991 AA128423	Hs.79006 Hs.40300	deoxythymidytate kinase (thymidytate kin calpain 3, (p94)	1.43 1.43	2.15 1.61	1.57 1.69
	439070	AI733278	Hs.7621	ESTs	1,43	2.10	1.40
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.43	2.09	1.24
50	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	2.13	1.54
30	442591 451668	AW292797 Z43948	Hs.326444	hypothetical protein MGC10772	1.43 1.43	2.11 1.49	1.61 1.16
	423639	AB037826	Hs.130411	cartilage acidic protein 1 KIAA1405 protein	1.42	2.08	1.51
	426234	BE314534	Hs.168159	apoptosis regulator	1.42	1.57	1.31
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.42	1,88	1.63
55	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	1.42	1.46	3.18
	447126 432241	AW150632 AI937060	Hs.170307 Hs.6298	Ral guanine nucleotide exchange factor R KIAA1151 protein	1.42 1.42	1.36 1.58	1.38 1.98
	412471	M63193	Hs.73946	endotheliat cell growth factor 1 (plate)	1,41	2.09	1.29
	434262	AF121858	Hs.12169	sorting nexin 8	1.41	3.07	1,41
60	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKF2p434K1815 (f	1.41	1.82	1.43
	402474 419897	X90826	Hs.93649	NM_004079:Homo sapiens cathepsin S (CTSS	1.41 1.41	1.32	1.24
	417621	AV654694	Hs.82316	upstream transcription factor 2, c-los i interferon-induced, hepatitis C-associat	1.41	1.69 1.22	1.80 1,74
	424441	X14850	Hs.147097	H2A histone family, member X	1.41	1.74	2.15
65	406663	U24683		immunoglobutin heavy constant mu	1.41	1.51	2.03
	409614	BE297412	Hs.55189	hypothetical protein	1,41	1.54	2.20
	443885 412276	H91806 BE262621	Hs. 15284 Hs. 73798	ESTs macrophage migration inhibitory factor (	1.41 1.40	1.19 1.88	1.41 1.24
	425179	AJ224442	Hs.155020	putative methyltransferase	1.40	1.84	1.47
70	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.40	1.27	2.79
	432403	AA550815	Hs.124840	ESTs	1.40	1.83	1.44
	417389	BE260964	Hs.82045	middine (neurite growth-promoting factor	1.40	1.65	2.51
	422596 435292	AF063611 N20514	Hs.118633 Hs.172965	2-5-oligoadenylate synthetase-like	1.40 1.40	2.57 1 91	1.44 1.43
75	435252	BE041820	Hs.38516	ESTs Homo sapiens, clone MGC:15887, mRNA, com	1.40	1.91 1.57	1.43
	425068	AL048716	Hs.154387	KIAA0103 gene product	1.39	1.27	3.18
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.39	2.26	1.40
	427740	BE242604	Hs.180616	CD36 antigen (collagen type I receptor,	1.39	1.76	0.99
80	403022 416111	AA033813	Hs.79018	C21000178*:gi[7341207]gb]AAF61215.1]AF22 chromatin assembly factor 1, subunit A (	1.39 1.39	1.74 1.72	1.36 1.39
30	410103	AW903666	ns./3010	gb:CM4-NN1032-280300-122-b02 NN1032 Homo	1.39	1.72	1.34
	439180	Al393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.39	1.35	1.79
	414057	A1815559	Hs.75730	signal recognition particle receptor (d	1.39	1.49	1.17

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.39	1.52	1.44
	423984	AF163825	Hs.136713	pre-B tymphocyte gene 3	1.39	3.02	1.52
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN cDNA 9430	1.38	1.81	1.39
-	436856	A1469355	Hs.127310	ESTs	1.38	1.35	0.99
5	437179	AA393508		serologically defined colon cancer antig	1.38	1.26	4.14
	437912	BE278594	Hs.5912	F-box only protein 7	1.38	2.03	1.40
	448664	AIB79317	Hs.334691	splicing factor 3a, subunit 1, 120kD	1.38	1.52	1.38
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	1.38	1.48	1.38
10	432812	A1935412	Hs.50162	ESTs	1.38	1.43	2.18
10	406826	AW\$16005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.38	1.87	1.28
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	1.38	1.46	2.23
	408787	NM_014784	Hs.47822	Rho guanine exchange factor (GEF) 11	1.38	1.98	1.50
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.38	1.29	2.04
16	412926	AI879076	Hs.75061	macrophage myristoylated atanine-rich C	1.38	1.52	2.62
15	418255	AW135405	Hs.37251	ESTs	1.38	1.44	1.75
	419745	AF042001	Hs.93005	stug (chicken homotog), zinc finger prot	1.37	1.51	1.37
	448977	X91809	Hs.22698	regulator of G-protein signalling 19	1.37	1.98	1.45
	422609	Z46023 F11872	Hs.118721	siafidase 1 (lysosomat siafidase)	1.37	1.75	1.31
20	435458 425081		Hs.4892	Homo sapiens clone 24841 mRNA sequence	1.37	1.38	2.80
20	429849	X74794 U33053	Hs.154443	minichromosome maintenance deficient (S.	1.37	1.61	1.62
	407103	AA424881	Hs.2499 Hs.256301	protein kinase C-like 1	1.37 1.37	1.71	1.45
	452923	BE276018	Hs.288940	hypothetical protein MGC13170	1.37	1.62 1.86	1.82
	453941	U39817	Hs.36820	five-span transmembrane protein M83 Bloom syndrome	1.37	1.59	1.37 1.37
25	446755	AW451473	Hs.16134	serine/threonine kinase 10	1.37	1.82	1.48
	439755	AW748482	Hs.77873	87 homotog 3	1.36	2.10	1.35
	447630	Al660149	Hs.44865	lymphoid enhancer-binding factor 1	1.36	1.79	1.67
	413821	AA844126	Hs.55964	ESTs, Wealthy similar to C4HU complement	1.36	1.91	1.39
	445823	AJ478563	Hs.145519	FKSG87 protein	1.36	1.29	0.33
30	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	1.36	1.33	2.01
	402542			Target Exon	1.36	1.66	1.46
	451050	AW937420		ESTs	1.36	2.00	1.36
	444501	AW247624	Hs.11342	ninjurin 1	1.36	1.59	1.14
~~	413291	NM_006278	Hs.75268	sialyttransferase 4C (beta-galactosidase	1.36	2.55	1.42
35	438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.36	1.46	1.32
	428398	A1249368	Hs.98558	ESTs	1.36	1.25	4.95
	439704	AW020018	Hs.293267	ESTs	1.36	1.84	1.48
	428782	X12830	Hs.193400	interleukin 6 receptor	1.36	1.27	0.58
40	437316	A1683454	Hs.46801	GCN5 (general control of amino-acid synt	1.35	2.10	1.29
40	439246	A1498072		membrane-associated tyrosine- and threon	1.35	1.81	1.63
	403409			NM_005929:Homo sapiens antigen p97 (meta	1.35	1.64	1.35
	446342	BE298665	Hs. 14846	Homo sapiens mRNA; cDNA DKF2p564D016 (fr	1.35	1.37	2.33
	437740	AA810265	Hs.122915	EST _S	1.35	1.91	1.35
45	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	1.35	1.53	1.10
73	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.35	1.89	1.57
	457760 439769	AA668123 AA448828	Hs.134170	ESTs	1.35	2.03	1.43
	406824	AW515961	Hs.30596 Hs.84298	Homo sapiens mRNA full length insert cDN	1.35	2.06	1.41
	429852	AB010445	Hs.225948	CD74 antigen (invariant polypeptide of m	1.35 1.35	1.77 1.52	1.27
50	421777	BE562088	Hs.108196	small inducible cytokine subfamily A (Cy HSPC037 protein	1.34	1.65	0.51 1.61
	400328	X87344	113.100130	transporter 2, ATP-binding cassette, sub	1.34	1,77	1.02
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.34	1,77	1.15
	428977	AK001404	Hs.194698	cyclin B2	1.34	1.53	1.82
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.34	1,33	3.45
55	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	1.34	2.11	1.32
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.34	1.27	1.97
	422758	AF152329	Hs.284180	protocadherin gamma subfamily C, 3	1.34	1.61	1.75
	421579	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	1.34	1.75	1.81
<b>60</b>	416374	NM_001154	Hs.300711	annexin AS	1.34	1.68	1.55
60	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.34	1.87	0.81
	424778	AA251048	Hs.153042	lymphocyte antigen 9	1.34	1.94	1.42
	421703	AI936513	Hs.1416	Fc tragment of IgE, low affinity II, rec	1.33	2.19	1.48
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.33	1.96	1.18
65	425923	NM_005026	Hs.162808	phospholnositide-3-kinase, catalytic, de	1.33	1.70	1.60
U.S	418803	U50079	Hs.88556	histone deacetylase 1	1.33	1.28	2.65
	427730	AW250549	Hs.180577	granutin	1.33	2.09	1.35
	441174	BE312775	Hs.294005	Homo sapiens, done IMAGE:3050476, mRNA,	1.33	2.05	1.33
	412738	N34731	Hs.74562 Hs.238954	siah binding protein 1; FBP interacting	1.33	1.85	1.35
70	424528 42 <b>259</b> 9	AW073971 BE387202		ESTs, Weakly similar to KIAA1204 protein	1.33	1.31	2.06
, 0	422997	BE018212	Hs.118638 Hs.122908	non-metastatic cells 1, protein (NM23A)	1.33	1.77	1.43
	415323			DNA replication factor	1.33	1.91	1.39
	409119	8E269352 AA531133	Hs.949 Hs.4253	neutrophil cytosofic factor 2 (65kD, chr hypothetical protein MGC2574	1.33 1.33	1.16	0.60
	419652	AL157485	Hs.91973	hypothetical protein	1.33	1.52 2.07	1.34 1.29
75	415697	AI365603	Hs. 198271	OKFZP566I1024 protein	1.32	2.07	1.33
	434359	AF129536	Hs.284226	F-box only protein 6	1.32	2.07	1.39
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	1.32	1.25	1,91
	444029	AW160993	Hs.326292	hypothetical gene DKFZp434A1114	1.32	1.63	1.44
	456974	M12529	Hs.169401	apolipoprotein E	1.32	1.47	0.85
80	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.32	251	1.23
	448610	NM_006157		nel (chicken)-like 1	1.31	3.12	1.31
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.31	1.21	1.65
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	1.31	1,68	1.47
				-			

	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.31	1.30	2.14
	407777	AA161071	Hs.71465	squatene epoxidase	1.31	1.45	1.43 0.90
	408536	AW381532	Hs.135188	ESTs	1.31 1.31	1.38 1.81	1.49
5	410423	AW402432	Hs.63489 Hs.117487	protein tyrosine phosphatase, non-recept gene near HD on 4p16.3 with homology to	1.31	1.63	1.31
3	422486 409154	BE514492 U72882	Hs.50842	interferon-induced protein 35	1.31	1.69	1.29
	425003	AF119046	Hs.154149	apurinic/apyrimidinic endonuclease(APEX	1.31	1.74	1.39
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	1.31	1.43	0.94
• •	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.30	2.53	1.34 1.38
10	417361	NM_000275	Hs.82027	oculoculaneous albinism II (pink-eye dil	1.30 1.30	1.38 2.11	1.36
	425676	AW410656	Hs.159161	Rho GDP dissociation inhibitor (GDI) atp phosphoserine aminotransferase	1.30	2.27	1.48
	427289 427747	AI097346 AW411425	Hs.180655	serine/threonine kinase 12	1.30	1.68	1.79
	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	1.30	1.50	1.30
15	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.30	1.42	2.13
	423062	NM_003655	Hs.5637	ESTs	1.30	1.58	1.30
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.30 1.30	1,77 1.57	1.35 1.51
	409340	BE174629	Hs.321130	hypothetical protein MGC2771 polymerase (RNA) II (DNA directed) polyp	1.30	1.67	1.44
20	416920 430451	AA176455 AA836472	Hs.80475 Hs.297939	cathebain B	1.30	1.49	1.16
20	457400	AF032906	Hs.252549	cathepsin Z	1.30	1.40	1.21
	403506	70 002000		C3001912:gij6677647[ref]NP_033602.1] zin	1.29	1.88	1.26
	424867	AI024860	Hs.153591	Not56 (D. metanogaster)-like protein	1.29	2.64	1.31 1.36
25	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	1.29 1.29	1.79 1.59	1.80
25	416322	8E019494	Hs.79217 Hs.99741	pyrroline-5-carboxytate reductase 1 ESTs, Weakly similar to PNL1_HUMAN PEANU	1.29	2.01	1.43
	440795 421846	AA262133 AA017707	Hs.1432	protein kinase C substrate 80K-H	1.29	1.70	1.34
	425966	NM 001761	Hs.1973	cyclin F	1.29	1.63	1.50
	446766	AF083208	Hs.16178	apoptosis antagonizing transcription fac	1.29	1,71	. 1.40
30	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.29	2.04	1.35 1.94
	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	1.29 1.29	1.41 1.24	1.29
	443086	AW977125 AW138909	Hs.156110	sine oculis homeobox (Drosophila) homolo immunoglobulin kappa constant	1.29	1.99	1.36
	439146 434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	1.29	1.18	1.32
35	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (COK	1.29	1.31	2.19
	400261			Eos Control	1,29	1.59	1.36
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	1.29	1.67	1.53 1.07
	412315	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo	1.28 1.28	1.26 1.85	1.40
40	420372	AW960049	Hs.293660	Homo sapiens, ctone IMAGE:3535476, mRNA, spteen focus forming virus (SFFV) provir	1.28	1.45	1.14
40	425449 454478	X52056 AW805749	Hs.157441	superoxide dismutase 2, mitochondrial	1.28	2.29	1.07
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	1.28	1.20	0.93
	406016			Target Exon	1.28	1.47	1.31
	449609	BE246434	Hs.289026	guanine πucleotide binding protein (G pr	1.28	1.26	3.02
45	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.28 1.28	1.76 1.60	1.23 1.30
	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR five-span transmembrane protein M83	1.28	1.51	1.22
	452700 408543	AI859390 N78098	Hs.288940 Hs.44289	ESTs	1.28	2.02	1.08
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	1.27	1.28	3.51
50	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.27	1.66	1.39
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.27	1.47	1.55
	430794	NM_000166		gap junction protein, beta 2, 26kD (conn	1.27 1.27	1.81 1,35	0.89 1.68
	430637	BE160081	Hs.256290 Hs.78281	S100 calcium-binding protein A11 (calgiz regulator of G-protein signalling 12	1.27	1.67	1.31
55	· 440502 441598	AI824113 AI733219	Hs.58262	ESTs	1,27	1.30	1.30
33	431921	N46466	Hs.58879	ESTs	1.27	2.00	1.15
	459345	AW503672		gb:UI-HF-BN0-ald-h-11-0-UI.r1 NIH_MGC_50	1.26	1.44	1.33
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A45010 X-lin	1.26	1.20	1.45 1.89
4٥	426334		Hs.169358	hypothetical protein	1.26 1.26	1.22 1.48	1.51
60	414044 405268		Hs.75721	profilin 1 ENSP00000223174°:KIAA0783 PROTEIN.	1.26	1.19	2.25
	416602		9 Hs.79389	Protein kinase C-binding protein NELL2	1.26	1.19	4.03
	439529		Hs.293984	hypothetical protein MGC13102	1.26	1.83	1.19
	421254		Hs. 102950	coat protein gamma-cop	1.26	1.61	1.23
65	417785		Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.26	1.84 1.66	0.68 1.34
	419395		Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	1.26	1.42	1.19
	418968			cholesteryl ester transfer protein, plas ESTs	1.26	1.29	1.28
	441553 445619			secreted phosphoprotein 1 (osteopontin,	1.25	1.22	0.65
70	424624		Hs.151301	Ca2+dependent activator protein for secr	1.25	1.17	2.95
. •	450087			MUM2 protein	1.25	1.78	1.28
	42960			hypothetical protein FLJ10989	1.25	1.18	1.25
	42938			secretory carrier membrane protein 3	1.25 1.25	2.22 1.90	1.25 1.39
75	44025			Homo sapiens, ctone IMAGE:3687782, mRNA, hypothetical protein FLJ10116	1.24	1.32	1.53
13	416759 43546			G protein beta subunit-like	1.24	1.96	1.32
	45062			hypothetical protein FLJ11354	1.24	1.61	1.27
	40021			NM_007002:Homo sapiens cell membrane gly	1.24	1.68	1.32
	43501	3 H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.24	1.76	1.25
80	41473		Hs.77171	minichromosome maintenance deficient (S.	1.24	1.82 1.68	1.42
	40685			major histocompatibility complex, class	1.24 1.24	1.73	1.19 1.29
	44849 44008		Hs.7718	ESTs hypothetical protein FLJ22678	1.24	1.70	1.38
	41000		19,7110				

	411355	M76477	Hs.289082	GM2 ganglioside activator protein	1.24	1.61	1.16
	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.24	2.65	1.24
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.24	1.49	1.50
_	427390	A1432163	Hs.268231	Homo sapiens cDNA; FLJ23111 fis, done L	1.24	1.17	2.10
5	429954	AI918130	Hs.21374	ESTs	1.23	1.19	4.77
	421178	BE267994	Hs.102419	zinc finger protein	1.23	1.62	1.28
	442609	AL020996	Hs.8518	setenoprotein N	1.23	2.30	1.24
	416188 410127	BE157260 AA354313	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.23 1.23	1.18	0.90
10	452244	N33530	Hs.58685 Hs.176674	CD5 antigen (p56-62) ESTs	1.23	1.68 2.93	1.23 1.23
10	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	1.23	1.56	1.29
	436939	AA853680	Hs.5345	arginyl aminopeptidase (aminopeptidase B	1.23	1.68	1.23
	414457	AW514320	Hs.76159	ATPase, H transporting, tysosomal (vacuo	1.23	1.58	1.20
	416929	N20535		melastatin 1	1.23	1.92	1.20
15	401106			Target Exon	1.23	1.82	1.29
	408981	AW500797	Hs.49427	Gem-interacting protein	1.23	1.40	1.59
	413317	U53225	Hs.75283	sorting nexin 1	1.23	1.43	1.44
	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.23	1.71	1.24
20	425455	AL137522	Hs.157777	casein kinase 1, gamma 1	1.23	1.95	1.29
20	451524	AK001466	Hs.26516	hypothetical protein FLJ 10604	1.23	2.07	1.27
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	1.22	1.87	1.19
	422034	AC006486	Hs.333069	Els2 repressor factor	1.22	1.55	1.21
	434224 429574	AA380731 BE268321	Hs.84 Hs.208912	interleukin 2 receptor, gamma (severe co	1.22 1.22	1.55	1.51
25	411742	AW247593	Hs.71819	hypothetical protein MGC861 eukaryotic translation initiation factor	1.22	1.49 1.64	1.46 1.40
23	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.22	1.63	1.30
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.22	1.24	0.71
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.22	2.20	1.26
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma	1.21	1.55	. 1.21
30	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	1.21	1.13	3.29
	404186			NM_019602:Homo sapiens butyrophilin-like	1.21	1.59	1.21
	447604	AW089933	Hs.301342	hypothetical protein MGC4342	1.21	1.25	2.00
	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	1.21	1.14	1.25
35	414509	AW161311	Hs.76294	CD63 antigen (metanoma 1 antigen)	1.21	1.39	1.25
رد	428468	AA171388	Hs.184482	DKFZP586D0624 protein	1.21	1.66	1.22
-	419700 430948	AF084935	Hs.92357	galactokinase 1	1.21	1.63	0.74
	448143	AI347578 AF039704	Hs.124015 Hs.20478	hypothetical protein MGC2605	1.21 1.20	1.48 1.75	1.21 1.23
	448499	BE613280	Hs.77550	ceroid-lipofuscinosis, neuronal 2, late hypothetical protein MGC1780	1.20	1.75	1.23
40	442173	N76101	Hs.8127	KIAA0144 gene product	1.20	1.54	1.31
. •	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	1.20	1.18	1.11
	448230	BE395949	Hs.94814	hypothetical protein MGC2865	1.20	1.83	1.19
	403817			NM_015271:Homo sapiens tripartite motif-	1.20	1.22	1.61
	411678	AI907114	Hs.71465	squatene epoxidase	1.20	1.15	2.01
45	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.20	1.79	1.20
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.20	2.34	1.20
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.20	1.93	1.20
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	1.20	1.32	1.52
50	446159	NM_013379	Hs.14089	dipeptidyl peptidase 7	1.19	1.64	1.22
50	434563 421541	AW083994	Hs.9469	pleckstrin homology domain-containing, f	1.19	1.53	1.45
	450706	NM_003942 AW167578	Hs.105584 Hs.14691	ribosomal protein S6 kinase, 90kD, polyp ESTs, Moderately similar to 138022 hypot	1.19	1.75	1.27 1.22
	430381	NM_006411	Hs.240534	1-acytglycerol-3-phosphate O-acytranste	1.19 1.19	1.71 1.66	1.22
	426329	AL389951	Hs.271623	nucleoporin 50kD	1.19	1.17	1.55
55	421612	AF161254	Hs. 106196	BD6 antigen	1.19	1.73	1.30
	410182	NM_001983	Hs.59544	excision repair cross-complementing rode	1.19	1.75	1.18
	434171	BE247688	Hs.347349	KIAA0948 protein	1.18	1.73	1.09
	424837	BE276113	Hs.333034	N-acetyltransferase, homolog of S. cerev	1.18	2.13	1.22
<b>C</b> O	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.18	1.45	1.30
60	453754	AW972580	Hs.172753	ESTs	1.18	1,71	1.35
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	1.18	1.60	1.23
	422256	M64673	Hs.1499	heat shock transcription factor 1	1.18	1,51	1.28
	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.18	1.89	1.18
65	430513 427283	AJ012008 AL119796	Hs.241586	G6C protein	1.18	2.07	0.81
UJ	441648	H05734	Hs.174185 Hs.30559	ectonucleofide pyrophosphatase/phosphodi ESTs	1.18 1.18	1.13 1.56	3.25 1.23
	418219	AA731836	Hs.137319	ESTs	1.18	1.77	1.23
	406422	741101000	16.151515	Target Exon	1.18	1.43	1.31
	414823	AA156531	Hs.103902	ESTs, Weakly similar to A44861 keratin.	1.18	1.66	1.23
70	425720	AA352394	Hs.293984	hypothetical protein MGC13102	1.18	1.58	1.15
_	419250	AW770185		U5 snRNP-specific protein, 116 kD	1.17	1.74	1.21
	454390	AB020713	Hs.56966	KJAA0906 protein	1,17	1.33	1.35
	428471	X57348	Hs.184510	stratifin	1.17	1.19	1.24
75	430200	BE613337	Hs.234896	geminin	1,17	1.13	1.96
75	412965	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	1,17	1.50	1.22
	430122	NM_013342		TCF3 (E2A) fusion partner (in childhood	1,17	1.69	1.32
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.17	1.12	2.44
	417080	BE392846	Hs.1063	small nuclear ribonucleoprotein polypept	1.17	1.93	1.18
80	423102	AW067812	Hs.303025	chromosome 11 open reading frame 24	1,17	1.89	1.17
ou	408393	AW015318 AA338432	Hs.23165	ESTs	1.16	1.10	1.91
	424292 446759	R61463	He tetes	gb:EST43554 Fetal brain I Homo sapiens c	1,16 1,16	1.61 1.45	1.21 1.23
	427324	AA159587	Hs.16165 Hs.285932	expressed in activated T/LAK lymphocytes hypothetical protein FLJ23322	1.16	1.43	1.23
	721024		*13.200332	yponicinos protein r se coece	1.19		1.40

	446055	AI815981	Hs.12909	mucolipin 1	1.16	1.49	1.10
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequen	1.16	1.67	1.20
	417900	BE250127	Hs.82906	COC20 (cell division cycle 20, S. cerevi	1.16	1.66	1.32
5	411305 438930	BE241596 AW843533	Hs.69547 Hs.343261	myelin basic protein	1.16 1.18	1.15 1.37	4.29 1.34
,	407239	AA076350	Hs.67846	hypothetical protein AL110115 teukocyte immunoglobulin-like receptor,	1.15	1.82	1.17
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU proteoglyca	1.15	1.46	1.32
	402160			Target Exon	1.14	1.23	1.12
10	416881	N32520	Hs_141358	ESTs	1.14	2.42	1.14
10	420223	N27807		ribosomal protein L4	1.14	1.23	1.14
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.14	1.38	1.27
	429538 428342	BE 182592 AI739168	Hs.139322	small proline-rich protein 2A	1.14 1.13	1.16 1.13	3.52 1.13
	436696	AA725678	Hs.120487	Homo sapiens cDNA FLJ13458 fis, clone PL ESTs	1.13	1.22	1.13
15	448950	AF288687	Hs.9275	CGI-152 protein	1.12	1.52	1.19
	437696	283844	Hs.5790	hypothetical protein dJ37E16.5	1.12	1.31	1.08
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	1.12	1.08	1.20
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.12	2.9	1.12
20	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	1.12	1.11	3.43
20	408116 450296	AA251393 AL041949	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	1,12	1.50	1.12
	420697	ALU41949 AAB27705	Hs.24756 Hs.26605	hepatocyte growth factor-regulated tyros ESTs	1.11 1.11	1.48 2.19	1.12 1.11
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1,11	2.73	1.11
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1,10	1.43	1,14
25	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.10	1.35	1.19
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	1.10	1.43	1.10
	408801	AI866590	Hs.63405	Homo sapiens, done IMAGE:3609337, mRNA,	1.10	1.53	1.14
	402622	AU 001040	44-4400	C1003392":gi]12314272 emb CAC00591.1] (A	1.10	1.59	1.06
30	418661 442680	NM_001949 BE270707	Hs.1189 Hs.8583	E2F transcription factor 3 similar to APOBEC1	1.09 1.09	1.82 1.49	1.09 1.24
50	439702	AW085525	Hs.55964	ESTs	1.09	1.68	1.09
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp43480650 (f	1.09	1.10	1.73
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.09	1.23	1.25
25	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	1.09	1.07	1.23
35	401558			ENSP00000220478*:SECRETOGRANIN III.	1.08	1.54	1.08
	428411	AW291464	Hs.10338	ESTs	1.08	1.07	6.19
	422051 414694	AW327546 NM_015362	Hs.111024 Hs.76907	solute carrier family 25 (mitochondrial HSPC002 protein	1.08 1.08	1.25	0.93
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.07	1.18 1.15	1.12 1.31
40	420856	BE513294	Hs.205736	HLA class II region expressed gene KE2	1.06	1.47	1.08
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.06	1.17	1.22
	429259	AA420450	Hs.292911	Plakophilin	1.06	1.08	0.73
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.05	1.04	0.84
45	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase 8	1.05	1.09	1.37
40	444438 407394	N32755 AF005081	Hs.322489	ESTs	1.04	1.13	1.05
	404960	AF 00300 I		gb:Homo sapiens skin-specific protein (x eyes absent (Drosophila) homolog 3	1.04 1.04	1.22 1.06	0.78 1.04
	408972	AL050100	Hs.49378	DKFZP586D0919 protein	1.04	1.09	1.13
	414477	U41635	Hs.76228	amplified in osteosarcoma	1.03	1.11	1.03
50	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.03	1.02	2.33
	435056	AW023337	Hs.5422	glycoprotein M6B	1.03	1.02	3.56
	415314	N88802	Hs.5422	glycoprotein M6B	1.02	1.02	4.02
	408591 401203	AF015224	Hs.46452	mammaglobin 1	1.00 1.00	1.41	0.05
55	400304	AF005082	Hs. 113261	Target Exon Homo sapiens skin-specific protein (xp33	1.00	1.02 1.49	0.98 0.56
	407395	AF005082	113.110201	gb:Homo sapiens skin-specific protein (x	1.00	1.69	0.91
	411388	X72925	Hs.69752	desmocollin t	1.00	3.12	1.00
	428618	AA885360		Target CAT	1.00	1.77	1.00
60	402860			ENSP0000239210:DJ50O24.4 (novel protein	1.00	1.53	1.00
OU	437211	AA382207	Hs.5509 Hs.22972	ecotropic viral integration site 2B	1.00	1.39	1.00
	409269 409190	AA576953 AU076536	Hs.50984	steroid 5 alpha-reductase 2-like; H5AR g sarcoma amplified sequence	1.00 1.00	1.46 0.60	1.00 1.00
	416143	Ai955650	113.30304	glutaminyl-peptide cyclotransferase (glu	1.00	1.96	1.00
	401588			C15000180*:gij544344 sp Q05859 FOR4_MOUS	1.00	2.04	1.00
65	419519	A1198719	Hs.176376	ESTs	1.00	1.91	1.00
	448816	AB033052	Hs.22151	KIAA1226 protein C	1.00	1.82	1.00
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	1.00	1.15	1.00
	418618	D66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.00	1.66	0.74
70	422836 452461	AL037365 N78223	Hs.194093 Hs.108106	AKAP-binding sperm protein ropporin transcription factor	1.00	2.21	1.00
, 0	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	1.00 1.00	1.61 1.42	1.00 1.00
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	1.00	1.81	1.00
	429477	AI275514	Hs.6658	ESTs	1.00	1.67	1.00
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	1.00	1.05	1.00
75	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	1.00	1.79	1.00
	451993	AA765776	Hs.122983	ESTs	1.00	2.15	1.00
	416947 441606	N23282 R37263	Hs.184341 Hs.21065	ESTs, Weakly similar to 834087 hypotheti ESTs, Moderately similar to PC4259 (erri	1.00	1.67	1.00
	442590	AI002686	Hs.130313	ESTs Moderately summar to PCA259 term ESTs	1.00 1.00	1.87 2.59	1.00 1.00
80	404831			C1002937*:gij7499208 pirljT20993 hypothe	1.00	1.44	1.00
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	1.00	1.47	1.00
	419717	H07970	Hs.92458	G protein-coupled receptor 19	1.00	1.78	1.00.
	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	1.00	1.64	1.00

	421666	AL035250	Hs.1408	endothelin 3	1.00	0.63	1.00	
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	1.00	1.60	1.00	
	423899	NM_001427	Hs.134989	engraited homolog 2	1.00	2.91	1.00	
_	423130	AW897586	Hs.21213	ESTs	1.00	1.65	1.00	
5	433843	AW021423	Hs.112819	ESTs	1.00	2.08	1.00	
	458574	AW384436	Hs.135265	Homo sapiens clone FLB8436 PRO2277 mRNA,	1.00	1.00	1.00	
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.00	1.41	1.00	
	427335	AA448542	Hs.251677	G antigen 7B	1.00	1.15	1.00	
	439951	Al347067	Hs.124636	ESTs	1.00	1.80	1.00	
10	420248	Al377191	Hs.44714	ESTs	1.00	2.15	1.00	
	446259	AA425204	Hs.334721	hypothetical protein FLJ13391	1.00	2.35	1.00	
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	1.00	1.53	1.00	
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.73	1.00	
	408758	NM_003686	Hs.47504	exonuclease 1	1.00	1.59	1.00	
15	453745	AA952989	Hs.63908	hypothetical protein MGC14726	1.00	1.73	1.00	
	436609	AI022514	Hs.131380	ESTs	1.00	1.96	1.00	
	419308	N40321		gb:yx80g07.r1 Soares melanocyte 2NbHM Ho	1.00	2.28	1.00	
	421650	AA781795	Hs.122587	ESTs	1.00	1.74	1.00	
	459578	AW612538	Hs.304491	EST	1.00	2.16	1.00	
20	446152	AI292036		ESTs	1.00	1.66	1.00	
	449579	AW207260	Hs.134014	ESTs, Wealthy similar to T46425 hypotheti	1.00	2.04	1.00	
	418573	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog (	1.00	1.75	1.00	
	415004	AA158925	Hs.240849	ESTs, Weakly similar to GBP1_HUMAN INTER	1.00	1.85	1.00	
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	1.00	1.92	1.00	
25	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	1.00	1.72	1.00	
	417791	AW965339	Hs.44269	ESTs	1.00	1.52	1.00	
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	2.02	1.00	
	416445	AL043004	Hs.79337	KIAA0135 protein	1.00	1.28	1.00	
	408375	A1224520	Hs.40930	ESTs	1.00	1.92	. 1.00	
30	406964	M21305		FGENES predicted novel secreted protein	1.00	0.46	1.00	
	408522	AI541214	Hs.46320	Small protine-rich protein SPRK (human,	1.00	1.00	2.48	
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	0.98	0.98	3.24	
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	0.95	0.96	3.06	
	446488	AB037782	Hs.15119	KIAA1361 protein	0.94	0.96	1.61	
35	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	0.94	0.94	0.76	
	409402	AF208234	Hs.695	cystatin B (stefin B)	0.93	0.91	1.55	
	423942	AF209704	Hs.169407	glycolipid transfer protein	0.92	0.93	2.09	
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	0.91	0.91	4.08	
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	0.90	0.81	0.73	
40	417632	R20855	Hs.5422	glycoprotein M6B	0.90	0.92	3.89	
	449092	U91641		alpha 2,8-sialyltransferase	0.89	0.79	0.84	
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	0.89	0.92	3.70	
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 28 (p1	0.88	0.90	2.02	
	408349	BE546947	Hs.44276	homeo box C10	0.88	0.87	0.73	
45	429345	R11141	Hs.199695	hypothetical protein	0.85	0.84	0.69	
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	0.84	0.85	1.32	
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	0.84	0.88	3.37	
	405885			Target Exon	0.81	0.71	1.00	
	407788	BE514982	Hs.38991	S100 catcium-binding protein A2	0.78	0.78	0.90	
50	417515	L24203	Hs.B2237	ataxia-telangiectasia group D-associated	0.77	0.73	0.71	,
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	0.75	0.78	4.69	
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.74	0.78	5.42	
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	0.70	0.75	4.29	
	412719	AW016610	Hs.816	ESTs	0.70	0.77	3.99	
55	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	0.69	0.73	3.79	
	437191	NM_006846		serine protease inhibitor, Kazal type, 5	0.65	0.64	1.11 3.20	
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	0.61	0.65	0.49	
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	0.61	0.22		
	439659			Homo sapiens cDNA FLJ14471 fis, clone MA	0.49	0.30	0.67 0.34	
60	419092		Hs.89603	mucin 1, transmembrane	0.41	0.11 0.30	0.35	
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	0.23	0.30	0.33	
							•	
	TABLE							
	Pkey:		ique Eos probeset					
65	CAT nu	mber: Ge	ene cluster number	` <u>.</u>				
	Access	ion: Ge	enbank accession r	numbers				
	Pkey	CAT Numb	er Accession	012195 NM_007126 AF100752 AL137377 Z70768 BM474	OCC DOTE 400C ALL	24226 0026	7202 00764420	PC775028 PC824418
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70			BM045810 AL	J120387 BG770238 BG886740 BG913323 B1739300 BG31 196861 BE856897 AA463876 AI375927 AA648810 AA948	102 A 440004E A44E	2001010 DE3	PIA RONONCIA DI	1843 A1131029 AW768399
			AI770171 BF1	196861 BE856897 AA463876 AI375927 AA648810 AA948 1337984 AW026150 BE466591 BE674599 AI818438 AA77:	193 AA49U910 AI43	3033 M43010	07E DC810097	MASS76A RE903567
			Al365196 AW	/337984 AW026150 BE466591 BE674599 AI618438 AA77 A043200 BE900263 BE900706 BE731097 BE390023 BG8	5131 WIDD 1351 WAA	100002001130	023 BGB 13003 1	5 RES01807 RE903610
			BE732715 BA	/043200 BE900263 BE900706 BE731097 BE390023 BG6 E560537 BE903782 BE732947 BI227204 BG761305 BE26	12304 DE30400 DE	. 200230 DIM	0350 DIEA7001	BIASONOO RE391391 RE259420
7.5			BE561530 BE	560537 BE903702 BE732947 BI227204 BG761305 BE20 N245422 A1423847 A1914618 H80534 BE301004 AL53179	2042 BEJ31040 BE	12 41 577202	AA 272266 DE7	46065 DE743630 RER79296
75			BE298109 AV	NZ45422 A1423847 A1914618 H80534 BE301004 AL53179 ID18598 A1689260 AW072450 F20201 AW151405 AW5175	11 AI433361 BF/331	12 AL3//303	163 00631530 001	1421728 BC767231 RM462953
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00			F13645 R413	194 AK025758 BG180977 BE349455 AA812018 AA740241 809493 AA481029 AA825718 A1347866 A1431670 AA8144	1 7002/122 AI 10030	U WWGGGJ32 /	AA724503 AID1	1399 AI537550 AA491103
80			AJ243844 AA	809493 AA481029 AA825718 AI347866 AI431670 AA8149 D7703 AA989120 AA746235 AW028983 AA789102 AU185	NO MIZO I IUS RUI / ( C761 AWAS 1466 AA	¥80€8+ ¥1¥40. ₩ ₩₩ 100000	21893 SWA1200	6 RE077936 BI860809
			AW008188 R	UTTUS MASSSTAU ARTADASS AVUZSSSS ARTOSTUZ AUTS DZJESE I DEGESOLS DIJJEJESE ALIESASOJ DEGISJOS USOL	,, ,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	-12-200 I M143		
				G746251 BE962912 BM454584 AL134894 BF104082 H80			•	
	43131	7 997174_1	AW970601 A	W613399 AA503435 AA502682 N91138				
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55		<b>-</b>	AA628934 AA659498 AA699617 H14450 H21758 H39576 AA095608 A1049973 BG054505 BG319545 A1742408 AA421324 A1580138 A1375883 A1374848 A1387857 A1374782 A1344678 AA017357 BF477168 A1373751 AA779885 A1801494 BE349021 A1220937 AW338397 AA253409 AA418327
22			AAR72682 AI572030 AI521517 AI572944 AI418670 AI266089 W72413 W76492 AI809207 AI915747 HZZZ3U HZ1951 HUX513 HZ5154
	416929 419250	14596_3 249447_1	BC017849 BC005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 BG755078 B1226909 N41827 AW404060 B1068921 H11253 AA461274 R05714 H00515 B1086965 A1032786 B1089613 BM171783 A1127382 A1660953
60			AW296271 A1592209 AA46995 A1376115 A1016900 BG055846 A1023644 AA767046 AA815039 AW403510 A1868663 AA815462 AA235654 AW292253 AW959582 AV725205 AW959578 AA300091 W24933 R05715 AW770185 H00465 N93714 H11254 T49555
UU	424292		AW966308 AA339512 AA338432
	420223 428342		AVOSC315 AID15524 AA724D79 RI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094
65	120		BF446026 AW118719 Al332765 AW500888 AW576556 AI859571 AW499564 AW614573 AW629495 AW505314 W74704 Al356361 Al923640
05			AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 155263
	407394	27110_2	BI002756 AA489664 BF827261 W74741 BF963166 AF005081 BG193848
70	428618		BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R85003 BG623286 H15003 BI562131 BG433772
70	416143	40539_2	0.0349900 AV706374 M3A469 AL 539369 R.C.186630 R.C.188697 R.C.181930 ALZDOAAD R.C.033721 BF968528 BF792647 AW2U4bbb AA922311 FU2/33
			AW342041 BG217293 BE619664 BE465887 AA745605 AI278924 AI278545 AI280994 AA809678 AA282134 T08599 AA732436 T05478 F04402 AA262267 AI989523 N25559 AI760218 BG217318 BF893160
75	419308		1 N40321 AA236322 AA236215
75	446152 449092		AK056270 AV706896 Al692935 Al681140 AW162481 AW087114 AW157019 Al689795 AW251085 AW206911 BF 438207 AW134945 BE041668
			BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AU929731 AW161524 R43753 BE779688
οΛ	TABLE	49C:	I being a who agreement in to m the emberal
80	Pkey: Ref:		Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:		sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. Indicates DNA strand from which exons were predicted.
	Juanu.		

	Nt_position:	: India	ates nucleotide	positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position				
_	402075	8117407	Ptus	121907-122035,122804-122921,124019-12416				
5	405451	7622517	Minus	145949-146227				
	401747	9789572	Minus	118596-118816,119119-119244,119609-11976				
	401454	9186923	Minus	114659-114832				
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182				
10	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941				
10	403328	8469085	Minus	120428-120703				
	405547 403532	1054740 8076842	Plus Minus	124351-124520,124914-125050 81750-81901				
	400750	8119067	Plus	198991-199168,199316-199548				
	405506	6466489	Plus	80014-80401,80593-81125				
15	400533	6981826	Minus	277132-277595				
	405779	7280331	Minus	33048-33856				
	402994	2996643	Minus	4727-4969				
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423				
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519				
20	403969	8569909	Plus	31237-31375,32405-32506				
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287				
	401797	6730720	Plus	6973-7118				
	401151	9438288	Plus	30848-31228				
25	404872	9650523	Minus	18540-18718				
23	402876	9864669	Plus	5679-6027,7485-7584				
	405204 402294	7230116 2282012	Plus Minus	126569-126754 2575-3000				
	402254	8096825	Ptus	159197-159320				
	401284	9800819	Minus	101307-101421				
30	402474	7547175	Minus	53526-53628,55755-55920,57530-57757				
-	403022	3132351	Plus	92097-92864				
	402542	9801558	Minus	67076-67594				
	403409	9438598	Plus	6860-7054,12573-12771				
	403506	7596863	Plus	105008-105650				
35	406016	8272661	Ptus	41341-41940				
•	405268	4156151	Minus	24404-24521				
	401106	8568931	Plus	122694-122893				
	404186	4481839	Ptus	829-1110				
40	403817 406422	8962065 9256411	Plus Plus	110297-111052 163003-163311				
40	402160	8516165	Plus	166063-166354				
	402622	9930984	Minus	129861-130099				
	401558	7139678	Plus	103510-104090				
	404960	7408010	Minus	146186-146377,147747-147943				
45	401203	9743387	Minus	172961-173056,173868-173928				
	402860	9588237	Minus	76423-76560				
	401588	7230871	Plus	46412-46561				
	404831	6624702	Minus	16833-17020,20007-20120,21605-21799,2333				
50	405885	7677703	Minus	42574-42998				
50								,
	Table 50	A lists about 3	98 aenes uprea	REGULATED IN PRIMARY MELANOMAS OR MELANO ulated in primary melanoma or melanoma metastases re	ative to benign nevi.	Genes we	re selected from 59	680 probesets on the
	Eos/Affyr	netrix HuO3 G	enechip array.	Gene expression data for each probeset obtained from the	is analysis was expr	essed as a	verage intensity (Al	), a normalized value reflecting the
55	relative k	evel of mRNA						
	Pkey:			set identifier number				
	ExAccn:			ion number, Genbank accession number				
	Unigenel		nigene number					
60	Unigene	Inte: U	nigene gene titl	; primary melanoma and melanoma melastasis Als divide	d by the maximum A	l of henina	nevi	
UU	R1: R2:	71	ous percentile of	primary melanoma and melanoma melastasis Als divide	d by the maximum A	d of benion	nevi. where the 15t	h perceptile of normal tissue Als
	rv.			om both the numerator and denominator	• •, •.•			
	Pkey	ExAcon	UnigenelE	Unigene Title	R	1	R2	
65	422424	AI186431	Hs.29663		13	3.73	16.82	
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11	1.67	11.84	
	407846	AA426202	Ps.40403	Cbp/p300-interacting transactivator, wit		35	7.59	
	444381	BE387335				63	7.90	•
70	417880	BE241595		selectin L (lymphocyte adhesion molecule		21	4.09	
70	424321	W74048	Hs,1765	lymphocyte-specific protein tyrosine kin		.13	6.10	
	447210	AF035269				.79 	6.26	
	417693	AW95974				.55	6.36	
	429500	X78565	Hs.28911			.43 .43	7.11	
75	414812	X72755	Hs.77367	monokine induced by gamma interferon ESTs, Wealdy similar to ALU7_HUMAN ALU		.31	7.51 4.28	
13	451736 418870	AW08035 AF147204				.20	4.32	
	428291	AA534009				.03	4.52	
	417308	H60720	Hs.81892			.01	6.78	
	448569	BE38265				.99	7.51	
80	439310	AF086120				.95	4.79	
	452838	U65011	Hs.30743		5	.95	5.55	
	422241	Y00062	Hs.17012	<ol> <li>protein tyrosine phosphatase, receptor t</li> </ol>		.76	4.82	
	442379	NM_0046	13 Hs.8265	transglutaminase 2 (C polypeptide, prote	5	.76	2.19	

	409274	NM_003930	Hs.52644	SKAP55 homologue	5.0	65	4.63
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.		3.41
	442711	AF151073	Hs.8645	hypothetical protein	5.4		5.79
5	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.		5.56
,	412918	BE563957	15-100000	activated RNA polymerase II transcriptio	5.		4.31
	428125 446921	AA393071	Hs.182579	leucine aminopepiidase	5.		4.83
	431183	AB012113	Hs.16530 Hs.250696	small inducible cytokine subfamily A (Cy	5.		5.13
	414219	NM_006855 W20010	Hs.75823	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic ALL1-fused gene from chromosome 1g		30 16	6.27 5.13
10	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible		05	13.72
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran		ល	4.93
	436701	AW959032		ESTs, Moderately similar to 178885 serin		03	3.42
	406648	AA563730	Hs.277477	major histocompatibility complex, class		99	3.36
	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C		98	5.30
15	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	4.	98	4.85
	432469	AL080084		CGI-100 protein	4.	97	4.46
	404854			Target Exon	4.	85	3.49
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.	82	4.8 )
20	425397	J04088	Hs. 156346	topoisomerase (DNA) II atpha (170kD)		81	5.26
20	408958	T99607	Hs.49346	signal recognition particle 54kD		78	2.34
	453949	AU077146	Hs.36927	heat shock 105kD		78	5.18
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992		77	4.13
	440245 412228	AK001913	Hs.7100	hypothetical protein		74	3.32
25	417834	AW503785 BE172058	Hs.73792 Hs.82689	complement component (3d/Epstein Barr vi tumor rejection antigen (gp96) 1		74 73	1.55 4.25
20	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)		67	4.69
	424571	BE379766	110.13012	polymerase (RNA) II (DNA directed) polyp		62	3.02
	434203	8E262677	Hs.283558	hypothetical protein PRO1855		61	5.45
	452268	NM_003512	Hs.28777	H2A histone family, member L		60	2.68
30	421311	N71848	Hs.2B3609	hypothetical protein PRO2032		60	3.24
-	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence		60	4.34
	425706	AW406678	Hs.122559	hypothetical protein FLJ22570		59	3.58
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	4.	57	3.82
26	406B36	AW514501	Hs.156110	immunoglobulin kappa constant	4.	.57	9.27
35	413441	AI929374	Hs.75367	Src-like-adapter	4	.53	3.60
	431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f		.48	4.89
	418506	AA084248	Hs.85339	G protein-coupled receptor 39		.47	3.72
	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN		.47	3.96
40	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),		.45	2.40
40	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1		.43	4.27
	448883 417274	BE614989	Hs.7503	hypothetical protein FLJ14153		.42	3.91
	419285	N92036 D31887	Hs.81848 Hs.89868	RAD21 (S. pombe) homolog KIAA0062 protein		.41	3.80
	418321	063477	Hs.84087	KIAA0143 protein		.40 .38	3.20 2.79
45	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito		.37	3.86
	428450	NM_014791	Hs.184339	KIAA0175 gene product		.36	4.65
	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito		.36	3.42
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha		.36	3.31
	409598	NM_014018	Hs.55097	mitochondrial ribosomal protein S28		.35	3.10
50	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4	.34	5.61
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4	.33	3.31
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance		.33	3.57
	452322	BE566343	Hs.28988	glutaredoxin (thiotransferase)		.32	2.20
55	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,		.32	3.60
55	449722 408380	BE280074 AF123050	Hs.23960 Hs.44532	cyclin B1		.31	5.79
	427127	AW802282	Hs.22265	diubiquitin pyruvate dehydrogenase phosphalase		.30 .28	3.62 4.18
	417933	X02308	Hs.82962	thymidylate synthetase		.28	5.06
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase		.25	4.15
60	450306	AL080080	Hs.24766	thioredoxin domain-containing		.24	3.15
	440266	AA088809	Hs.19525	hypothetical protein FLJ22794		.23	3.65
	407951	W77762	Hs.79015	antigen identified by monoctonal antibod		.22	4.21
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	4	.20	4.11
65	408989	AW361666	Hs.49500	KIAA0746 protein	4	1.20	4.26
65	449626	AA774247	Hs.301637	zinc finger protein 258		1.19	2.65
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, dC		l.18	6.80
	415726	T89844	Hs.78712	aminolevulinate, delta-, synthase 1		1.16	4.28
	444207	A1565004	U= 00004	cathepsin D (lysosomal aspartyl protease		1.16	1.89
70	416980 438718	AA381133 AL040058	Hs.80684	high-mobility group (nonhistone chromoso		1.14	3.32
	437802	AI475995	Hs.6375 Hs.122910	uncharacterized hypothalamus protein HTO		1.14	3.02
	446392	AF142419	Hs.15020	ESTs homolog of mouse quaking QKI (KH domain		l.12 l.12	4,18 3.67
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor		1.12 1.11	3.80
_	427247	AW504221	Hs.174103	integrin, atoha L (antigen CD11A (p180).		1.11 1.11	5.71
75	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob		1.10	4.25
-	450071	AA018283	Hs.24359	Homo sapiens cONA FLJ11174 fis, clone PL		1.10	2.91
	452882	AW972990	Hs.196270	folate transporter/carrier		4.10	4.25
	414522	AW518944	Hs.76325	Immunoglobulin J chain		1.09	3.99
00	407756	AA116021	Hs.38260	ubiquitin specific protease 18		1.09	4.60
80	405506			Target Exon		4.08	3.64
	444677	AL110212	Hs.301005	purine-rich element binding protein B		4.07	2.43
	417497	AW402482	Hs.82212	CD53 antigen		4.07	6.55
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	•	4.06	3.27

	421508	NM_004833	Hs.105115	absent in melanoma 2	4.05	4.39
	408688 439453	A1634522 BE264974	Hs.152925 Hs.6566	KIAA1268 protein	. 4.05 4.04	3.32 3.53
	445701	AF055581	Hs.13131	thyroid hormone receptor interactor 13 lymphocyte adaptor protein	4.02	4.20
5	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	4.01	3.96
	449291	BE176893	Hs.23440	KIAA1105 prolein	4.01	2.34
	443071	AL080021	Hs.8986	complement component 1, q subcomponent.	4.00	6.97
	417615 408246	BE548641 N55669	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.27
10	408246	N00000 AW1634B3	Hs.333823 Hs.48320	mitochondrial ribosomal protein L13 doubte ring-linger protein, Dorlin	3.98 3.98	3.66 3.76
••	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	3.97	2.38
	418942	AI566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	3.97	3.40
	424756	AW504657	Hs.152931	tamin 8 receptor	3.93	2.67
15	421958	AA357185	Hs.109918	ras homolog gene family, member H	3.89	2.39
13	440692 433001	AL031591 AF217513	Hs.7370 Hs.279905	phosphotidylinositol transfer protein, b clone HQ0310 PRO0310p1	3.88 3.88	3.23 4.24
	418255	AW135405	Hs.37251	ESTs	3.87	2.53
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.29
20	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	3.85	3.73
20	416114	Al695549	Hs.183868	glucuronidase, beta	3.85	3.74
	440598 417020	H13032 T78413	Hs.103378	hypothetical protein MGC11034 heterogeneous nuclear ribonucleoprotein	3.84 3.82	1.90 2.04
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	3.81	3.07
~-	446506	Al123118	Hs.15159	chemotine-like factor, alternatively spl	3.81	3.69
25	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.80	6.01
	410668	BE379794	Hs.159651	hypothetical protein	3.80	5.22
	420107 446071	AL043980 N51527	Hs.7886 Hs.13659	pellino (Drosophila) homolog 1 hypothetical protein DKFZp586F2423	3.79 3.79	3.93 2.74
	419731	S47242	Hs.92909	SON DNA binding protein	3.77	1.85
30	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.98
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	7.42
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.76	3.55
	419381 423979	AB023420 AF229181	Hs.90093 Hs.136644	heat shock 70kD protein 4 CS box-containing WD protein	3.76 3.76	3.81
35	402474	A 223101	113.130014	NM_004079:Homo sapiens cathepsin S (CTSS	3.76	3.97 4.01
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.75	3.77
	454080	A1199711	Hs.576	fucosidase, alpha-L- 1, tissue	3.74	6.15
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	3.74	2.92
40	426096 417105	D87436 X60992	Hs.166318 Hs.81226	lipin 2 CDG antigen	3.72 3.72	2.98 2.78
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.72	3.37
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.70	4.09
	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.79
45	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.69	2.94
40	428398 423494	AI249368 AW504365	Hs.98558 Hs.24143	ESTs Winkert Aldrich gundrome austoin interna	3.68	3.82 3.52
	413235	BE243445	Hs.75248	Wiskoti-Aldrich syndrome protein interac topoisomerase (DNA) II beta (180kD)	3.67 3.67	2.79
	423712	W46802	Hs.81988	disabled (Drosophila) hornolog 2 (mitogen	3.66	3.42
50	409703	NM_006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	3.66	6.44
50	447225	R62676	Hs.17820	Rho-associated, coiled-coil containing p	3.65	2.93
	414829 400219	AA321568	Hs.77436	pleckstrin Eos Control	3.65 3.64	2.30 2.76
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	2.73
<i>E E</i>	422445	M23114	Hs.1526	ATPase, Ca transporting, cardiac muscle,	3.62	3.60
55	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 ffs, clone PL	3.62	3.62
	424460 427609	BE275979 AK000436	Hs.296014 Hs.179791	polymerase (RNA) II (DNA directed) polyp	3.62	3.06
	400750	A1400430	113.173731	hypothetical protein FLJ20429 Target Exon	3.62 3.61	2.31 2.74
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	3.61	2.25
60	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.60	4.20
	433867	AK000596	Hs.3618	hippocalcin-like 1	3.59	4.19
	421986 414841	AL137438 H55601	Hs.110454 Hs.77490	SEC15 (S. cerevisiae)-like	3.59 3.58	1.58 1.00
	429693	BE254962	Hs.211612	glutathione S-transferase theta 1 SEC24 (S. cerevisiae) related gene famil	3.57	3.00
65	425204	NM_002436	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.56	3.09
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HE	3.56	3.26
	442043	BE567620	Hs.99210	ESTs	3.55	3.56
	406636 446341	L12064 AL040763	Hs.310735	gb:Homo sapiens (clone WR4.12VL) anti-th ESTs, Moderately similar to ALU7_HUMAN A	3.55 3.54	3.83
70	432485	N90866	Hs.276770	COW52 antigen (CAMPATH-1 antigen)	3.54 3.54	3.52 4.66
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.54	3.25
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fis, clone C	3.54	1.87
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	3.53	3.96
75	425177 426643	AF127577 AA857131	Hs.155017 Hs.171595	nuclear receptor interacting protein 1 HIV TAT specific factor 1	3.53 3.51	3.40
	420137	AA306478	Hs.95327	CO3D antigen, delta polypeptide (TiT3 co	3.51 3.51	2.21 2.51
	429248	U96759	Hs.198307	von Hippel-Lindau binding protein 1	3.51	2.85
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.51	2.71
80	451791	278407 AAR14100	Hs.27023	vesicle transport-related protein	3.49	2.91
50	418310 406858	AA814100 AA505445	Hs.86693 Hs.300597	ESTs immunoglobulin heavy constant gamma 3 (G	3.49 3.48	1.45 6.81
	400200			NM_002788*:Homo sapiers proteasome (pros	3.48	2.51
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.94

				WA 40000	2.47	3.38
	441646		Hs.7935	KIAA0952 protein cathepsin S	3.47 3.45	2.71
	427968 440201	AI857607 AL359588	Hs.181301 Hs.7041	typothetical protein DKFZp7628226	3.45	3.45
	434608	AAB05443	Hs.179909	hypothetical protein FLJ22995	3.44	3.68
5	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.44	6.70 2.72
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenasa	3.44 3.43	2.76
	435550 453857	AJ224456 AL080235	Hs.324507 Hs.35861	H.sapiens polyA site DNA DKFZP586E1621 protein	3.43	3.64
	423392	AA195037	Hs.169341	HTPAP protein	3.43	2.29
10	418460	M26315	Hs.85258	CD8 antigen, atpha polypeptide (p32)	3.43	2.78
	453915	AA588721	Hs.285218	ribosomal protein L44	3.41 3.41	3.06 4.23
	442485	BE092285	Hs.29724 Hs.3066	hypothetical protein FLJ13187 granzyme K (serine protease, granzyme 3;	3.40	3.93
	432606 417410	NM_002104 AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	3.40	2.12
15	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	4.70
	422545	X02761	Hs.287820	fibronectin 1	3.39 3.36	7.58 4.12
	409142	AL136877	Hs.50758 Hs.22265	SMC4 (structural maintenance of chromoso pyruvate dehydrogenase phosphatase	3.34	5.05
	434826 448410	AF155661 AK000227	Hs.21126	hypothetical protein FLJ20220	3.33	4.31
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.33	4.60
	432642	BE297635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	3.32	4.49 4.22
	425234	AW152225	Hs.165909	ESTs, Wealthy similar to 138022 hypotheti complement component 1, q subcomponent.	3.24 3.23	12.31
	443623 426490	AA345519 NM_001621	Hs.9641 Hs.170087	aryl hydrocarbon receptor	3.23	5.07
25	443958	BE241880	Hs.10029	cathepsin C	3.16	4.97
	412577	Z22968	Hs.74076	CD163 antigen	3.14	4.75 4.00
	414050	NM_004766	Hs.75724	coatomer protein complex, subunit beta 2	3.13 3.12	4.45
	421633	AF121B60 AF113676	Hs.106260 Hs.297681	sorting nexin 10 serine (or cysteine) proteinase inhibito	3.11	4.00
30	413936 428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (1	3.10	4.03
50	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.06	4.49
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.04 3.03	4.98 4.49
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxyfic Homo sapiens cDNA: FLJ21482 fis, clone C	3.01	4.75
35	452139 439237	AA099969 AW408158	Hs.16331 Hs.318893	ESTs, Wealthy similar to A47582 B-cell gr	2.95	5.55
	422684	BE561617	Hs.119192	H2A histone family, member Z	2.94	4.64
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.93	10.28 5.40
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3 chloride intracellular channel 4	2.91 2.90	4.86
40	450455 427528	AL117424 AU077143	Hs.25035 Hs.179565	minichromosome maintenance deficient (S.	2.89	4.04
70	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.87	9.61
	423605	AF047826	Hs.129887	cadherin 19, type 2	2.83	4.86
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82 2.60	5.02 4.30
45	419956	AL137939 NM_006762	Hs.40096 Hs.79356	cadherin 19, type 2 Lysosomal-associated multispanning membr	2.79	5.80
40	416511 429732	U20158	Hs.2488	tymphocyte cytosolic protein 2 (SH2 doma	2.78	4.21
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	2.78	4.23
	416784	AA334592	Hs.79914	turnican	2.78 2.77	4.40 4.23
50	427792	M63928 AA219691	Hs.180841 Hs.73625	tumor necrosis factor receptor superfami RAB5 interacting, kinesin-like (rabkines	2.77	4.17
50	412140 427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.76	4.43
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.20
	437179	AA393508		serologically defined colon cancer antig	2.74 2.72	4.07 4.63
55	429402	AF116571	Hs.201671 Hs.103839	SRY (sex determining region Y)-box 13 erythrocyte membrane protein band 4.1-li	2.71	4.93
,,,	421360 409202	AA297012 AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.15
	426124	AJ268389	Hs.250697	phosphatidylinositol glycan, class F	2.68	4.00
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.67 2.65	4.72 7.77
60	417389	BE260964	Hs.82045 Hs.6083	midkine (neurite growth-promoting factor Homo sapiens cDNA: FLJ21028 fis, clone C	2.65	4,47
00	409415 410341	AA579258 AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	5.61
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.63	4.34
	424687	J05070	Hs.151738	matrix metalloproleinase 9 (gelatinase B	2.62 2.60	4.95 6.00
65	409430		Hs.346735 Hs.153053	splicing factor, arginine/serine-rich 5 CD37 antigen	2.60	4.27
03	424779 409354	*******	Hs.159472	Homo sapiens cONA: FLJ22224 fis, clone H	2.60	4.64
	427550		Hs.311609	nuclear RNA helicase, DECD variant of DE	2.57	4.27
	426143			proteasome (prosome, macropain) subunit,	2.56 2.56	4.20 4.13
70	421563			granutysin proteoglycan 1, secretory granule	2.55 2.55	5.46
70	425593 428169		Hs.1908 Hs.182793	golgi phosphoprotein 2	2.54	5.78
	429800			antizyme inhibitor	2.50	5.15
	407241			gb:Human omega light chain protein 14.1	2.50	4.98
75	421739			UDP-Gal:betaGicNAc beta 1,4- galactosyll	2.45 2.45	5.58 7.20
75	412819		Hs.24048	FK506 binding protein precursor Wiskott-Aldrich syndrome protein interac	2.44	4.11
	412025 435523		Hs.24143 Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.67
	445350			tysophospholipase (	2.44	5.44
00	44929	6 AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	2.41 2.41	4.31 4.25
80	44006		Hs.266331	hypothetical protein MGC4595 Eos Control	2.39	5.68
	40022 42265		Hs.250175	homolog of yeast long chain polyunsatura	2.39	6.62
	43162			interteron, atpha-inducible protein (clo	2.38	7.22

	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.21
	415149	X12451	Hs.78056	cathepsin L	2.37	7.71
	435099 427407	AC004770 BE268649	Hs.4756 Hs.177766	flap structure-specific endonuclease 1 ADP-ribosyttransferase (NAD; poly (ADP-r	2.37 2.31	5.68 4.89
5	426432	AF001601	Hs.169857	paraoxonase 2	2.29	4.83
	430555	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fs, clone HE	2.27	5.03
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	2.25	4.14
	412617 447547	AK001364 NM_007229	Hs.808 Hs.18842	heterogeneous nuclear ribonucleoprotein	2.21 2.19	4.31 4.62
10	416232	AW502678	Hs.79090	protein kinase C and casein kinase subst exportin 1 (CRM1, yeast, homolog)	2.18	4.84
- •	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.14	4.22
	411358	R47479	Hs.94761	KIAA 1691 protein	2.13	4.65
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.03
15	406687 417331	M31126 AW411297	Hs.81972	matrix metalloproteinase 11 (stromelysin SHC (Src homology 2 domain-containing) t	2.11 2.11	4.16 4.25
13	450344	AW994032	Hs.8768	hypothetical protein FLJ10849	211	4.09
	429642	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (	2.11	5.42
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	6.42
20	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	2.10	4.00
20	453352 409220	T10446 BE243323	Hs.51233	ESTs furnor necrosis factor receptor superfami	2.09 2.09	4.48 4.98
	414045	NM_002951	Hs.75722	ribophorin ()	2.07	4.59
	422451	AA310753	Hs.42491	ESTs, Wealdy similar to S65657 alpha-1C-	2.07	4.09
25	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.06	5.06
25	452363 438393	AI582743 AA351815	Hs.94953 Hs.50740	Homo sapiens, Similar to complement comp Homo sapiens cDNA: FLJ22272 fis, clone H	2.04 2.03	11.17 4.36
	413313	NM_002047	Hs.283108	glycyl-IRNA synthetase	2.02	4.79
	412994	032257	Hs.75113	general transcription factor IIIA	2.00	4.67
20	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.79
30	421897 442159	AW583693 AW163390	Hs.109253 Hs.278554	N-terminal acetyltransferase complex and	1.98 1.95	4.17 7.53
	429451	BE409861	Hs.202833	heterochromatin-like protein 1 heme oxygenase (decycling) 1	1.95	4.63
	416967	BE616731	Hs.80645	Interferon regulatory factor 1	1.95	4.31
25	400203			Eos Control	1.94	5.03
35	437317	AA748613	Hs.311977	ESTs, Highly similar to SWI/SNF related.	1.94	4.03
	414945 416224	BE076358 NM_002902	Hs.77667 Hs.79088	tymphocyte antigen 6 complex, tocus E reticutocalbin 2, EF-hand calcium bindin	1.93 1.92	4.68 4.12
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	1.91	4.23
40	413945	NM_000591	Hs.75627	CD14 antigen	1.90	5.00
40	413317	U53225	Hs.75283	sorting nexin 1	1.89	4.20
	448719 430838	AA033627 N46664	Hs.21858 Hs.169395	trinucleotide repeat containing 3 hypothetical protein FLJ12015	1.89 1.88	4.26 4.15
	427239	BE270447	113, 103333	ubiquitin carrier protein	1.87	5.72
4.5	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.87	5.81
45	433671	AW138797	Hs.132906	19A24 protein	1.85	4.27
	413190 414915	AA151802 NM_002462	Hs.40368 Hs.76391	adaptor-related protein complex 1, sigma	1.85 1.85	5.19 4.31
	430040	AW503115	Hs.227823	myxovirus (influenza) resistance 1, homo pM5 protein	1.83	5.57
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.82	4.29
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.39
	414416 428977	AW409985 AK001404	Hs.76084	hypothetical protein MGC2721	1.80	4.20
	418707	U97502	Hs.194698 Hs.87497	cyclin B2 butyrophilin, subfamily 3, member A2	1,79 1,78	4.17 4.30
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.78	5.44
55	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.77	5.11
	422009 424909	AI742845 S78187	Hs.110713 Hs.153752	DEK oncogene (DNA binding)	1.77	4.37
	409154	U72882	Hs.50842	cell division cycle 258 interferon-induced protein 35	1.74 1.74	5.00 4.86
	413892	AI878921	Hs.75607	myristoylated alanine-rich protein kinas	1.73	4.37
60	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1,71	5.02
	424263 424825	M77640 AF207069	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.70	4.68
	427378	BE515037	Hs.153357 Hs.177556	procollagen-lysine, 2-oxoglutarate 5-dio melanoma antigen, family D, 1	1.70 1.67	4.59 5.59
	413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.39
65	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4.03
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.24
	422976 443051	AU076657 AA333660	Hs.1600 Hs.71331	chaperonin containing TCP1, subunit 5 (e hypothetical protein MGC5350	1.64 1.64	4.91 4.08
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4.41
70	446143	BE245342	Hs.306079	sec61 homotog	1.62	4.70
	431142	AA852596	Hs.250641	tropomyosin 4	1.62	4.86
	407752 416322	AA573581 BE019494	Hs.13328 Hs.79217	ESTs pyrroline-5-carboxylate reductase 1	1.62 1.61	4.19 4.51
	414572	AU077174	Hs.288181	cathensin H	1.60	5.25
75	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.56
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.58	5.46
	413976	BE295452	Hs.75655	procollagen-profine, 2-oxoglutarate 4-di	1.58	4.05
	414420 419638	AA043424 N46504	Hs.76095 Hs.91747	immediate early response 3 profilin 2	1.58 1.57	4.00 5.57
80	422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.57	4.44
	415819	AU077330		transcription elongation factor A (SII),	1.55	4.89
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.66
	425243	N89487	Hs.155291	KIAA0005 gene product	1.54	4.38
				53.6		

	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-	1.53	4.22	
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.53	7.41	
	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.51	4.12	
•	416879	AW162087	Hs.5437	Tax1 (human T-cell leukemia virus type 1	1.50	4.02	
5	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	1.50	4.18	
	415661	AF057307 AU077258	Hs.78575	prosaposin (variant Gaucher disease and	1.49 1.49	4.19 5.74	
	428098 452264	AU077013	Hs.182429 Hs.28757	protein disuffide isomerase-related prot transmembrane 9 superfamily member 2	1.48	4.53	
	415198	AW009480	Hs.943	natural killer cell transcript 4	1,47	4.95	
10	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	1.45	4.61	
10	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	1.45	4.15	
	421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	1.42	4.67	
	415089	N25117	Hs.299465	ribosomal protein S26	1.41	5.19	
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.41	4.03	
15	400202			NM_002795*:Homo sapiens proteasome (pros	1.41	4,44	
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.41	4.57	
	412968	AW500508	Hs.75102	alanyl-IRNA synthetase	1.40	4.25	
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	4.11	
20	447099	AB030656	Hs.17377	coronin, actin-binding protein, 1C	1.39	4.51	
20	428511	AA019912	Hs.184693	transcription elongation factor B (SIII)	1.38	4.90	
	413825 441737	BE299181	Hs.75564	CD151 antigen	1.37 1.36	4.44 4.29	
	440087	X79449 W28969	Hs.7957 Hs.7718	adenosine deaminase, RNA-specific hypothetical protein FLJ 22678	1.36	4.29	
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.35	4.50	
25	413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.35	5.14	
	433026	AW160616	Hs.279921	HSPC035 protein	1.35	4.14	
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	1.34	4.35	
	428289	M26301	Hs.2253	complement component 2	1.33	4.23	
	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.32	4.61	•
30	425299	AW505214	Hs.155560	calnexin	1.31	4.76	
	422242	AJ251760	Hs.273385	guanine nucleotide binding protein (G pr	1.30	5.30	
	448483	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	1.29	6.09	
	407143	C14076	Hs.332329	EST	1.29	4.56	
35	413125	BE244589	Hs.75207	glyoxalase I	1.26 1.26	5.56 4.98	
33	439053 413929	BE244588 BE501689	Hs.6456 Hs.75617	chaperonin containing TCP1, subunit 2 (b collagen, type IV, alpha 2	1.25	4.76	
•	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	1.24	4.56	
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.21	8.96	
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.21	4.02	
40	425335	BE394327	Hs.296267	follistatin-like 1	1.18	4.29	
	446211	AJ021993	Hs.14331	S100 calcium-binding protein A13	1,17	4.32	
	428542	NM_014899	Hs.10432	KIAA0878 protein	1.13	4.17	
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	1.10	4.00	
4.5	428216	M18468	Hs.183037	protein kinase, cAMP-dependent, regulato	1.09	4.40	
45	431211	MB6849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.00	4.70	
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	0.98	4.40	
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	0.90	4.78	
	TABLE S	nn.					
50	TABLE 5 Pkey:		nua Ean arabacat ida	atifar aurahas			
30	CAT nur		que Eos probeset ide le cluster number	HUHER HUTTIDES			
	Accessio		bank accession num	hers			2
	Pkey	CAT Number	Accession				
55	412918	2764_3		009 AV755430 AV756363 AV711927 BI523434 AI521	453 AAB46815 AV	V024829 AW949	702 BG218926 AA626658 AI445621 AI452815
		_		1580 AA612925 BG105326 BG532618 AW513994 AW			
				0378 AA483698 BE066066 BE066067 BE066062 AW3			
				2971 H97042 D58090 BI046351 H81248 AI750112 AV	/372079 C05492 (	)58287 D57835	AA935095 BF700910 BG215802 BG195459
۷0				5535 BG533177 BI087962 BE541579 BF130753			
60	436701	28142_1		I3 BM353155 AI473754 AI147901 AI803109 AA84329			
				234 AA394157 BF378047 BE467036 AA319724 AW29			
				02 N36920 H50440 AI919034 AI004399 AI383862 AI1			
			AW149064 AI70	911 AW194733 AA213447 AI290291 BF437165 AA75 BE30 AI00031	1332 BF000304 A	11333U32 A1133.	2400 DL 440000 VI330221, DE330043
65	432469	58644_1		1029 N9002 1 6365 NM 016040 AF151858 BIS61037 AW966873 AV	/067/07 DE210/6	2 DE019650 AW	770511 AWAGOOG AWA70122 BM150181
0,5	432403	30044_1		135 A1632346 A1129838 BM147664 A1292112 BE244			
				00 AW087624 AA668793 AL080084 BI335866 BI8209			
				54201 BM145846 BG111760 AI750065 BG655794 AA			
				1602 AI343932 AW136586 AW029464 AI708651 AA82			
70				537 AA609603 AI873901 AI859995 AA833589 AA765			
			N69889 BE2431	85 AA282179 AA831098 AA112676 AI702407 BG6217	'52 BE006492 AA	353202 BG6742	56 N46921 BI048774 AW300233 BF739890
			AW966879 AA39	3405 BF115146 AA910851 AA013099 N28878 AA287	713 BE348728 B	3616446 AL5999	353 AL599952 BF381073 AW505056 AA094735
				14 H27168 R54718 BF792697 AV693603 AV685883 E			
75				1997 AA490239 AW388161 BE842126 BG165309 N7			
75				3098 H00297 AW576477 AW150918 AW591371 AI38		497 AI285602 A	A745055 AI281647 BF 377670 T65207
				21680 AA285143 H27167 AW500235 BG494497 BF66			
	424571	9758_1	BE379766 AW1	52643 AI803450 AI564343 AI092711 AI140525 AW152	156 Al620740 Al	034669 AU161209	AIZ9UZ4Z AI339/45 AI374611 AI347368
				529 Al366124 AA493912 AA406235 AA493889 Al0571			
80				63 N70628 AA424577 AA983537 BF003004 AA62668 1777 A1359198 AA993793 BE614394 BE738239 AA12			
30			N3/630 A13703	1777 AIJ59198 AA993793 BE614394 BE738239 AA12 15 BE244980 AA548596 AW449675 AI191008 BF2237	1003 NIU34344 I 10 N70753 N979	A 500100 PULLER &	M300104 M11031003 MA302103 MA301200 128001 AIA19106 RE215661 RESQ1648
				13 BE244380 AAS46336 AW443673 ATTS 1008 BF2237 1968 BE858217 BF793358 AV756758 BG483603 A109			
			00072330 NI4/		O. O.O.O.O. L		

_	444207	9172_3	BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BC533994 AA513783 AI887309 AA280056 AW972006 AW873028 AI924914 AI818810 AW152786 AW084946 AI521413 AI659583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF811528 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353220 BE843111 AW819036 AW393133 BG9697291 AV548670 AV654332 AV687530 BG566964 AI807430
5			AIG76072 AAB37010 AI452482 AIG25817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AAG32893 BEG74169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA502956 AA483492 AA518178 AW802049 BCG75859 AV658871 BCG78B60 AI565004 AW819026 BE843092 AV658437 AV723049 BCG16948 AI911647 AI743494 AID91058 BCF87251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BCG36641 BCG17830 AA235802 BE774885 BE006682 BF342375 AA903144 BF338033 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847
10	450515	13638_2	BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299605 AL589870 AA847598 A470122 BE39896 AL304356 BE223045 BF435800 AL334207 A708171 AW025415 AL079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 H99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW7842369 H06848 H05608 H81745 H15016 R51905 AA860423 AL860904 AA876023
15	417020	74857_1	AK024824 BI089104 AL596792 AIB80004 BF959921 BE349489 AAB43097 AI475644 AW576123 AW731676 AI339951 AI128503 AW243903 BG231992 BGQ57353 AA987811 AA575927 AI889162 N68847 AA464693 AA9872541 AA844323 AI989578 AI830997 AW71626 H7792 AI338984 R24078 AI128953 T88696 AA868038 AA694545 H02091 BF439007 AI188980 AI279912 AA730423 R26552 AA45W71626 H77926 AJ446015 R19187 D51331 T24484 AI522034 AV771528 BI056540 BG009879 AW371388 Z36733 BE707682 BG501334 BG187547 H48381 BF055495 AI948528 AW994256 BF109394 AI817046 W58758 H48807 H01994 T78413 BG750345 R24132 N92060 R2530.
20	400219	8366_1	BC002552 L10284 NM_001746 A1271880 BIB34281 BI597016 AU133331 BI568332 BI465073 BG720694 ALQ46728 BH46138 BI4451052 AV647588 BG6232863 AW889757 BE001258 AA312566 AA47646 AU098976 AA312196 BF749977 M94859 A6707646 BG564195 BG623597 AU117332 BG6889653 BI6670033 AU134542 AU138830 A761759 BG675882 AA209406 AW512644 AW514813 AI570635 BE547592 BG655518 A459204 BF725673 BB877032 BF001988 ALQ47245 BF724470 BF058818 H18415 BE076849 BE076857 BE076848 BE075827 BED76856 AV708887 AA380923 BE076831 F0818 L18887 BF795701 AU128383 BE908383 AW673350 AW500108 BE077837 BE929419 BF686758 AW503373 AW580528 BE005524 BI917505 BI457781 BE833812 BI668159 AA213643 AA374821 BF968974 BM480200 AU136152 BE395635 AV685066 AV693755 ALQ40984 AA676820
25 30			BG896408 BC082272 BE082312 C05287 BE082264 AA379850 AW672902 AI625955 BF033526 AW296557 AA728815 BE077058 AW081700 AA911707 AA362640 BE707179 BG913228 BG116191 BG752367 AA074678 AL036937 BG113760 H03524 BG681802 AI564688 AU149556 BE178600 AB13488 A4652433 AZ08989 AA599392 AA580385 AA466274 AA6528899 AA555929 AA114046 AA094252 BM450328 BG529998 R63320 BE076792 BE090073 BE076855 BE076859 BE076829 AA36719 AA379164 AI202712 BG223315 BE122741 BG534531 AA965494 H24978 BF032674 BF085150 BE739158 AA352904 C21593 BG697597 AA134969 AA374612 BE566182 BE871838 BE076911 AW579175 BF969599 BI548594 BG386452 BG311195 BM456787 N40286 T80096 N39642 H42119 BG483861 AW381621 R69347 AW128895 AI367416 AI095285 AA099344 BE568161 AA180109 BF246488
	406636 400200	0_0 3806_1	BI561938 AW579170 BGS67212 L12064 L12063 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423
35			AA465237 A1376096 AA035579 A1087306 AA448162 AA129977 A1090903 A1080686 A128939 N33004 A1801240 AW021546 A1370773 A1086064 AA669528 A1250053 A1870113 AA853181 AA8581014 BC055562 BC9339559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 A1582295 A4417525 A1563975 A1093366 A1704743 A1280741 AW073417 BE875418 BM264076 BC876884 A1680533 AW854219 BE774635 AW854212 BC952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BC878291 BC876450 AW819099 A1908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473
40	406782 437179	0_0 12239_1	AA430373 AA968771 AK055109 BC019085 AA187684 BG655226 BM023227 A1932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 A1859222 A1348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 A1092259 AI028416 A1074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 A1400988 R54266 R31422
45	426143	3806_1	BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436785 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240586 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI093903 AI080686 AI288939 N33004 AI240 AW021546 AI370773 AI086064 AA669528 AI250053 AIB70113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H3021400 AW021546 AIM_002788 AA641134 AI582285 AI417525 AI563975 AI0933566 A707743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212
50	400223	2368_1	BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA246473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599 AL521812 BG705730 BI495545 BH95546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375
55	,		BM019558 BM023382 BG164174 N55999 B167064 BM023464 AI207475 BM311415 BG758439 BG758807 AI934826 N90351 BC422026 BE910312 AI027778 AI081950 AI356980 AI080915 AI191829 BG759697 AI138728 AA399403 AI355589 AI354677 AA588702 AA393560 AA025127 BG027630 AA962774 AA6817224 BG940967 BE791087 AA57315 W81685 AA393525 BG944103 AI339125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA888954 AA975844 AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI6011114 AW135664 AI206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 B1160457 H64512 BG503396
60	406687 453352	0_0 12299_2	M31126 BGG19646 AA367158 B1850421 AW998556 BF107010 BF969630 BF185964 AA361080 AW960026 AA147486 AI807023 AW770262 BI492178 BM145577 AA829932 AW021238 AW629477 AI337862 AI457141 BI712705 BM194542 BI712465 AI380070 N27407 AI609764 AI274152 AI206228 AI076874 AI261827 AI610982 AI469158 AI420690 AI168768 AA491675 C16249 C16232 C16209 C16275 C16243 C23287 BF246254 R66738
65	400203	11774_1	R23212 C14593 NM_002794 D26599 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 A1189162 A1831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133131997 AA284572 AA453009 BF938258 AA152127 AA393918 BF765307 BE247542 BF934697 BF341798 BE253409 AA470620 A1828932 AW379902 AV762678 AV741784 AV760892 A1025755 AA678562 AA630630 AA761708 AA862518 AA865831 AA862947 N53065 AA131821 AA293499 N23342 N26856 A1147346 AW951549 AA772963 BE245986 BG208493 A1831666
70	427239	20459_2	BG474873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA43583 AI002710 AW276192 AU149842 BG214797 BG198193 AW197923 AW67799 T39663 BG194788 BG2164565 BF345258 BG716363 AI066528 BI546220 AA393815 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735966 BG198438 BG216840 BG198438 BG400762 AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
75	415010	40015 *	AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 A1334909 AI802853 A1345036 A1348921 A1340734 A1307478 A1251289 AW302327 AW075200 A1312145 AW073656 AW072513 AW071289 A130515959 AA875186 T29587 A1307493 A125068 A1252868 A1252889 AW074809 A1252926 A1252160 A1251652 A1251626 A1251262 A1610913 A120787 A1270156 A125075 AW073469 AW072901 AW072496 AW071400 A1305762 A1254764 AI802837 A1251264 AW073049 AW071311 A1340643 BE138965 BE138502 AW073456 A1334733 A1054335 BE139260 A1054302 A1054060 A1054057 A1053722 A1289711 BE139228 AW47078 AW271039 AW302085 BE041872 A1254494 A1271496 A1252427 BF718773 BF718645 AW074866 BE857822 BF571807 DAM467094 A 140006 BF57264 FEFSTRONG APPRILATE PROFITS AND ARAPTAL SAMPAGANGANGANGANGANGANGANGANGANGANGANGANGAN
80	415819	40015_1	BE739429 BM460292 AL549095 BF752457 BE783002 BC035869 AW601528 AI880413 BF593762 AA974415 AW305318 AA716501 AI936239 AI809485 AI744171 AW80M992 BF108747 AW804693 BE219333 AI807707 AA306963 B0012140 BF74161B BF741618 BF741619 AW052543 AA155832 AU151381 AU158043 AU150410 AU145605 AU150252 AA188205 AU153035 AI147293 AA084507 AA688165 AI887120 AI468336 AW023112 H44035 F01513 AA747672 AW779630 AA757298 R77738 AU150931 R38473 AA189022 H96984 AL550490 AW949737 AU150194 AU149258 AI749453 AW172950 AW276160 AI753604 AI421762 AW575512 AI275633 AW516120 AI340167 AI567728 AI797326 AI471532 AI074080 AI633122 AW674646 AW316571 AA258187 AA102780 AA258186 AI363307 AA862862 AI206836 AA629555 AA486287 AI185097 AI872389 BE465687
			529

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A1246746 A1351453 A1189679 AA594582 A1038639 AA862764 AA644332 AA912423 AA601562 AW014502 AA694605 AW068949 BF941650 AW297886 BF941649 A1077854 A1027442 AA705602 AW020757 BH91734 AA977135 AA653973 B1522334 AA398723 A1280083 A1419671 AW009199 AA496011 AU144081 A1538440 BF741690 BF741660 H41990 AV724108 AW955578 BE698790 T29312 BG954488 R33179 B1832621 BF742040 AA95011 AU144081 IALS8440 BF /41650 BF /41680 HA1950 AV/4108 AW953578 BESS4780 IASJ16 BESS4780 RSJ179 BIASG47 BF /4280 BEGS1438 HSP2128 BG614897 AW953759 AZ15552 H44107 AA395350 BE F17315 B G258556 BF5716878 BA489308 BF741676 R54496 BE IR3198 H97097 AW062534 BF036430 AW192614 BF431707 N30258 AA629072 BG954496 A401616 BG960957 BEF73590 BF745945 AA156007 AA573157 AW7847610 AA516337 N79563 BM83306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 BF972880 BG11942 BI094093 AL538757 BEZ71653 BR55538 BC909573 BG109826 BE78430 BES99255 BR333973 BM010809 BEG21321 BG664956 BE904726 BB871370 AV708990 BF971483 BE298241 BI197007 BEZ72092 BG103074 AW963599 BE590572 AV744947 BG943041 AW327463 BC904726 BB871370 AV708990 BF971483 BE298241 BI197007 BEZ72092 BG103074 AW963599 BE590572 AV744947 BG943041 AW327463 BC904726 BB871370 AV708290 BF971483 BE298241 BI197007 BEZ72092 BG103074 AW963599 BE590577 AV744947 BG943041 AW327463 BC96476 BW744947 BG943041 AW327463 BC96476 BW744947 BG943041 AW327463 BC96476 BW744947 BG943041 AW327463 BW744947 5 400202 11771_2 BEG472870 BE333997 N2833 AA316042 N42043 AW40426 AW992094 AA379385 AW801110 AW406977 AA373791 BE341889 BE076254 AA360459
AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AA494241 W32225 BF745937 AJ383690 BG202360 10 TABLE 50C: Plusy: Ref: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. 15 Indicates DNA strand from which exons were predicted. Strand: Nt_position: Indicates nucleotide positions of predicted exons. Nt_position 14260-14537 Pkey 404854 20 7143420 Plus 80014-80401,80593-81125 53526-53628,55755-55920,57530-57757 405506 402474 7547175 Minus 198991-199168,199316-199548 8119067 400750 25 TABLE 51A: ABOUT 453 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO NORMAL SKIN Table 51A Kas about 453 genes upregulated in primary melanomas relative to normal skin. Cenes were selected from 59680 probesets on the Eos/Alfymetrix Hu/03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. Unique Eos probeset identifier number 30 Exemplar Accession number, Genbank accession number ExAcon: UnigenelD: Unigene number Unigene gene title Unigene Title: 90th percentile of primary metanoma Als divided by 90th percentile of normal skin Als 90th percentile of primary melanoma Als divided by 90th percentile of normal skin Als, where the 15th percentile of normal tissue Als was subtracted from both R2: 35 the numerator and denominator UnigenelD Hs.30743 Unigene Title preferentially expressed antigen in mela Pkey 452838 ExAccn U65011 14.06 13.64 15.56 11.62 NM_001922 NM_000372 Hs.301865 Hs.2053 dopachrome tautomerase (dopachrome delta tyrosinase (oculocutaneous albinism IA) 430377 40 426555 12.78 BE386801 AI186431 trinucleotide repeat containing 3 prostate differentiation factor 13.80 438549 Hs.21858 Hs 295638 422424 426600 Hs.171014 VGF nerve growth factor inducible 10.14 22,45 glyceraldehyde-3-phosphate dehydrogenase ESTs, Weakly similar to S51797 vasodilat chondroitin sulfate proteoglycan BEHAB/b 7.25 9.62 430822 AJ005371 Hs.248017 8.66 7.87 45 Hs.32399 457211 AW972565 Hs.6194 Hs.82002 438380 T06430 D13168 endothelin receptor type B 7.66 7.38 4.63 9.04 417355 447210 AF035269 AA319146 Hs.17752 Hs.75426 phosphatidylserine-specific phospholipas secretogranin II (chromogranin C) 7.32 4.65 413554 50 415752 BE314524 Hs.78776 putative transmembrane protein 6.46 absent in melanoma 2 7.00 Hs.105115 NM 004833 421508 AW960707 Hs.148324 Hs.181874 ESTs 6.43 6.27 5 92 AF026939 interferon-induced protein with tetratri 426312 small inducible cytokine sublamily A (Cy hexabrachion (tenascin C, cytotactin) 3.70 446921 AB012113 3.92 7.73 55 Hs.289114 429500 X78565 6.04 6.04 X72755 monokine induced by gamma interferon 414812 5.89 452973 H88409 Hs.40527 **FSTs** 5.96 5.72 2.50 5.29 ENSP00000251056*:Plasma membrane calcium 402075 436856 A1469355 Hs.127310 **ESTs** hypothetical protein FLJ12015 5.68 5.62 5.88 6.30 60 AA663372 Hs.169395 425088 AF086120 NM_001394 439310 Hs.102793 ESTs 5.62 5.36 5.36 5.35 5.28 5.23 5.20 5.14 5.09 5.04 4.94 4.88 4.87 4.74 4.74 4.72 4.68 3.30 Hs.2359 dual specificity phosphatase 4 429170 AB000115 AW979187 hypothetical protein, expressed in osteo melanoma differentiation associated prot 4.28 413670 Hs.75470 409512 Hs.293591 65 Homo sapiens cDNA: FLJ22105 fis, clone H 4.64 Hs.27935 hypothetical protein MGC4837 4.31 BF390513 436315 hypothetical protein MGC48370 glycoprotein M6B 442426 AI373062 Hs.332938 4 03 435056 AW023337 Hs.5422 5.52 4.82 Hs.287402 chondroitin 4-sullotransferase 432828 AB042326 70 AI538226 AK000680 Hs.32976 Hs.266175 guarrine nucleotide binding protein 4 phosphoprotein associated with GEMs 430294 431639 4.35 430838 N46664 Hs.169395 Hs.7155 hypothetical protein FLJ12015 ESTs, Moderately similar to 2115357A TYK 3.68 AA737033 414004 gb:Homo sapiens cig33 mRNA, partial sequ fls485 AF026942 AA305159 Hs.17518 6.29 75 Hs.113019 422192 silver (mouse homolog) like 6.00 42020B BE276055 NM_004403 W03476 deafness, autosomal dominant 5 hypothetical protein MGC4595 446006 Hs.13530 9.85 5.75 Hs.266331 440065 421574 440274 AJ000152 R24595 Hs.105924 defensin, beta 2 80 Hs.7122 scrapie responsive protein 1 2.78 AA431323 N88802 Hs.42146 Hs.5422 417166 **ESTs** 4.29

glycoprotein M6B

ESTs

415314

443983

H04482

Hs.163724

	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	4.62 4.62	2.87 5.08
	437179 417933	AA393508 X02308	Hs.82962	serologically defined colon cancer antig thymidylate synthetase	4.58	3.02
	431620	AA126109	Hs.264981	2-5-ofigoadenylate synthetase 2 (69-71	4.50	4.37
5	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	4.49	16.82
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.44 4.42	5.95 2.94
	409264	NM_014937 BE262677	Hs.52463 Hs.283558	KIAA0966 protein hypothetical protein PRO1855	4,42 4,42	3.54
	434203 422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	4.38	3.30
10	449722	BE280074	Hs.23960	cyclin B1	4.32	4.07
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.30	3.82
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	4.28 4.27	4.36 3.05
	424247 413916	X14008 N49813	Hs.234734 Hs.75615	hysozyme (renal amytoidosis) apolipoprotein C-II	4.25	4.68
15	420267	N37030	Hs.173337	ESTs	4.24	4.24
	442739	NM_007274	Hs.8679	cytosotic acyl coenzyme A thioester hydr	4.21	3.00
	433576	BE080715	Hs.161091	ESTs	4.20 4.20	6.31 2.73
	412652 438209	AI801777 AL120659	Hs.6111	ESTs aryl-hydrocarbon receptor nuclear transl	4.20	5.18
20	441553	AA281219	Hs.121296	ESTs	4.14	4.94
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	4.14	3.14
	439926	AW014875	Hs.137007	ESTs	4.12	4.76
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.12 4.10	4.85 5.20
25	400860 409415	AA579258	Hs.6083	Target Exon Homo sapiens cDNA: FLJ21028 fis, clone C	4.08	6.02
23	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.08	2.42
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	4.06	2.96
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	4.06 4.01	2.28 2.96
30	417632 418064	R20855 BE387287	Hs.5422 Hs.83384	glycoprotein M6B S100 calcium-binding protein, beta (neur	4.00	4.62
30	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.00	2.82
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.00	2.90
	451668	Z43948	Hs.326444	cartilage acidic protein 1	3.99	5.17
35	430015	AW768399	11- 2020	ESTs	3.96 3.94	3.89 2.91
33	407756 430223	AA115021 NM_002514	Hs.38260 Hs.235935	ubiquitin specific protease 18 nephroblastoma overexpressed gene	3.93	3.89
	433364	AI075407	Hs.296083	ESTs, Moderately similar to 154374 gene	3.93	4.70
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	3.92	7.78
40	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.87	3.34 3.69
40	402609 408083	BE383668	Hs.42484	KIAA1209 protein hypothetical protein FLJ10618	3.87 3.86	4.04
	409703	NM_006187	Hs.56009	2-5-oigoadenyiate synthetase 3 (100 k	3.85	3.64
	420218	AW958037		ribosomal protein L4	3.84	3.20
4.5	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.84	5,19
45	410600	AW575742	LL 120000	ESTs, Moderately similar to S65657 alpha	3.82 3.82	5.74 2.96
	442117 428513	AW664964 BE220806	Hs.128899 Hs.184697	ESTs; hypothetical protein for IMAGE:447 Homo sapiens clone 23785 mRNA sequence	3.82	4.03
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	3.80	3.56
50	432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	3.79	3.23
50	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela cadherin 19, type 2	3.77 3.72	3.66 2.28
	423605 407846	AF047826 AA426202	Hs.129887 Hs.40403	Cbp/p300-interacting transactivator, wit	3.72	5.34
	442578	AK001643	Hs.8395	hypothetical protein FLJ10781	3.71	3.42
	448965	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.68	3.31
55	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.68 3.68	4.24 2.74
	400750 447217	BE465754	Hs.17778	Target Exon neuropilin 2	3.66	3.60
	459373	BE408266	Hs.301406		3.66	3.48
<b>60</b>	419528	H67546	Hs.49768	ESTs	3.62	4.13
60	406868	AA505445	Hs.300697		3.61 3.59	4.40 3.53
	421866 421709	M24470 AA159394	Hs.1435 Hs.107056	guanosine monophosphate reductase CED-6 protein	3.57	2.63
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	3.54
<i>(</i> =	408962	8E386436	Hs.44317	SRY (sex determining region Y)-box 10	3.55	2.70
65	425139	AW630488	Hs.25338	protease, serine, 23	3.50	280 258
	428411 452744	AW291464 AJ267652	Hs.10338 Hs.246107	ESTs Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.49 3.48	2.58 4.61
	411305		Hs.69547	myelin basic protein	3.48	3.37
70	447343	AA256641	Hs.236894		3.47	2.68
70	429954		Hs.21374	ESTs	3.47 3.46	2.63 2.34
	417621 435256		Hs.82316 Hs.13872	interferon-induced, hepatitis C-associat cytokina-fike protein C17	3.46	2.47
	450534		Hs.25132	KIAA0470 gene product	3.42	3.65
~-	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	3.41	2.63
75	418506		Hs.85339	G protein-coupled receptor 39	3.40	4.02
	442711		Hs.8645 Hs.44571	hypothetical protein ESTs	3.39 3.38	2.95 2.38
	453344 436700		Hs.445/1 Hs.30140		3.36	4.60
	418007		Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	2.61
80	433867	AK000596	Hs.3618	hippocalcin-like 1	3.36	4.26
	408393				3.36 3.36	2.10 2.49
	447484 412828		Hs.29256 Hs.74621	- 1995-1 . N	3.35	2.45
	112020					

	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.35	2.58
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	3.34	2.55
	420602	AF060877	Hs.99235	regulator of G-protein signalling 20	3.34 3.34	5.96 2.73
5	439963 406663	AW247529 U24683	Hs.6793	platelet-activating factor acetythydrola immunoglobulin heavy constant mu	3.31	5.21
•	427540	R12014	Hs.20976	ESTs	3.30	3.40
	412141	A1183838	Hs.48938	hypothetical protein FLJ21802	3.29	2.80
	400282			NM_005313:Homo sapiens glucose regulated	3.29 3.28	3.46 5.20
10	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs epithelial membrane protein 1	3.28	2.79
10	416539 431518	Y07909 AA743462	Hs.79368 Hs.165337	ESTs	3.27	2.51
	402994	744 10102	1.0.100001	NM_002463°:Homo sapiens myxovirus (influ	3.26	6.38
	419956	AL137939	Hs.40096	cadherin 19, type 2	3.26	4.48
16	421379	Y15221	Hs.103982	small inducible cytoldine subfamily 8 (Cy	3.26 3.25	3.71 3.72
15	444371 432874	BE540274 W94322	Hs.239 Hs.279651	forkhead box M1 metanoma inhibitory activity	3.25	5.33
	417282	AA195203	113.213031	RAB5C, member RAS oncogene family	3.24	3.20
	439569	AW602166	Hs.222399	CEGP1 protein	3.24	2.32
~~	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.24	6.20
20	403817			NM_015271:Homo sapiens tripartite motif-	3.23 3.22	3.70 2.49
	407857 426334	A1928445 BE305081	Hs.92254 Hs.169358	synaptotagmin-like 2 hypothetical protein	321	2.46
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	3.19	5.50
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.18	2.04
25	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	3.18	3.73
	424090	X99699	Hs.139262	XIAP associated factor-1 Homo sapiens clone 25218 mRNA sequence	3.18 3.18	4.44 3.26
	410491 408418	AA465131 AW963897	Hs.64001 Hs.44743	KIAA1435 protein	3.16	2.21
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.16	4.04
30	402829			C1002500:gij6754254 ref[NP_034610.1] hea	3.15	4.57
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.15 3.14	3.07 3.08
	425935 417124	Z98200 BE122762	Hs.163724 Hs.25338	HSPC019 protein ESTs	3.14	2.73
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.11	2.16
35	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.10	2.43
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.10	2.83
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.10 3.10	1.78 3.17
	429083 437673	Y09397 AW665665	Hs.227817 Hs.153034	BCL2-related protein A1 ESTs	3.10	3.32
40	407813	AL120247	Hs.40109	KIAA0872 protein	3.10	3.90
	445745	AB007924	Hs.13245	KIAA0455 gene product	3,10	3.35
	451537	R56631	Hs.26550	retinoid X receptor, gamma	3.09 3.08	4.45 3.65
	408654	BE018882	Hs.46721	UCC1 protein hypothetical protein FLJ11264	3.08	2.12
45	444484 446019	AK002126 AI362520	Hs.11260	histone deacetylase 3	3.08	2.26
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	3.08	5.29
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.06	3.36
	403532	414003000	11. 121212	NM_024638:Homo sapiens hypothetical prot TASP for testis-specific adriamycin sens	3.06 3.04	3,37 3.17
50	433160 446341	AW207002 AL040763	Hs.134342 Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	3.03	2.98
-	426501	AW043782	Hs.293616		3.03	2.01
	450325	AI935962	Hs.91973	ESTs	3.02	2.19
	418941	AA452970	Hs.239527	E18-55kDa-associated protein 5	3.02 3.02	3.29 2.54
55	431797 442064	BE169641 AI422867	Hs.270134 Hs.88594	hypothetical protein FLJ20280 ESTs	3.00	1.96
-	405451	74422001		dihydropyrimidinase-like 3	3.00	2.98
	414915	NM_002462		myxovirus (influenza) resistance 1, homo	2.99	6.41
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.98 2.98	3.25 4.14
60	452958 427647	AA883929 W19744	Hs.40527 Hs.180059	ESTs Homo sapiens cDNA FLJ20653 fis, clone KA	2.96	3.30
•	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.96	2.47
	428819	AL135623	Hs.193914		2.96	4.16
	428450	NM_014791			2.96 2.95	2.41 2.79
65	414219 411358	W20010 R47479	Hs.75823 Hs.94761	ALL1-fused gene from chromosome 1q KIAA1691 protein	2.95	4.70
03	432467	T03667	Hs.239388		2.94	2.65
	400222			NM_002082":Homo sapiens G protein-couple	2.94	2.69
	405785			NM_025184*:Homo sapiens hypothetical pro	2.94	2.55
70	409760		Hs.83484	gb:EST10534 Adipose tissue, white I Homo SRY (sex determining region Y)-box 4	2.94 2.93	2.57 2.52
70	418113 409038		Hs.50002		2.93	2.43
	456760		Hs.12782		2.92	3.20
	459710		Hs.12159		2.91	4.45
75	411395		Hs.7542	KIAA1802 protein	2.90 2.90	2.72 2.27
75	427528 406964		Hs.17956	5 minichromosome maintenance deficient (S. FGENES predicted novel secreted protein	290	2.27
	428834		Hs.33931		2.89	3.55
	413190		Hs.40368	adaptor-related protein complex 1, sigma	2.89	3.87
00	438619	AB032773	44	TU1281-TY protein	2.88	2.37
80	442432		Hs.38178 Hs.19340		2.87 2.86	2.00 2.51
	428782 454027		Hs.21527		2.86	3.07
	453107				2.86	5.58

	414737	AI160386		ESTs	2.84	2.79
	412140	AA219691		RAB6 interacting, kinesin-like (rabkines	2.84 2.83	3.80 2.11
	447735			Homo sapiens cDNA: FLJ23020 fis, clone L defensin, beta 3	283	3.32
5	416091 442445	AF295370 AA082665		KIAA1715 protein	2.81	2.17
,	408208	BE018717	12,20000	ESTs	2.81	2.43
	430066	A1929659	Hs.237825	signat recognition particle 72kD	2.80	2.25
	424755	AB033094	Hs.152925	KIAA1268 protein	2.80 2.79	2.74 2.01
10	422616	BE300330	Hs.118725	selenophosphate synthetase 2	278	265
10	405506	ALATOCOO	Hs.71040	Target Exon hypothetical protein FLJ20425	2.78	3.10
	411619 400236	AJ418609	115.71040	Eas Control	2.78	2.21
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.78	3.15
	446488	AB037782	Hs.15119	KIAA1361 protein	2.78	2.80
15	439778	AL109729	Hs.99364	putative transmembrane protein	2.78	3.78
	420005	AW271106	Hs.133294	ESTs	2.78 2.77	2.86 . 3.07
	428642	NM_014899 N35187	Hs.10432	KIAA0878 protein 28kD interferon responsive protein	2.76	4.56
	453779 425289	AW139342	Hs.43388 Hs.155530	interferon, garrima-inducible protein 16	2.76	1.83
20	437723	AI672731	Hs.13256	ESTs	2.76	4.23
	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76	2.98
	426153	AF057169	Hs.1B2771	vitelliform macular dystrophy (Best dise	2.76	3.21
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.76 2.74	3.97 3.50
25	421351	AU076667	Hs.103755 Hs.198253	receptor-interacting serine-threonine to major histocompatibility complex, class	2.74	3.24
23	406673 427268	M34996 X78520	Hs.174139	chloride channel 3	2.74	2.82
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	2.74	1.95
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.74	2.99
	419705	AW368634	Hs.154331	ESTs	2.74	2.28
30	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.72 2.72	3.60 2.43
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reductase vipirin; similar to inflammatory respon	2.72	4.77
	447164 430594	AF026941 AK000790	Hs.17518 Hs.246885	hypothetical protein FLJ20783	2.72	3.67
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.71	12.06
35	424572	M19650	Hs.179600	2,3-cyclic nucleotide 3 phosphodieste	2.70	2.40
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.70	3.81
	425996	W67330		hypothetical protein AL110115	2.69	3.85
	430441	BE398091	11- 0202	desmoplakin (DPI, DPII)	2.68 2.68	2.55 1.67
40	442355 421362	AA456539 AK000050	Hs.8262 Hs.103853	lysosomal-associated membrane protein 2 hypothetical protein FLJ20043	2.68	2.94
40	421302	AW090198	15.103033	KIAA1150 protein	2.68	1.89
	412315	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo	2.68	2.80
	432878	BE386490	Hs.279663	Pirin	2.68	2.58
40	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.68	2.74
45	426759	AI590401	Hs.21213	ESTs	2.68 2.67	2.35 2.70
	405486	A1268000	Hs.47650	Target Exon ESTs	2.67	3.33
	410326 434040	AI368909 AW444613	Hs.288809	hypothetical protein FLJ20159	2.66	2.54
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.66	1.91
50	412719	AW016610	Hs.816	ESTs	2.66	4.21
	451708	A1306536	Hs.60975	ESTs	2.66	5.69
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.66 2.66	2.31 2.73
	425017	AL119305	Hs.26409	ESTs NM_005336:Homo sapiens high density lipo	2.66	2.79
55	400235 444809	BE207568	Hs.208219	oculospanin	2.64	2.86
55	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.64	2.33
	406382			C16001275*:gij12698037 dbjjBAB21837.1  (	2.64	2.48
	432241	AI937060	Hs.6298	KIAA1151 protein	2.63	3.16
60	417308	H60720	Hs.81892	KIAA0101 gene product	2.63 2.62	2.10 2.43
00	429294	AA095971 Al633770	Hs.198793 Hs.42572	Homo sapiens cDNA: FLJ22463 fis, clone H ESTs	2.62	1.99
	453935 401454	AI053770	115.42312	NM_014226*:Horno sapiens renal turnor anti	2.62	3.01
	436456	AW292677	Hs.248122		2.62	5.94
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.61	3.02
65	453256	AI565587	Hs.32556	KIAA0379 protein	2.60	2.68
	451622		Hs.30579	Homo sapiens cDNA: FLJ23070 fis, clone L	2.60 2.60	2.51 2.56
	424006		Hs.137548 Hs.159472		2.59	3.00
	409354 425392		Hs.15220	zinc finger protein 106	2.58	3.52
70	427286			epidermal growth factor receptor pathway	2.58	1.86
. •	418166			Cdc42 effector protein 3	2.58	2.15
	413794		Hs.61638	myosin X	2.58	2.54
	445707		Hs.114390		2.58 2.57	1.95 2.46
75	416640		Hs.79404	neuron-specific protein	2.56	1.74
75	427982 439453		6 Hs.181326 Hs.6566	5 KIAA1073 protein thyroid hormone receptor interactor 13	2.56	2.22
	455839		1.5.0500	gb:MR0-HT0208-101299-202-a04 HT0208 Homo	2.55	2.34
	447737		Hs.19404	DKFZP564L0862 protein	2.55	2.31
~~	423799	AW026300	Hs.13290	5 19A24 protein	2.54	211
80	442762	AF035119	Hs.8700	deleted in fiver cancer 1	2.54 2.54	2.47 3.99
	432888		Hs.27970		2.54 2.54	2.96
	440676 424481		7 Hs.11237 Hs.1787	groteofipid protein 1 (Pelizaeus-Merzbac	2.53	6.98
	45-40	1113733		historian history . It autones marress		

	422340			RAB7, member RAS oncogene family-like 1	2.53	3.06
	428844	AW972635		hypothetical protein FLJ12671	2.53 2.53	3.13 1.63
	458997 419591	AW937420 AF090900		ESTs Homo sapiens cDNA: FLJ21887 fis, clone H	2.52	2.30
5	414807	AI738616		hydroxyprostagiandin dehydrogenase 15-(N	2.52	1.80
•	429238	NM_002849		protein tyrosine phosphatase, receptor I	2.52	3.02
	432882	NM_013257		serum/glucocorticoid regulated kinase-li	252	3.05
	407260	L09095		gb:Homo sapiens mRNA fragment.	2.50 2.49	5.00 6.16
10	431186	NM_012249		ras-like protein progestagen-associated endometrial prote	2.49	4.71
10	417542 419556	J04129 U29615		chitinase 1 (chitotriosidase)	2.48	5.77
	408209	NM_004454		ets variant gene 5 (ets-related molecule	2.48	3.77
	405885			Target Exon	2.46	3.11
	406837	R70292	Hs.156110	immunoglobulin kappa constant	2.44	310
15	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.44 2.44	4.90 4.31
	421633	AF121860	Hs.106260 Hs.49344	sorting nexin 10 hypothetical protein FLJ 11006	2.42	3.19
	415929 413171	AA724373 AA318325	Hs.75219	tyrosinase-related protein 1	2.37	3.00
	406621	X57809	Hs.8997	immunoglobulin lambda locus	2.36	5.87
20	414142	AW368397	Hs.334485	hemicentin (fibufin 6)	2.36	3.04
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.36 2.34	3.66 4.95
	414283	AW960011	Hs.154993	ESTs ESTs	2.34	4.18
	453931 422515	AL121278 AW500470	Hs.25144 Hs.117950	multifunctional polypeptide similar to S	2.32	3.45
25	435292	N20514	Hs.172965	ESTs	2.32	4.94
	412926	A1879076	Hs.75061	macrophage myristoylated alanine-rich C	2.31	3.78
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	2.30 2.29	3.96 5.08
	425262	D87119	Hs.155418	GS3955 protein	2.28	4.05
30	439979 403969	AW600291	Hs.6823	hypothetical protein FLJ10430 ENSP00000034663:Zinc finger protein 131	2.28	3.64
50	421686	AB011156	Hs.106794	KIAA0584 protein	2.26	3.31
	432800	BE391046	Hs.278962	AIM-1 protein	2.24	4.08
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.24	3.47
25	415539	A1733881	Hs.72472	BMP-R1B	2.22 2.20	3.66 3.43
35	447523	BE613328 AB038651	Hs.21938 Hs.31854	hypothetical protein FLJ 12492 K562 cell-derived leucine-zipper-like pr	2.20	3.52
	433180 415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	2.19	3.76
	407241	M34516		gb:Human omega light chain protein 14.1	2.18	3,17
40	422243	AW803733	Hs.23585	hypothetical protein MGC12250	2.18	3.28
40	417324	AW265494		ESTs	2.16 2.14	5.85 3.49
	412819	T25829	Hs.24048 Hs.274404	FK506 binding protein precursor plasminogen activator, tissue	2.13	4.39
	432342 427923	AL036128 AW274357	Hs.301406	hypothetical protein PP3501	2.13	5.48
	417437	U52682	Hs.82132	interferon regulatory factor 4	2.13	3.08
45	425535	AB007937	Hs.158287	KIAA0468 gene product	2.13	8.66
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.12 2.12	3.01 4.66
	409154	U72882 AL040521	Hs.50842 Hs.15220	interferon-induced protein 35 zinc finger protein 106	2.12	3.71
	429951 418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	211	4.27
50	419200	AW966405		EST	2.11	3.58
	416448	L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10	5.34
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	2.07 2.06	7.86 3.68
	445133 411492	AW157646 T46848	Hs.198689 Hs.70337	ESTs immunoglobulin superfamily, member 4	2.04	3.36
55	408015	AW135771	Hs.244349	epidermal differentiation complex protei	2.03	3.41
-	424412	H15512	Hs.10043	hypothetical protein FLJ13074	2.03	3.82
	431657	A1345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	2.02	3.03
	427536	BE277141	Hs.115803	gb:601178666F1 NIH_MGC_20 Homo sapiens c	2.02 2.00	3.09 3.29
60	400533 432680	T47364	Hs.278613	ENSP00000209376*:PRED65 protein (Fragmen interferon, alpha-inducible protein 27	1.99	3.07
00	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.97	4.52
	417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (	1.97	3.26
	423952	AW877787	Hs.136102		1.94	3.79
65	455705	AW161061	11- 220010	ESTs, Weakly similar to zinc linger prot	1.93 1.93	3.16 3.11
03	419723 438866		Hs.339810 Hs.325495		1.93	3.47
	448410		Hs.21126	hypothetical protein FLJ20220	1.92	3.00
	400292		Hs.72472	BMP-R1B	1.92	4.07
70	436797		Hs.334477		1.90	3.04
70	406851		11- 404936	major histocompatibility complex, class	1.90 1.89	6.53 3.39
	428437 431836		Hs.184325 Hs.271411		1.89	4.04
	424687		Hs.151738		1.87	3.64
	426322		Hs.2012	transcobalamin I (vitamin B12 binding pr	1.85	4.21
75	425221		Hs.155188		1.85	3.13
	420162		Hs.95577	cyclin-dependent kinase 4	1.85 1.85	3.04 3.20
	443530 433671		Hs.9552 Hs.132906	binder of Arl Two 5 19A24 protein	1.84	3.39
_	424415				1.82	3.22
80	400991	1		Target Exon	1.82	4.11
	418677		Hs.87224		1.82 1.81	3.43 3.12
	424441		Hs.14709		1.79	5.31
	424825	AF207 <b>0</b> 69	Hs.15335	hororade where candings are sain	1,73	5.51

	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.79	3.40
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	1.78	3.38
	414945	BE076358	Hs.77667	tymphocyte antigen 6 comptex, locus E	1.77	3.69
_	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.77	3.12
5	401591			Target Exon	1.75	4.30
	425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.75	3.68
	412844 417237	A1828045 H86385	Hs.18016 Hs.81737	Homo sapiens mRNA; cDNA DKFZpS86H0324 (f palmitoyl-protein thioesterase 2	1,74 1,73	3.53 3.06
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	1.72	4.38
10	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.72	4.38
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.72	3.61
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	1.72	3.06
	430148	BE387620	Hs.234489	lactate dehydrogenase B	1.71	4.38
15	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.70 1,70	3.13 3.08
13	413317 417333	U53225 AL157545	Hs.75283 Hs.173179	sorting nexin 1 bromodomain and PHD finger containing, 3	1.68	3.15
	407223	H96850	10.173173	gb:yw03b12.s1 Soares melanocyte 2NbHM Ho	1,68	4.19
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.67	5.74
	404067			Target Exon	1.67	4.73
20	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	1.66	3.22
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	1.65	3.17
	427747 437912	AW411425 BE278594	Hs.180655 Hs.5912	serine/threonine kinase 12 F-box only protein 7	1.64 1.64	3.35 3.24
	404140	BE210394	ns.3312	NM_006510:Homo sapiens ret finger protei	1.64	3.10
25	414214	D49958	Hs.75819	glycoprotein M6A	1.64	3.45
-•	427239	BE270447		ubiquitin carrier protein	1.62	3.58
	427289	AI097346		phosphoserine aminotransferase	1.62	5.89
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.62	3.23
30	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.62 1.61	4.00 5.00
30	439627 451489	BE621702 NM_005503	Hs.29076 Hs.26468	hypothetical protein FLJ21841 amyloid beta (A4) precursor protein-bind	1.60	3.06
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	1.58	3.34
	411825	AK000334		hypothetical protein FLJ20327	1.56	3.18
26	438552	AJ245820	Hs.6314	type i transmembrane receptor (seizure-r	1.56	3.23
35	428081	AA421048	Hs.95011	syntrophin, beta 1 (dystrophin-associate	1.55	3.10
	401914			Target Exon	1.54	3.33
	424902 441648	NM_003866 H05734	Hs.153687 Hs.30559	inositol polyphosphate-4-phosphatase, ty ESTs	1.54 1.52	3.15 3.36
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.52	3.17
40	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.52	4.93
	413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.52	3.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.52	3.83
	422596	AF063611	Hs.118633	2-5-oligoadenylate synthetase-like	1.50	3.04
45	421851 448499	R18686 BE613280	Hs.108896 Hs.77550	lambda-crystallin	1.47 1.44	3.10 3.07
73	427378	BE515037	Hs.177556	hypothetical protein MGC1780 melanoma antigen, family D, 1	1.44	3.00
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	1.42	3.66
	448143	AF039704	Hs.20478	ceroid-tipofuscinosis, neuronal 2, late	1.42	4,16
50	413291	NM_006278	Hs.75268	sialyltransferase 4C (beta-galactosidase	1,41	3.30
50	435968	AW161481	Hs.111577	integral membrane protein 3	1.41	3.30
	422486 443759	BE514492 BE390832	Hs.117487	gene near HD on 4p16.3 with homology to	1.40 1.39	3.01 3.82
	444441	AW613841	Hs.134729 Hs.301394	FXYO domain-containing ion transport reg hypothetical protein MGC3101	1.39	3.43
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.36	3.32
55	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.35	3.03
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.34	6.25
	426890	AA393167	Hs.41294	ESTs	1.34	3.66
	433320 450358	D60647 AB010098	Hs.250879 Hs.24907	ESTs, Highly similar to CTXN RAT CORTEXI coronin, actin-binding protein, 28	1.34 1.33	3.18 3.19
60	421612	AF161254	Hs.106196	806 antigen	1.33	3.03
••	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.32	3.68
	428342	AI739168		Homo sapiens cDNA FLI 13458 fis, clone PL	1.32	3.10
	449444	AW818436		solute carrier family 16 (monocarboxylic	1.30	3.30
65	404700			Target Exon	1.30	3.14
UJ	403043 409858	NM_006586	Hs.56828	Target Exon trinucleotide repeat containing 5	1.30 1.29	4.22 3.09
	424679	AL117477	Hs.119960		1.27	3.13
	406908	Z25437	1.0.110000	gb;H.sapiens protein-tyrosine kinase gen	1.27	3.66
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.26	3.09
70	423130	AW897586	Hs.21213	ESTs	1.24	3.34
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	1.24	3.15
	442680	BE270707	Hs.8583	similar to APOBEC1	1.22	3.94
	422319 402408	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD NM_030920*:Homo sapiens hypothetical pro	1.21 1.04	3.36 3.37
75	424905	NM_002497	Hs.153704		1.00	3.02
				,	,	

# TABLE 51B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

	430540	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395988 BM048875 BE881070 BE313689 BE879144 BM03834 AW245847 AI770171 BF196861 BE856697 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ420408 A191843 A1131029 AW768399 AJ365196 AW337984 AW026150 BE465591 BE674599 AJ818438 AA772197 AJ651927 AW151143 BI198825 BG819083 BM458764 BE903567
5			BE732715 BM043200 BE900253 BE900706 BE731097 BE390023 BG975304 BF996406 BF98830 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903785 BE732947 BI277204 BG761305 BE25642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE590420 AW24627 BM237874 BM247847 BM2478 BM247847 BM24787 BM24787 BM24787 BM24787 BM2478 BM2478 BM2478 BM2478 BM2478 BM2478 BM2478
10			ALSS493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 A421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 B1041891 BG332385 BG253168 BG759470 BF389329 BF38132 BE2599418 BE785738 B1091658 N72512 W58732 W85690 BG358989 AIE05206 H19721 W17051 W77958 B1262010 AA844319 W74143 W727214 N85194 BE785738 B164099 AA931069 F13645 R41394 AK025758 BC180977 BE349455 AA812018 AA740241 A1027722 A150356 AA886395 AW977627 BE220225 AA884002 AW518114 AA243844 AA809493 AA81029 AA825718 A1347866 A431670 AA814436 A1251109 R07704 AA765606 AA724593 A1918399 A1537550 AA491103
			AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809
15	437179	12239_1	BE002760 BG746251 BE962912 BMA54584 AL134894 BF104082 H80591 AK055109 BC019985 AA187684 BG656226 BM023227 AI323211 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AU092259 AU29416 AI074114 BG656536 BE501577 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226
			PGGG31 FD4125 CD2343 AA115589 R56480 AI400988 R54266 R31422
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25			BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA453876 AI375927 AA648810 AA948193 AA499916 AI459893 AU458188 AU440408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AB18438 AA772197 AI651927 AW151143 B188825 BG819083 BM458764 BE903367 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
			BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
30			A1359493 BM018598 A1689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 A1421728 BG767231 BM452953 BG340524 W52564 BA4113434 BE7857348 BI041981 BG832385 BG253168 BG759470 BF368329 BF981332 BE2598188 BE785738 B1091658 N72512 BG759470 BF36894 BF368738 BF36738 B1091658 N72512 W567372 W56690 BF36896 A196706 H19721 W17051 W77958 B1262010 AA844319 W72143 W72214 N85194 BE734033 BG164099 AA931069
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45	417282	2142_2	AW991405 BG739837 AA287804 AW801855 AL568814 AW384099 AW384058 AW754178 AI001019 R33917 BE814037 AI557164  AK05474 JU1303 AF741304 RM424202 AI 539379 AI 554793 AI 543707 AI 549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347
		_	BIB3B505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 U310U3 AA234218 A1420466 RM0R3921 BE856788 BE669957 BF430992 AW614978 AW205958 BF110763 BF222758 AA195232 AI341353 AI698676
50			A093230 A1123522 A1656594 A1208758 AA975916 A1089224 A1264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 AL576975 BF689524 AL563130 B1658155 AA417889 AL513995 AL568815 AU160693 AA836028 H84388
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	408208	642734_1	81757837 AWA39843 AW172765 RE018717 RE464329 RE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387
	400236		M80355 NM_002376 AU132239 AU120606 AU124963 AU065116 BE900808 BF968374 AI806648 BG774205 AW250728 BE265845 AA290719 AU125196 BG428863 AA333580 AA604551 W73300 AI932646 AA082201 AA627618 BF038887 BF337051 BI021159 AW057581 AI983156 AI268004
65			T71031 T00003 AW104000 H93959 A1742843 A1935080 RE041751 H93970 AW797399 W05032 T87824 T82912 AW129639 A1221821 AJ911810
			AA703093 AA160135 AW779124 AA102559 AA969546 D29560 BI915937 AA707716 BI085679 AA700887 AA081085
	416730 425996		RMDDGGG1 AA3G71G2 AWGG37DG AIG31R33 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557G33 AA7800G5
70	42,550	100010_1	AI218139 AW194264 D20120 AI082715 AI959980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AI431759 AI796526 AI521794
70	430441	1438_6	AI796380 AW117545 AI749657 AI537634 N50122 BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080
	437158	59575_1	R00283 C15236 AW327776 D80759 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552
75		_	AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370
	412315	1163860_	AW611634 H41653 A468349 H19588 AW090198 AW043993 R39847 1 AW936678 AW936621 AW936683 AW936822 AW936781 AW936817 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812
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5			BE712902 BE BF060840 BG A1720319 AIRE	17292 BE712975 BE712970 BE712933 BE712929 BE712922 BE712975 BE712866 BE712861 BE712860 BE712854 BE712853 172897 BE712912 BG984910 BE712903 BE764759 BE715723 BE715745 BE712915 AA441839 BE713040 BE715755 BF872528 193104 BG744878 AU124081 AU89823 AU801072 AU633102 AU673670 AU93508 AW194294 AU545555 AU686735 AW154477 AU419496 18190 AA047013 AA039625 BE049622 AA369065 AA025686 AU570198 AA706304 AW439251 HG4553 AW168006 AU807479 AW81999 181490 BF886341 AW591246 AU90143 AU151074 AU499541 AU650934 AA402167 AA382049 T16207 T03299 AU932691 AW571663
10			BG479797 BE W25087 BM45 BF948864 BE R72666 H395	5 1930 BF-86531 19791426 AT 191143 A
15			W80749 BF23 AA064680 N8 BF923672 BIO	33 16 (279768 AA325106 T19241 BE409339 BF852119 W23803 T54011 AW392638 B1465185 AW516784 AA211335 B1159846 8814 BE279768 AA325106 T19241 BE409339 BF852119 W23803 T54011 AW392638 B1465185 AW516784 AA211335 B1159846 0615 W49676 BF851406 R88120 AA434028 H44546 T61029 M44804 AA114948 H26960 B1261965 AA582599 BG469385 BF818172 274270 AW362633 BE833122 BM470779 BE933750 AW856056 AW856103 BE826607 AW381799 AL 121058 BE828618 BE769545 2749978 B1770417 B1862544 AH110687 AF08262 BE740347 BE874864 AJ305113 BE513675 BE091369 B1048660 BE091453 B1046548 868704 AW25179 BF356840 BF886357 BF886313 BG951884 AJ347880 AW627563 BF932535 AW820377 BF739372 BF831620 BE068264
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	419200	9531_1	BG951874 AI BF036043 AI	N190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345
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40			BM128728 A AA625761 A AIR63R60 HC	53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL 118798 A193411 AW444709 AW952455 AB87612 BF431948 BH96876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595 B872909 A1826790 AA328366 BE827416 F75951 D6918 R681729 BE827388 AL118797 A1184164 AA164411 B1495332 BE858113 B660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
45	455705	77478_2	AA864334 A	ES13812 AA1333SS AW581719 BF434402 AL600619 BG699731 BI551395 AW027136 AW055130 BF939512 A(076048 H18584 AW161061 IB16101 BE049456 AW044012 AA954079 A1274682 A1370526 AW131990 AA853195 AA853191 BG118295 AA761620 BG705371 F336596 AA360497 H28072 BG198352 AW364709 H40926 H44214 AA836538 B1059563
73	406851	0_0	AAROQ7RA R	97304
	427239	20459_2	AW075006 /	E794750 AA582906 AID15067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 XW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 XW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809
50	427220	1020.2	AI252926 AI AI802837 AI	252160 Al251662 Al251262 Al510913 Al270787 Al270156 Al252075 AW073469 AW072901 AW072496 AW071420 Al305762 Al254764 251264 AW073049 AW071311 Al340643 BE138965 BE138965 AW073455 Al334733 Al054335 BE139260 Al054302 Al054050 Al054057 289711 BE139228 AW470478 AW271039 AW302085 BE041872 Al254494 Al271496 AL252427 BF718773 BF718645 AW074866 BE857822 IG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 Al889380 AA868504
55	427289	1820_2	AW512968 AW612240 AV703420 F	aasoora aits1211 n26980 aisakoo aat47849 BF 154926 BF477185 aa649647 R39135 ait50216 T35363 W36278 aw09375 a aasos495 aas15380 BG760793 aw370651 BG766029 aw370595 BF229885 BG762422 BG766407 T50662 aa025671 aw915715 165047 aar85582 R56188 H90385 R59913 B1261497 Bi018403 BF376945 T75678 BF933225 BF932853 BC502266 aw868934 av683504
	411825	7891_1	AK000695 /	41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199 KK000489 BC001688 BG235988 AW006329 AI887644 AI207230 A1148213 AI304333 AI634653 AW662636 AI281247 AA946921 AA424487 KIB30688 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 BI906631 AW083424 AA625199 NM_017767
60	406827	0_0	AK000334 ( AA971409	3F984048 AW815634 AL573992 AA430612 AA928390 AA46447 AW340827 AA424290 AI927759 BG951502 AW881353 BI765535
	428342	6712_1	AK056315 /	NO15524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 NW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI366361 AI923640
65			AI985564 A	AIS21500 AL042095 AAG09309 AA761319 A381489 H45700 AA761333 AW265424 AA909524 AAG35311 AAG49040 A1392620 Z40708 W263513 AA913892 AIG93486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263
	449444	2735_1	BI002756 A U59185 NN AU155762	A489664 BF827261 W74741 BF963166 L 004596 AV734324 A1245349 AA399517 H88760 D79128 AA970406 HD1059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 R73508 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BG429539 BE929862 BF811258
70	432665	27095_3	8G165971	BE143233 ALS77712 AI400326 AA769318 AA427866 AW088714 AI150755 AI924874 AI186243 AA804195 AA768972 AW574769 AW204520 AA235336 AI005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 AI690331 AI673409 AA627727 AI923685 AA931499 AI249783 AI810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840
75	TADIF	E1C·		
,,	TABLE : Pkey: Ref:		Sequence source, sequence of huma	presponding to an Eos probesel The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA on chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402-489-495.
80	Strand: Nt_posi		Indicates DNA str	and from which exons were predicted. te positions of predicted exons.
	Pkey 402075	Ref 8117407	Strand Plus	Nt_position 121907-122035,122604-122921,124019-12416

	400850	9757499	Minus	151830-152104,152649-152744
	402609	9926445	Minus	113464-113633,114264-114654
	400750	8119067	Ptus	198991-199168,199316-199548
_	402994	2996643	Minus	4727-4969
5	403817	8962065	Plus	110297-111052
	402829	8918414	Plus	101532-101852,102006-102263
	403532	8076842	Minus	81750-81901
	405451	7622517	Minus	145949-146227
	405785	9581533	Minus	98702-98925
10	405506	6466489	Plus	80014-80401,80593-81125
	405486	6651379	Plus	179441-179598
	406382	9256148	Plus	122336-122851
	401454	9186923	Minus	114659-114832
	405885	7677703	Minus	42574-42998
15	403969	8569909	Plus	31237-31375,32405-32506
	400533	6981826	Minus	277132-277595
	400991	8096825	Plus	159197-159320
	401591	9966977	Minus	55410-55835
	404067	3282162	Plus	1415-2071
20	404140	9843520	Plus	37761-38147
	401914	9369520	Plus	62537-62945,63155-63308
	404700	9800123	Minus	159621-160203
	403043	7768753	Minus	314423-316252
	402408	9796239	Minus	110326-110491
25				

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES
Table 52A fists about 204 genes upregutated in primary metanomas relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:

ExAcon:

Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number

Uniquenel Title:

Unique Eos probeset identifier number

Uniquenel Title:

Unique Eos probeset identifier number

Uniquenel Title:

Vingene number

Uniquenel Title:

90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

35

30

Unique Eos probeset identifier number
Exemplar Accession number, Gentbank accession number
Unigene number
Unigene number
Unigene gene title
90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Ais
90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Ais, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
40	421948	L42583	Hs.334309	keratin 6A	21.90	16.66
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	21.36	43.65
	401781			Target Exon	18.70	18.58
	401780			NM_005557*:Homo sapiens keratin 16 (foca	15.34	16.00
	431360	NM 000427	Hs.251680	koricrin	12.34	9.86
45	409632	W74001	Hs.55279	serine (or cysteine) proteinase Inhibito	11.24	8.73
	412636	NM 004415		desmoplakin (OPI, DPII)	11.20	6.62
	417366	BE185289	Hs.1076	small proline-rich protein 18 (comifin)	10.46	12.75
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	10.41	25.49
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	9.20	8.63
50	420783	AI659838	Hs.99923	tectin, galactoside-binding, soluble, 7	8.11	11.14
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	7.90	8.92
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	7,14	22.14
	427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	7.03	8.90
	430686	NM_001942	Hs.2633	desmogtein 1	6.88	5.39
55	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	6.60	12.79
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.44	6.19
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	6.34	7.77
	422166	W72424	Hs.112405	S100 catcium-binding protein A9 (catgran	6.15	8.91
	418067	AI127958	Hs.83393	cystatin E/M	6.08	9.24
60	408535	AW381532	Hs.135188	ESTs	6.04	17.40
	402075			ENSP00000251056*:Plasma membrane calcium	5.96	8.41
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.46	3.32
	410001	AB041036	Hs.57771	katlikrein 11	5.38	5.36
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	5.32	3.84
65	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.19	5.30
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	5.03	7.94
	429504	X99133	Hs.204238	lipocatin 2 (oncogene 24p3) (NGAL)	4.86	5.22
	421773	W69233	Hs.112457	ESTs	4.82	12.41
	442577	AA292998	Hs.163900	ESTs	4.82	4.40
70	401760			Target Exon	4.60	11.03
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	4.50	11.35
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.47	12.43
	431211	MB6849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.45	2.99
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.39	4.23
75	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.38	4.55
	418663	AK001100	Hs.41690	desmocollin 3	4.36	5.16
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	4.29	5.19
	401747			Homo sapiens keratin 17 (KRT 17)	4.28	5.41
	414807	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	4.24	2.30
80	411274	NM_002776		kaltikrein 10	4.22	4.82
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.21	8.26
	420039	NM_004605		sulfotransferase family, cytosolic, 2B,	4.18	4.73
	429538	BE182592	Hs.139322	small profine-rich protein 2A	4.16	7.30

	418686	236830	Hs.87268	annexin A8	4.12	4.09
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.08 4.08	2.13 4.38
	421733 416091	AL119671 AF295370	Hs.1420 Hs.283082	fibroblast growth factor receptor 3 (ach defensin, beta 3	4.06	5.38
5	442757	AI739528	Hs.28345	ESTs	3.94	4.28
	427318	AF 186081	Hs.175783	zinc transporter	3.92	3.07
	453309	A1791809	Hs.32949	defensin, beta 1 fis485	3.90 3.88	4.30 2.81
,	422192 424012	AA305159 AW368377	Hs.113019 Hs.137569	tumor protein 63 kDa with strong hornolog	3.86	5.03
10	429365	AA451798	Hs.99249	ESTs	3.76	4.05
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.72	6.35
	425580	L11144	Hs.1907 Hs.86149	galanin phosphoinositol 3-phosphate-binding prot	3.68 3.68	3.65 2.75
	448966 444946	AW372914 AW139205	Hs.156457	hypothetical protein FLJ22408	3.59	5.72
15	408591	AF015224	Hs.46452	mammaglobin 1	3.58	4.73
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.58 3.56	2.62 2.61
	438501 421574	Z44110 AJ000152	Hs.86149 Hs.105924	phosphoinositol 3-phosphate-binding prot defensin, beta 2	3.56	4.6-
	402294	2000132	10.100024	Target Exon	3.48	4.38
20	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.44	2.95
	401785	*****	11- 00460	NM_002275*:Homo sapiens keratin 15 (KRT1	3.42 3.36	4.92 4.24
	418007 418394	M13509 AF132818	Hs.83169 Hs.84728	matrix metafloproteinase 1 (interstitial Kruppel-like factor 5 (intestinal)	3.31	5.42
	452392	L20815	Hs.507	comeodesmosin	3.30	8.56
25	445183	AB007877	Hs.12385	KIAA0417 gene product	3.30	2.35
	433124	U51712	Hs.13775	hypothetical protein SMAP31	3.26 3.25	2.15 4.34
	419098 421978	AA234041 AJ243662	Hs.87271 Hs.110196	ESTs NICE-1 protein	3.17	5.86
	445493	AJ915771		metallothionein 1E (functional)	3.16	2.98
30	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	3.14	2.07
	445745	AB007924	Hs.13245 Hs.61635	KIAA0455 gene product six transmembrane epithelial antigen of	3.10 3.06	2.39 2.71
	410268 407839	AA316181 AA045144	Hs.161566	ESTs	3.06	3.54
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.04	4.64
35	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	3.04	2.78 4.79
	452240 409190	AJ591147 AU076536	Hs.61232 Hs.50984	ESTs sarcoma amplified sequence	3.00 2.96	3.05
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.94	10.53
40	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.91	3.01
40	406964	M21305	11- 2000	FGENES predicted novel secreted protein	2.90 2.89	5.34 6.64
	451541 454027	BE279383 R40192	Hs.26557 Hs.21527	plakophilin 3 Human DNA sequence from clone GS1-115M3	2.86	2.81
	414737	A1160386	Hs.125087	ESTs	2.84	1.76
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.82	1.83
45	405542	AE447070	U= 150953	Target Exon	2.80 2.78	2.77 5.17
	442503 402970	AF147078	Hs.150853	p53-responsive gene 5 C20000886°:gi]9280563 gb AAF86472.1  (AF	2.78	3.37
	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76	2.76
50	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	2.75 2.72	2.76 2.86
50	447164 409453	AF026941 AI885516	Hs.17518 Hs.95612	vipinin; similar to inflammatory respon ESTs	2.72	6.68
	428824	W23624	Hs.173059	ESTs	2.67	2.75
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.65	3.07
55	430630	AW269920	Hs.2621	cystatin A (stefin A)	2.63 2.61	2.38 2.44
33	433339 444670	AF019226 H58373	· Hs.8036 Hs.332938	gfioblastoma overexpressed hypothetical protein MGC5370	2.57	1.74
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	2.54	3.66
	400995	44000043	11- 47CCD4	C11000295*:gij12737279 ref XP_012163.1	2.54 2.53	2.93 7.36
60	423515 417359	AA327017 T99264	Hs.176594 Hs.191117	ESTs ESTs	2.53	2.54
v	432426	AW973152	Hs.31050	ESTs	2.52	2.15
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.52	3.05
	414987 407748	AA524394 AL079409	Hs.294022 Hs.38176	hypothetical protein FLJ14950 KIAA0606 protein; SCN Circadian Oscillat	2.52 2.48	3.85 1.76
65	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.47	1.92
	413392	AW021404	Hs.13021	ESTs	2.47	2.56
	442762	AF035119	Hs.8700	deteted in fiver cancer 1	2.46	1.90
	444781	NM_014400 AW383226		GPI-anchored metastasis-associated prote ESTs. Wealdy similar to G01763 atrophin-	2.46 2.46	7.90 2.66
70	424364 420568	F09247	Hs.247735	protocadherin alpha 10	2.45	3.01
	405885			Target Exon	2.46	2.82
	412633		Hs.74304	periplakin	2.46 2.45	5.01 3.35
	429852 429624		Hs.225948 Hs.99476	small inducible cytokine subfamily A (Cy ESTs, Wealdy similar to 13131848 alpha 1	2.45 2.44	2.33
75	429624 407325		Hs.328476	ESTs, Wealdy similar to atternatively so	2.44	211
	431441		Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.43	3.66
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	2.42	3.12
	430168			DKFZP434I1735 protein bullous pemphigoid antigen 1 (230/240kD)	241 240	2.75 3.67
80	408000 404049		Hs.198689	NM_018937*:Homo sapiens protocadherin be	2.39	1.89
	433576	BE080715	Hs.161091	ESTs	2.39	1.59
	444083			gb:co17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.38 2.37	2.59 2.12
	408208	BE018717		ESTs .	231	2.12

	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	2.36	2.23
	453931	AL121278	Hs.25144	ESTs	2.34 2.31	1.99 3.82
	452308 431048	AI167560 R50253	Hs.61297 Hs.249129	ESTs cell death-inducing DFFA-like effector a	2.31	2.18
5	403752	N30233	NS.243123	NM_002753*:Homo sapiens mitogen-activate	2.30	2.38
-	402525			NM_002699":Homo sapiens POU domain, clas	2.30	2.36
	420223	N27807		ribosomat protein L4	2.30 2.29	1.73 4.54
	452023 443172	AB032999	Hs.27566 Hs.199061	KIAA1173 protein p300/CBP-associated factor	2.28	2.02
10	439979	AW662964 AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	1.71
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.27	1.81
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.26	2.17
	436895	AF037335	Hs.5338	carbonic anhydrase XII	2.26 2.26	2.51 2.19
15	404029 424049	AB014524	Hs.138380	NM_018936":Homo sapiens protocadherin be NIAA0624 protein	2.26	2.99
• 5	442423	BE326264	Hs.246842	ESTs	2.26	1.75
	408452	AA054683	Hs.192455	ESTs, Wealdy similar to ALU7_HUMAN ALU S	2.26	2.29
	428471	X57348	Hs.184510	stratifin	2.25 2.24	2.40 2.46
20	410541	AA065003 AI733881	Hs.64179 Hs.72472	syntenin-2 protein BMP-R1B	2.22	1.64
20	415539 425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	2.22	3.04
	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	2.22	3.24
	409178	BE393948	Hs.50915	kalikrein 5	2.19	4.74
25	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.19 2.17	7.96 3.56
23	430171 401994	AF086289	Hs.234766	skin-specific protein Target Exon	2.14	3.34
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.11	5.52
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.11	5.78
30	426150	NM_003658	Hs.167218	Bart-like homeobox 2	2.05 2.04	2.96 4.17
30	452554 443162	AW452434 T49951	Hs.58006 Hs.9029	ESTs, Wealtly similar to ALU5_HUMAN ALU S DKFZP434G032 protein	1.98	3.20
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.94	3.20
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.92	3.24
35	412507	L36645	Hs.73964	EphA4	1.92 1.90	3.06 3.18
35	410310	J02931 M13903	Hs.62192 Hs.157091	coagulation factor III (thromboplastin, involucrin	1.89	5.26
	425415 417324	AW265494	FS. 13/V91	ESTs	1.88	3.82
	412446	AJ768015		ESTs	1.88	3.36
40	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.87	3.75
40	444726	NM_006147	ı	interferon regutatory factor 6 Al905687:IL-BT095-190199-019 BT095 Homo	1.86 1.85	4.11 4.20
	424399 434346	AI905687 AA630445		ESTs	1.84	3.08
	446051	BE048061	Hs.37054	ephrin-A3	1.83	3.44
4.5	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	1.78	3.45
45	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.76 1.74	2.99 3.60
	411908 445656	L27943 W22050	Hs.72924 Hs.21299	cytidine deaminase ESTs, Wealdy simitar to AF151840 1 CGI-8	1.71	3.56
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.71	3.38
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.70	3.92
50	425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	1.68	3.25
	429299	AJ620463	Hs.347408 Hs.2340	hypothetical protein MGC13102 junction plakoglobin	1.67 1.66	2.92 3.35
	429002 421335	AW248439 X99977	Hs.103505	ARS component B	1.66	4.31
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.65	3.55
55	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.64	4.04
	414214	D49958	Hs.75819	glycoprotein M6A hypothetical protein FLJ22969	1.64 1.62	3.59 3.13
	437897 426350	AA770561 NM_00324	Hs.146170 5 Hs.2022	transglutaminase 3 (E polypeptide, prote	1.62	2.92
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	1.57	3.09
60	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.53	3.39
	427751	AF000152	11- 444250	conserved gene amplified in osteosarcoma	1.52 1.52	3.53 3.06
	416881 435013	N32520 H91923	Hs.141358 Hs.110024	ESTs NM_020142:Homo sapiens NADH:ubiquinone o	1.49	2.91
	434574		Hs.33470	ESTs	1.48	3.05
65	454478			superoxide dismutase 2, mitochondrial	1.48	3.54
	447330		Hs.18141	tadinin 1	1.46	4.48
	414583			proline arginine-rich end leucine-rich r Horno sapiens cDNA: FLJ23538 fis, clone L	1.41 1.40	2.99 3.71
	433640 427461			hypothetical protein MGC13010	1.36	2.98
70	430205			carbonic anhydrase XIV	1,36	3.14
	450798			envoptakin	1.34	3.74
	407394			gb:Homo sapiens skin-specific protein (x	1.30 1.28	3.26 3.26
	430513 411388		Hs.241586 Hs.69752	G6C protein desmocollin 1	1.20	3.64
75	431089			ESTs, Weakly similar to unknown protein	1.14	3.71
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.00	3.20
	443672			butyrobetaine (gamma), 2-oxoglutarate di	1.00	3.26
	***	enn.				
80	TABLE Pkey:		inique Eos probese	et identifier number		
	CAT m	ımber: G	ene cluster numbe	ar .		
	Access		enbank accession	u'numpeus		

	Pkey	CAT Numbe	er Accession	
	412636	1438_1	M77830 NM 0	04415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813
		_	J05211 BG698	865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164
5			BF149266 BE	940187 BIO50445 BIO50444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 #770253 BE160433 BI039775 AW886475 BA462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859
,			RE993352 RG	223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467
			BE819069 BE	819048 BI036306 BC990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265
			AW995615 BE	E814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175
10			AW847688 BE	B18280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 N847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254
10			AWU6884U AY	931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG386845 AA131128 AA099891 W39488 C04715 BF096124
			RERESSA1 AV	v799304 ALF03116 RE149760 RE705967 RE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115
			BE696084 AV	VB48371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089
15			BE713297 BE	713298 BE179915 AW799309 BF872345 BF088576 BE705939 AW752599 BC005197 BF350086 BE715196 BE715155 BF752396 831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467
13			AI100500 AIS	54403 A1303036 ALLISRA77 RIA67353 ALLIS9919 A1760816 RF082516 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963
			AI142882 AA	139975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702
			AW166R07 A	134607R W9507D AA149191 AA026R64 AIR30049 AW780435 AI078449 AI819984 AI858282 BI458588 AI860584 AI025932 AA026047
20			AA703232 AA	658154 AA515500 AW192085 AA918281 T77851 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 X782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330
20			RG681425 BI	T06/169 W19201 W02136 AW130036 AX022101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 107101 1071
			AW799118 B	F087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290
			A1686869 A15	68892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 E939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937
25			AW850878 B	ES39707 BE189700 BE714004 BE714903 BE714908 BE714705 BG350104 BE7143010 AM353131 BG350403 BE605272 BI 315305 1905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE695209 BE696210
23			RIDS94R3 RF	006273 RE872225 AW391912 RE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291
			BG961498 B	G678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837
			BG949393 B	E714441 AW996245 BE711801 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 W365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A4498487
30	445493	423456_1		1809338 AI808768 AI240593 AI915771
	416730	1988296_	1 H80564 T999	937 170802
	444083	10908_12	BI836699 AI	123195 V439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387
	408208 420223	642734_1 191648_1		9439843 AWITZT65 GEUTATT BE494329 BE302263 H39902 BE417901 BE314300 BE010733 H39300 F13301 56634 BE276324
35	417324	292720_1	BG775668 B	G680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
			BG951874 A	1572169
	412446	63467_1	BC021735 A	1669212 AL120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 A987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF962020 BF963134 BI035538 BF908052 BF908057
			BF090026 B	F943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838
40			AA617929 B	F947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
	444726	3503_2	BG285809 8	IE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 N698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327
			AWEE4EER	NGGC46 BE073294 AW297633 AA136332 AUT7322 AB16734 AT15634 AT15634 AT16434 AA877495 BF001575 A1824693 AW849604
			AWR49405 /	4W849396 AW849173 RE673179 A1611327 AA705753 BE715478 AW849414 AW849399 A1085759 A1140849 T67412 A1889885 AW104647
45			AI912495 AI	889874 A1744241 BE717113 BE717108 BE715564 A1872527 AA029457 C00338 A1469558 BE715577 AA045413 BF843813
	424399	2196_1	NM_058173 RG218084 F	AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624
			R75793 BG	202313 AI905837 BE815853
50	434346	MH1094_	14 AK056896 A	N924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AI274929 AI281211 AI821178 BC020841 BF352476 BF843140
50	427751	15028_1	8F917041 V	V80832 AA630445 BF350167 BE162052 BE931808 AI572329 BG536379 W751975 W39241 BF808798 W22600 BF082190 AA031290 R42801 H98235 H17925 AI631236 AI933786 H42736 AF000152 AU123911
	421731	13020_1	AW410526	BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 U81556
			Al422831 A	L154008 AA147822 AA873109 A1089244 A1360868 AW168024 A1819848 AA811327 A1355616 AA281629 A1880578 A1274316 AW014622
55			A1268660 A	1270283 aa171981 a1349410 aa402469 a1421985 a1004864 a1423497 a1361503 a1363096 aw805345 al539979 aa553967 aw502264 22420 a1281054 a1500699 aw342095 c75122 aw504577 a1130811 a1423567 r79086 a1860451 be222885 a1697830 a1279575 bf438693
33			AW576277	BE218210 AI952376 AA506609 AI147566 AI391690 AA991622 AI696368 AI784664 AA741555 AI002681 AW474554 AW474508 D25623
			AJ493929 A	A179800 W73566 AW411368 AA147971 AA088581 8F804510 AU145809 AU148108 AA223219 AU157840 AW169757 AI537862 N42341
			AI128667 A	W327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 A1905211 BF802713 N40338 BF752939 BE250441 H64761 BF853011 H81877 H96088 AL576453 W73585 H39990 AW438965 BF899684 A1040299 AL561879 AA293821
60	•		H27760 BC	018922 ALS33396 BE513580 BF432649 AI884985 AA404264 AW024396 AW167863 AW027036 AI302177 AI660487 AW026086 BF432564
•			BF091011	N193156 AA744623 AI859510 BI063081 BI061541 AA777036 BG058486 BI063555 AI349411 BF874521 AW139801 AI268585 AA401267
			A1905209 R	164276 N72043 AF022231 B1256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 B1041697 W192840 AW410527 A1697435 AW006631 AW504124 AL048926 A1085476 AW327855 AA459344 AW207516 AW204875 BM142514
			8F436650	AA960980 AW242609 BI012363 AW837102 BE703126 BE814612 BE837991 BE703141 BF343101 R47375 AA031413 N40264 BG027363
65			DESOSSEN I	DE301363 AA380103 DE304043 RE350630 AH147734 AH146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603
			BE857292	AJ719393 AU155418 BC770385 AA339673 BC337748 H42694 BEB34346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280
	454478	4273_16		8F304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
	407394	27110_2		
70	431089	125941_	.2 BG940189	AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	TABLE	52C:		
	Pkey:	JEU.	Unique number co	presponding to an Eos probesel
~-	Ref:		Sequence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
75				an chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
	Strand: Nt_posi	tion:		and from which exons were predicted. de positions of predicted exons.
80	Pkey	Ref	Strand	M_position
60	401781 401780			83215-83435,83531-83656,83740-83901,8423 28397-28617,28920-29045,29135-29296,2941
	402075	811740	7 Plus	121907-122035,122804-122921,124019-12416
	401760		9 Ptus	83126-83250,85320-85540,94719-95287



	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	402294	2282012	Minus	2575-3000
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
_	405542	9857564	Plus	71331-72183
5	402970	9650703	Minus	124891-125049
	400995	8099094	Plus	141186-141601
	405885	7677703	Minus	42574-42998
	404049	3688074	Minus	75765-78155
	403752	7678B57	Plus	33704-33828
10	402525	9800048	Minus	19748-20683
	404029	7671252	Plus	108716-111112
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519

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mRNA express Pkey: ExAcon: UnigeneID: Unigene Title: R1 R2

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unique number
Unique number
Unique e number
Unique gene title
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als, where the 15th percentile of normal tissue Als was
subtracted from both the numerator and denominator

	Pkey	ExAcon	UnigenelD	Unigene Title	RI		R2 11.32
	407245	X90568	Hs.172004	tiin	9.2		6.14
30	412228 426752	AW503785	Hs.73792 Hs.172004	complement component (3d/Epstein Barr vi	8.7		10.44
30	420732 418310	X69490 AA814100	Hs.86693	titin ESTs	8.6		6.49
	414522	AW518944	Hs.76325	tmmunogtobulin J chain	8.3		4.39
	433447	U29195	Hs.3281	neuronal pentraxin II	8.3		7.25
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	7.		6.70
35	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com			9.02
	428087	AA100573	Hs.182421	troponin C2, fast		45	7.65
	436485	X59135	Hs.156110	immunoglobulin kappa constant	7.3	35	6.18
	414646	AA353776	Hs.901	CD48 antigen (8-cell membrane protein)	6.	97	5.75
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	6.		6.33
40	430280	AA361258	Hs.237868	interleukin 7 receptor	6.		3.11
	449078	AK001256	Hs.22975	KIAA1576 protein			8.55
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled			5.36
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3			5.57
4.5	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3			6.40
45	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992		.72	4.76
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule		.71	5.00
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor		.69	3.84
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com		.37	4.12 6.02
50	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G		.31 .29	7.97
30	428804	AK000713	Hs.193736	hypothetical protein FLJ20706		.26	2.93
	410361	BE391804	Hs.62661 Hs.146065	guanylate binding protein 1, interferon- ESTs		.12	3.10
	445784 409461	AI253155 AA382169	Hs.54483	N-myc (and STAT) interactor		.05	3.41
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous		.59	4.00
55	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif		.47	3.92
23	453857	AL080235	Hs.35861	OKFZP586E1621 protein		.46	3.61
	428242	H55709	Hs.2250	leukernia inhibitory factor (cholinergic		.37	3.22
	414829	AA321568	Hs.77436	pleckstrin	4	1.35	3.35
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H		1.35	2.68
60	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4	1.27	2.67
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2		1.27	3.67
	441623	AA315805		desmoglein 2		4.24	3.66
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t		4.22	3.60
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam		4.20	2.58
65	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,		4.16	5.82
	430770	AA765694	Hs.123296	ESTs		4.15	5.10
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy		4.12	5.06
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletał mu		4.11	3.82
70	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito		4,10 4.04	2.68 4.10
70	432306	Y18207 X60992	Hs.303090 Hs.81226	protein phosphatase 1, regulatory (inhib		4.03	4.51
	417105	AB033025	Hs.50081	CD6 antigen		4.02	3.72
	409041 432485	N90866	Hs.276770	Hypothetical protein, XP_051860 (KIAA119 CDW52 antigen (CAMPATH-1 antigen)		3.99	4.87
	415165	AW887604	Hs.78065	comptement component 7		3.97	3.98
75	421181	NM_005574				3.96	3.19
,,	421712	AK000140	Hs.107139			3.95	7.34
	408380	AF123050	Hs.44532	diubiquifin		3.94	2.45
	422423	AF283777	Hs.116481			3.93	3.29
	408989	AW361666	Hs.49500	KIAA0746 protein		3.90	3.02
80	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin		3.84	3.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co		3.84	4.84
	424922	BE386547	Hs.217112			3.78	3.04
	400440	X83957	Hs.83870	nebutin		3.77	4.89
					551		

		•				
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.74	3.91
	450293	N36754	Hs.171118	hypothetical protein FL100026	3.74	2.89
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3; ESTs, Wealdy similar to ALUC_HUMAN !!!!	3.72 3.72	2.65 2.43
5	408548 429490	AA055449 AJ971131	Hs.63187 Hs.23889	ESTS, Wealdy similar to ALU7_HUMAN ALU S	3.71	2.23
_	414821	M63835	Hs.77424	Fc tragment of IgG, high affinity Ia, re	3.70	2.36
	419749	X73608	Hs.93029	sparo/osteonectin, owov and kazal-like d	3.67	3.30
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	3.67 2.66	6.72
10	433658 424153	L03678	Hs.156110 Hs.141496	immunoglobulin kappa constant MAGE-like 2	3.66 3.64	2.49 2.65
10	421666	AA451737 AL035250	Hs.1408	endothetin 3	3.64	5.92
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.61	2.69
	429732	U20158	Hs.2488	lymphocyte cytosotic protein 2 (SH2 doma	3.60	1.95
1.5	422173	BE385828	Hs.250619	phorbofin-like protein MDS019 (CEM15)	3.59 3.57	3.08 11.26
15	413778 442379	AA090235 NM_004613	Hs.75535 Hs.8265	myosin, light polypeptide 2, regulatory, transglutaminase 2 (C polypeptide, prote	3.56	4.91
	439859	AW292872	Hs.124554	ESTs	3.53	4.15
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.51	2.88
20	411252	AB018549	Hs.69328	MD-2 protein	3.46	1.82
20	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.45 3.42	4.65 2.47
	420286 413385	AJ796395 M34455	Hs.111377 Hs.840	ESTs indoleamine-pyrrole 2,3 dioxygenase	3.42	3.09
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.41	2.22
~-	405545			Target Exon	3.40	2.46
25	416373	AA195845		ESTs, Weakly similar to S12658 cysteine-	3.40	5.64 4.27
	417410	AF063020 AA605038	Hs.82110 Hs.7149	PC4 and SFRS1 interacting protein 1 Homo sapiens cDNA: FLJ21950 fis, clone H	3.37 3.33	2.37
	418522 433470	AW960564	113.7143	transmembrane 4 superfamily member 1	3.33	3.13
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.32	2.51
30	442149	AB014550	Hs.8118	KIAA0650 protein	3.30	2.29
	411852	AA528140	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti	3.29 3.24	3.85 2.79
	447023 421566	AA356764 NM_000399	Hs.17109 Hs.1395	integral membrane protein 2A early growth response 2 (Krox-20 (Drosop	3.23	1.78
	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	3.22	2.90
35	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.16
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.17	3.59
	424148	BE242274 AA563730	Hs.1741 Hs.277477	integrin, beta 7 major histocompatibility complex, class	3.14 3.13	2.29 3.05
	406648 429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	3.13	2.36
40	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.12	2.55
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.12	5.54
	443885	H91806	Hs.15284	ESTs	3.08 3.08	3.55 2.20
	418203 417640	X54942 D30857	Hs.83758 Hs.82353	CDC28 protein kinase 2 protein C receptor, endothelial (EPCR)	3.06	3.21
45	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	3.05	3.36
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04	2.07
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.04	2.24
	421834 444666	BE543205 BE293347	Hs.288771 Hs.11638	DKFZP586A0522 protein long-chain fatty acid coenzyme A ligase	3.03 3.01	1.91 3.43
50	425295	AA431366	Hs.37251	ESTs	3.01	3.07
• •	429109	AL008637	Hs.196352	neutrophil cytosofic factor 4 (40kD)	2.99	2.55
	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TiT3 com	2.98	5.98
	418968	NM_000078	Hs.89538 Hs.10727	cholesteryl ester transfer protein, plas	2.97 2.97	2.68 2.19
55	438914 418391	N93892 NM_003281		ESTs troponin I, skeletal, slow	2.96	2.68
•••	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	2.96	3.94
	449523	NM_000579		chemokine (C-C motif) receptor 5	2.96	4.02
	450847 418460	NM_003155	Hs.25590 Hs.85258	stanniocalcin 1 CD8 antigen, alpha polypeptide (p32)	2.96 2.95	3.24 2.73
60	426711	M26315 AA383471	Hs.343800		2.94	2.36
• • •	426559	AB001914	Hs.170414		2.93	2.17
	424528	AW073971	Hs.238954		2.93	2.70
	408633	AW963372	Hs.46677 Hs.193063	PRO2000 protein Homo sapiens cDNA FLJ14201 fis, clone NT	2.92 2.92	2.16 2.92
65	443195 425234	BE 148235 AW 152225	Hs.165909		2.90	2.09
0.5	437802	AJ475995	Hs.122910		2.90	3.71
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.90	3.56
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	2.90 2.87	2.60 2.07
70	414555 421958	N98569 AA357185	Hs.76422 Hs.109918	phospholipase A2, group tIA (platelets, ras homolog gene family, member H	2.87	3.48
, 0	420224	M84371	Hs.96023	CD19 antigen	2.86	4,77
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.85	5.44
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	2.84	2.55
75	427527	AI809057	Hs.153261 3 Hs.14453	immunoglobulin heavy constant mu interferon consensus sequence binding pr	2.84 2.83	4.16 2.97
13	446231 408838	NM_002163 AI669535	Hs.40369	ESTs	2.82	1.82
	429124	AW505086	Hs.196914	minor histocompatibility antigen HA-1	2.82	4.21
	425023	AW956889	Hs.154210		2.79	4.00
80	425388		Hs.156110	) immunoglobutin kappa constant ESTs	2.79 2.78	2.28 3.19
οv	414290 418255		Hs.71721 Hs.37251	ESTs	2.76	3.27
	451952		Hs.30166	3 ESTs	2.75	1.74
	424865		Hs.15356	3 lymphocyte antigen 75	2.75	3.10

	409245	AA361037		tRNA isopentenylpyrophosphate transferas	2.74 2.74	2.12 3.08
	453920	AI133148	Hs.36602	I factor (complement) KIAA0955 protein	2.74	2.34
	443958 434094	AA287702 AA305599	Hs.10031 Hs.238205	hypothetical protein PRO2013	2.73	1.67
5	436476	AA326108	Hs.33829	bHLH protein DEC2	2.72	1.70
	428398	A1249368	Hs.98558	ESTs	2.72	2.06 2.55
	417141 427080	U22662	U- 201176	nuclear receptor subfamily 1, group H, m ras-related C3 botulinum toxin substrate	2.70 2.69	3.15
	442485	AW068287 BE092285	Hs.301175 Hs.29724	hypothetical protein FLI 13187	2.69	1.99
10	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	2.69	1.70
	443998	AI620651	Hs.296276	ESTs	2.69	2.30
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	2.68 2.68	3.23 3.01
	414291 448861	AL049951	Hs.13040 Hs.22370	G protein-coupled receptor 86 Homo sapiens mRNA; cDNA DKFZp564O0122 (!	2.66	2.51
15	432435	BE218886	Hs.282070	ESTs	2.65	3.28
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	2.65	3.04
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	2.64 2.64	3.82 1.9.7,
	414696 420991	AF002020 AW504814	Hs.76918 Hs.287379	Niemann-Pick disease, type C1 Homo sapiens mRNA for FLJ00111 protein,	2.64	2.51
20	401566	A11304014	113.201313	NM_005159:Homo sapiens actin, alpha, car	263	3.74
	444119	R41231	Hs.184261	ESTs, Wealty similar to T26686 hypotheti	263	2.13
	425231	AA527161		ESTs	2.61 2.61	2.95 1.90
	417427	M90391 Al358105	Hs.82127 Hs.123164	interleukin 16 (lymphocyte chemoattracta ESTs, Weakly similar to match to ESTs AA	2.60	4.45
25	437669 413856	D13639	Hs.75586	cyclin D2	2.60	5.71
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.59	2.68
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.58	2.77 9.28
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro lg superfamily protein	2.58 2.58	9.20 4.49
30	443021 424779	AA368546 AL046851	Hs.8904 Hs.153053	CD37 antigen	2.58	3.88
50	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.57	2.09
	424265	AF173901	Hs.144287	hairy/enhancer-of-split related with YRP	2.57	3.57
	426780	BE242284	Hs.172199	adenylate cyclase 7 sotute carner family 37 (glycerol-3-pho	2.57 2.56	1.86 2.90
35	452721 442904	AJ269529 AW575008	Hs.301871 Hs.11355	thymopoietin	2.56	3.39
	433646	AA603319	Hs.155195	ESTs	2.54	2.19
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.53	4.56
	422640	M37984	Hs.118845	troponin C, slow	2.53 2.53	5.38 2.08
40	448413 429536	AI745379 AA873016	Hs.42911 Hs.206097	ESTs oncogene TC21	2.52	2.49
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.52	3.46
	424378	W28020	Hs.167988	neural cell adhesion molecule 1	2.52	2.91
	410257	BE244044	Hs.61469	hypothetical protein	2.51 2.51	3.67 3.11
45	427609 424868	AK000436 AI568170	Hs.179791 Hs.96886	hypothetical protein FLJ20429 ESTs	2.51	230
73	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.50	264
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.50	3.04
	413441	AJ929374	Hs.75367	Src-like-adapter	2.49 2.49	2.37 1.82
50	414761 429493	AU077228 AL134708	Hs.77256 Hs.145998	enhancer of zeste (Drosophila) homolog 2 ESTs	2.49	2.40
50	419631	AW188117	113.143330	popeye protein 3	2.48	1.85
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.48	2.32
	421552	AF026692	Hs.105700		2.47 2.47	4.17 2.62
55	420158 453987	AI791905 AA323750	Hs.95549 Hs.235026	hypothetical protein Homo sapiens, clone IMAGE:4247529, mRNA,	2.47	2.49
33	429640	U83508	Hs.2463	angiopoietin 1	2.47	2.57
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA OKFZp761J1112 (f	2.46	2.42
	426969	AI936504		CDC-like kinase 1	2.46 2.46	2.41 2.17
60	427674 405547	NM_003528	Hs.2178	H2B histone family, member Q NM_018833":Homo sapiens transporter 2, A	2.46	2.84
00	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	2.45	2.69
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	2.45	3.40
	428746	AW503820	Hs.192861		2.43 2.39	6.25 4.01
65	453953 427759	AW408337 BE245578	Hs.36972 Hs.2200	CD7 antigen (p41) perforin 1 (pore forming protein)	2.39	4.56
03	443071	AL080021	Hs.8986	complement component 1, q subcompone	2.39	3.31
	437211	AA382207	Hs.5509	ecotropic viral integration site 28	2.38	3.15
	440596		Hs.103378		2.37	3.68 4.08
70	452651 421563		Hs.30209 Hs.105806	KIAA0854 protein grandysin	2.36 2.34	3.25
70	421924		Hs.109606		2.33	3.38
	449092	U91641		alpha2,8-sialyttransferase	2.32	3.53
	425367		Hs.155975		2.32	7.02
75	418117		Hs.83496	linker for activation of T cells	2.30 2.26	3.56 3.42
13	425795 428111		Hs.15954 Hs.2243	B EDG-6 (endothetial differentiation, G-p B tymphoid tyrosine kinase	2.25	3.69
	439981		Hs.12467	5 ESTs, Wealdy similar to T14742 hypotheti	2.25	4.05
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.25	3.44
90	436648		Un 20002	ESTs	2.24 2.23	3.23 3.08
80	452250 441715		Hs.28607 Hs.34265	hypothetical protein A-211C6.1  Homo sapiens cDNA FLJ13289 fis, clone OV	2.23	3.30
	423397			chemokine (C-C motif) receptor 7	2.22	3.25
	449626		Hs.30163		2.21	3.14

				_		
	412975	170956	Hs.75106	clusterin (complement lysis inhibitor, S	2.18	3.41
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.15	3.62 5.21
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2 (ICAM	2.09 2.07	3.81
5	436420 418174	AA443966	Hs.31595 Hs.83656	ESTs  Rho GDP dissociation inhibitor (GDI) bet	2.05	3.14
,	420626	L20688 AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.01	4.42
	428289	M26301	Hs.2253	complement component 2	2.00	3.33
	429683	AF148213	Hs.211604	a disintegrin-like and metalloprotease (	2.00	3.75
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.96	3.68
10	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	1,91	4.84
	416445	AL043004	Hs.79337	KIAA0135 protein	1.91	3.41
	409817	BE295464	Hs.56607	Williams-Beuren syndrome chromosome regi	1.87	3.53
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.86 1.85	3.55 3.79
15	437740 437938	AA810265 A1950087	Hs.122915	ESTs gb:wg05c02.x1 NCt_CGAP_Kid12 Homo sapien	1.83	3.42
13	425240	AA306495	Hs.1869	phosphoglucomutase 1	1.83	3.75
	406972	M32053	10.1003	gb:Human H19 RNA gene, complete cds.	1.80	4.03
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	1.78	3.53
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	1.78	3.39
20	416350	AF188625	Hs.189507	phosphotipase A2, group IID	1.78	5.48
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	1.78	4.88
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.77	5.79
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.74 1.74	3.41 3.80
25	427278 418618	AL031428 U66097	Hs.174174 Hs.86724	KIAA0601 protein GTP cyclohydrolase 1 (dopa-responsive dy	1.73	4.21
23	420397	NM_007018	Hs.97437	centrosomal protein 1	1.73	3.21
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.73	3.77
	459245	BE242623	Hs.31939	manic fringe (Drosophila) homolog	1.72	3.12
••	425356	BE244879	Hs.155939	inositol polyphosphate-5-phosphatase, 14	1.71	3.55
30	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.70	7.70
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.70	3.10
	451579	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.68	4.19 5.76
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	1.68 1.67	3.17
35	416819 409896	U77735 AW205479	Hs.80205 Hs.279780	pim-2 oncogene NY-REN-18 antigen	1.67	3.74
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.66	3.62
	426666	AW500131	Hs.171763	CD22 antigen	1.65	4.67
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.65	3.43
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.64	3.66
40	430449	AA352723	Hs.241471	RNB6	1.62	3.09
	424661	M29551	Hs. 151531	protein phosphatase 3 (formerly 28), cat	1.61	3.37
	453027	AI879341	Hs.539	ribosomal protein S29	1.61 1.60	11.60 3.28
	410068 440446	AI633888 NM_013385	Hs.58435 Hs.7189	FYN-binding protein (FYB-120/130) pleckstrin homology, Sec7 and coiled/coi	1.59	3.14
45	453657	W23237	Hs.296162	AD037 protein	1.59	3.12
	418102	R58958	Hs.26608	hypothetical protein MGC15880	1.58	3.55
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.58	3.07
	406791	A1220684	Hs.347939	hemoglobin, alpha 2	1.55	5.06
60	421703	AI936513	Hs.1416	Fc fragment of IgE, low affinity II, rec	1.53	3.59
50	421859	AA356620	Hs.108947	KIAA0050 gene product	1.52	3.41 3.28
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	1.52 1.47	3.26 3.34
	456086 425783	AL161999 AI026740	Hs.77324 Hs.1948	eukaryotic translation termination facto ribosomal protein S21	1.46	4.95
	407682	AL035858	Hs.3807	FXYO domain-containing ion transport reg	1.46	3.48
55	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	1.45	3.25
	435624	AF218942	Hs.24889	formin 2	1.45	3.11
	413969	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidylin	1.45	3.33
	426530	U24578	Hs.278625		1.44	4.27
60	425928	S55736	Hs.238852		1,44 1,43	3.65 4.01
OU	418219 429071	AA731836 AW794126	Hs.137319 Hs.195453		1.43	4.23
	418473	AA243335	Hs.309943		1,41	3.29
	423766	AA303799	Hs.300141		1.40	3.22
	430150	L05148	Hs.234569		1.39	3.29
65	416370	N90470	Hs.203697	CD38 antigen (p45)	1.36	3.08
	406758	AA552326	Hs.77039	ATP synthase, H transporting, mitochondr	1.32	3.29
	448610	NM_006157		nel (chicken)-like 1	1.31	3.85
	444674	BE562200	Hs.244	amino-terminal enhancer of split	1.30	3,10
70	407694 427349	U77594 AA360154	Hs.37682 Hs.177415	refinoic acid receptor responder (lazaro Finkel-Biskis-Reitly murine sarcoma viru	1.30 1.28	3.91 3.59
, 0	419032	W81330	Hs.99877	ESTs, Highly similar to JAK3B [H.sapiens	1.28	3.21
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.27	4.00
	415138	C18356	Hs.295944		1.24	3.25
	406623	X69392		ribosomal protein L26	1.24	3.31
75	437895	AB014558	Hs.5898	KtAA0668 protein	1.21	3.33
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing le	1.18	3.35

TABLE 538:

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Genbank accession numbers

Pkey CAT Number Accession



5	441623	3362_1	BC022413 BE395396 BF754175 AAS06621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AJ337912 AU390244 AW090300 BE219837 AI623661 BE501576 BE501734 AJ742232 AJ023964 A4458424 AA975373 AJ288904 AJ89483 AA890325 N32562 AJ358102 AW371694 AJ038448 AJ672071 AU018393 AA576391 AA977374 AW189392 W37448 AA612894 AJ277548 H89551 AI699774 H89355 AA315805 AW579186 BC014584 BC014581 AW780125 AB72414 BE328145 AW60919 BC03306 AW172758 BE708322 AA345675 BE875779 H28241 H28318 BF540913 BG175688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822
	416373	3442_1	A122760 BE718200 AW887496 AA149420 BE706307 BE533995 BE748765 A1373633 R75904 BF979185 BF691393 BC495595 BI094458 BE706702 BC496559 BF248373 BC494800 AK056582 AW755525 AL596757 BF827376 BF827373 BF827375 BF827369 BF826900 F01252 BC022888 BI850312 AA195845 BF825671 BF574821 Z21656 F32854 AA211780 F21569 A1288453 A1803678 AA180309 A1074627 AA192950 AA661688 F36698 F32290 F28773 F22692 AA424993
10	433470	6624_1	AW340328 AA192247 BF672229 BF575143 BF673106 BF693623 X75684 AL573167 AU45461 AU453743 AU993655 AI564644 AA977180 AI694111 AI591358 AW071625 AIG78712 AI720939 AI927759 BE439795 AJ963432 AA292956 AW192593 AI856838 AI696905 AU424384 A161312 AI911921 AI597801 BI494959 AI240988 AU492554 AW262737 BE044033 AW07870 AW679636 RU49458 AAA78439 AA76657 BF727870 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186
15			AAQ43217 BE219784 A179814 AA129575 A1671727 A1470033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW775048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1592846 A1061065 H80983 R79933 A1950893 A143632 A1349380 AA148284 A1788502 AA487893 A1671320 AW194272 C063365 AA953883 BE858936 A1918523 A1672628 A1927217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A1363829 A1693030 AA603586 BE773488 AW333301
20			BE773489 BE773462 BE773495 AI650338 BE773499 A7745717 BE811475 BE811470 BE811464 BE811419 BE811410 BE811409 BE811399 BE811389 BE811332 BE773301 BE773494 BE773486 BE773474 BE773470 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW6734145 CONTRO JERGOSAD DRTSSS AI468237 AI437033 AA498962 R21752 BP002457 AA588237 AIL574095 AL576200 AL571074 AL574525
25			AL578810 BG498381 AI528364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811390 BE811399 BF991711 BF757734 BE925037 A3777596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 A1744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI25230 AA948565 BE706942 BE156360 T65026 AW742958 AW197954 BE905184 AA722206 AI344943 AI346877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242
30			AN343943 AL34887 AL34880 BE-21857 BE 158280 AAA390427 T91782 AAQ35075 AAB37326 T10930 BF906587 BIT55027 BC506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BIZ59821 BG741786 BI868522 AU135866 BI552770 BIZ59210 BIZ56520 BIZ55559 BC4885098 BIZ59228 BC498501 BBA044512 AU133984 AL556586 BE745111 BIZ22633 AU133917 BC288151 BIZ60715 BIS50550 BG500773 BIS51761 BG707601 BB18593 BF691383 BG721129 BG541578 BE206666 BG751098 BIZ24133 BG40746 BG478055 BE730436 AW080233 AU137549 BC429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BIZ560895
35			AW651691 BM048974 BM043805 BG142185 AA315188 AH46615 C06300 BG49764 AA088544 AB15987 BG528631 BE519182 AW2.9185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BB870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF700713 BG788075 BF788864 AA21353 B721870 AA011722 T975755
40	409245	3199_2	AF030234 BC017465 BC008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI869732 R66856 H01374 BI257369 BI259830 AW960845 BM466232 AW956813 BE766847 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 A695683 BG505078 AV654024 BF093291 AW0721929 H22650 AA499715 BC49650718 BI254209 BC499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BC490948 W37195 BF372041 BE883796 BF537202 BF367329 BF909744 AW366003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 A435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189661 AI221962 AI378034 AW118897 AW665247 AW340077
45			N11605 AA77819 AA683875 AB58250 AA463379 A1292305 BED45947 AA971089 A1125820 BG940947 A1080745 AA884934 A1125/02 A138633 AA931835 A135631 AW439905 A1027833 A1399648 A014533 AA347831 AA738251 N67374 N69481 A1768667 AA948472 A819214 AA293133 A1186725 AA889214 A1222635 B1495143 N29605 N48812 AA769041 A1492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12455 BG\$34562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 B1255749 B1492848 H16217 H21980 H22651 H88179 H87354 H44052 H23155 H44128
50	417141	9517_1	A391712 UZ2662 NM_005693 AW166878 BF339795 A1970974 A1521157 A1336082 AW339789 A1288682 BF477594 BF477593 A1703008 A1290961 A1049684 AW770753 A1208561 A1699406 F33996 AA630563 A1985346 A1927058 AA533882 AW204589 A1206938 AW590068 A1263769 AA991550 A192005 A1559946 A1524373 A1516239 A1560848 A1580658 A1719135 AW026500 A1698217 A1872977 A1670983 A1654870 AA493407 AA548525 A1016420 AA843563 W15576 H61726 AA913245 BF438146 A1524338 B1762380 AU136488 B1759892 AV655930 T78977 B1524075 BE538944 AA527161 BG211784 AA527065 AA505489 AW512550
55	425231 419631	235504_1 2743_1	BC022323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA661832 H84897 AI382294 AA662874 AW993380 BE813742 H84368 A1188074 N20482 HR4369
	426959	12113_1	M59287 AI936504 AI694705 AI679216 AI679235 BF110184 AW518110 AI679811 AW054981 BE455531 BE327409 AW339105 BI714787 AI871568 AW179115 AUAG080 AI232300 AW139086 AA387771 BC654699 AU144657 RE437422 AI478374 AA492513 AU157562 AI826962 AU145528
60	•		A951093 AW513819 AA042856 AA725690 AA733176 A1028702 A1251890 AIB11729 AW975208 AW339589 A1147668 AU157862 AA629327 BF476670 BE464795 AW510511 AA399098 AA398210 A1291988 A1160296 AU158075 N34811 BE326407 A1270528 AA496923 AA50802 A1270284 A1139504 BF437009 A1354626 A19363336 AA287250 AA491853 BF445818 AA688026 AA2847510 AW151054 AA412072 AA709241 H89332 BF445769 BF989466 BF989472 AA631105 A1129915 W85362 AA515277 AA541513 L29222 AV758119 D62109 AL00456 BE2444413 AV64586 D6246321 BE246314 D82116 AL036176 AA331779 AU100106 BE243857 AU076865 AW972327 AA497087 A1687039 AW072798 A1174455 AU156788 AA044001 AA046086
65			BE244986 AI634456 BE242945 BE242093 AU156034 BE244982 AL567955 BI005141 AA040426 AW630506 BF155668 AU118544 BG573573 W96436 AA373395 BE710347 AL564154 AI708332 AA729530 N9Z729 AI573015 T29655 N89333 H85847 AI886473 AW189990 ND2905 AI811986 AU157753
	406678 449092		W86829 A020844 AU158204 AA057356 AA283466 AA405504 AA017027 W94754 AA226498 W72391 H66461 C00442 H01925 BI912232 U77534 U77534 U77537 AK056270 AV706896 AI692935 AI681140 AW162481 AW087114 AW157019 AI689795 AW251085 AW266911 BF438207 AW134945 BE041668
70	436648	_	BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AI929731 AW161524 R43753 BE779688
75	437938	66997_1	H10426 R11851 T65264 R18737
80	406623	0_0	X69392 T24055
30	TABLE Pkey:	<b>53C</b> :	Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Ref:

Nt_position:

Strand 405545 1054740

Nt_position 118677-118807,119091-119296,121626-12182 96277-96420,96979-97160 124361-124520,124914-125050 Plus Minus Plus 401566 405547 8469090 1054740

10

TABLE 54A: ABOUT 161 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER

Table 54A fisis about 161 genes upregulated in primary metanomas from tumors that later metastasized relative to primary metanomas that did not metastasize later. These genes were selected from 59680 probasets on the Ecos/Affymetrix Hu03 Genechip array. Gene expression data for each probaset obtained from this analysis was expressed as average intensity (Af), a normalized vature reflecting the relative level of mRNA expression.

Pkcy: Unique Ecos probaset identifier number

ExAcon: Exemplar Accession number, Genbank accession number 15

Unigene number

20

UnigenelD: Unigene Title: R1: Unigene gene title

Whigene gene title

Whigene gene title

Whigene gene title

White gene title

Whit R2:

25	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.15	3.41
	413916	N49813	Hs.75615	apolipoprotein C-II	5.93	6.55
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	5.64	2.98
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	5.03	4.56
30	440274	R24595	Hs.7122	scrapie responsive protein 1	4.98	4.83
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	4.96	7.07
	427882	AA640987	Hs.193767	ESTs	4.68	4.68
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.29	3.06
20	407907	A1752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	3.94	3.86
35	424410	W79027	Hs.271762	ESTs -	3.67	3.19
	429083	Y09397	Hs.227817	BCL2-related protein A1	3.46	2.49
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	3.31	3.06
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.27	2.12
40	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.22	2.69
40	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.20	1.85 4.61
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.18	2.11
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.13	3.31
	430643	AW970065	Hs.287425	MEGF10 protein	3.10	3.31
45	412262	W26406		seven in absentia (Drosophila) homolog 1	3.06	3.94
43	438328	AJ492261	Hs.32450	ESTs	3.05	2.65
	409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	3.01 2.94	1.86
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.91	3.70
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.88	2.53
50	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	2.88	2.00
ου	453935	AI633770	Hs.42572	ESTs	2.84	6.47
	452689	F33868	Hs.284176	transferrin	283	4.74
	449550	AA353125	Hs.184721	ESTs	2.82	2.43
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.82	2.08
55	438898	AI819863	Hs.106243	ESTs	2.80	2.69
33	430191	A1149880	Hs.188809	ESTs	2.79	1.75
	408418	AW963897	Hs.44743	KIAA1435 protein	2.77	3.40
	450157	AW961576	Hs.60178	ESTs	2.77	4.28
	420380	AA640891	Hs.102406	ESTs	2.75	2.88
60	443172	AW662964	Hs.199061	p300/CBP-associated factor histone deacetylase 3	2.72	2.24
OO	456629	AW891965 AI928445	Hs.92254	synaptotagmin-like 2	2.72	1.93
	407857	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.68	2.59
	421097	AI690734	NS. 123232	Homo sapiens cDNA: FLJ22562 fis, done H	2.67	2.79
	436280			gb:H.sapiens mRNA for CD58 T7 protein.	2.65	1.98
65	407550 427871	Y10515 AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.64	1.76
05	427899	AA829286	Hs.332053	serum amyloid A1	2.59	3.01
	442793	AI017798	113.332033	ESTs. Weakly similar to TI47_HUMAN CARGO	2.58	1.60
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.57	1.91
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.57	2.13
70	458247	R14439	Hs.209194	ESTs	2.56	2.61
,,	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.52	2.74
	433980	AA137152	Hs.285049	phosphoserine aminotransferase	2.51	1.88
	412719	AW016610	Hs.816	ESTs	2.50	1.68
	441789	052059	Hs.7972	KIAA0871 protein	2.50	3.11
75	405885	032033	119.7572	Target Exon	2.50	3.15
,,	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.48	3.33
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	2.48	1.66
	450202	AW969756		ESTs, Weakly similar to B49647 GTP-bindi	2.47	2.79
	436825	AW341123		ESTs	2.47	2.55
80	424762		Hs.183684	eukaryotic translation initiation factor	2.42	2.28
00	432426	AW973152		ESTs	2.42	1.76
	409095	AW337272		ESTs, Moderately similar to S72481 proba	2.41	2.41
	403752		113,250000	NM_002753*:Homo sapiens mitogen-activate	2.41	2.87
	403/32			Zanaa an anna andamina mendicinanana		

	40					
	404489	A + CCCCCCC		Target Exon	2.39	1.97
	411690 439195	AA669253 H89360		RNA, U2 small nuclear	2.37	2.54
	453582	AW854339	Hs.33476	gb:yw28d08.s1 Morton Fetal Cochlea Horno hypothetical protein FLJ11937	2.37 2.36	2.27 2.81
5	438461	AW075485	Hs.286049	phosphoserine aminotransterase	2.35	2.01
•	432878	BE386490	Hs.279663	Pirin	2.35	2.28
	416647	BE297139	Hs.79411	replication protein A2 (32kD)	2.33	1.97
	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	2.32	2.92
10	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	231	2.63
10	421282	AA286914	Hs.40782	ESTs	2.31	1.85
	434418	AF134707	Hs.278679	a disintegrin and metalloproteinase doma	231	2.21
	413204	BE071603	000700	gb:QV3-BT0510-161299-032-03 BT0510 Homo	2.31	1.49
	449720 451838	AA311152	Hs.288708	hypothetical protein FLJ21562	2.30	1.78
15	410943	AW005866 AW968322	Hs.193969 Hs.11156	ESTs	2.28	2.05
13	459711	BE386801	Hs.21858	tow motecular mass ubiquinone-binding pr binucleotide repeat containing 3	2.28 2.27	2.39 2.39
	429489	AF008203	Hs.204039	aristatess-like homeobox 3	2.26	1.97
	429493	AL134708	Hs.145998	ESTs	2.26	2.77
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.26	1.78
20	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	2.26	1.84
	419352	A1675008	Hs.199493	ESTs	2.25	1.47
	427393	AB029018	Hs.177635	KIAA 1095 protein	2.25	1.83
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	2.24	2.42
25	433468	AA832055	Hs.172843	ESTs, Wealthy similar to ALU1_HUMAN ALU S	2.24	1.76
23	452782 443910	AA028166	Hs.17733	ESTs Set-	2.24	2.34
	408832	AW051711 AW085690	Hs.132440 Hs.63428	ESTs ESTs, Wealdy similar to 2195_HUMAN ZINC	2.24	1.79
	407283	T51008	F15.03420	gb:yb55e08.s1 Stratagene ovary (937217)	2.22 2.22	1.52 1.31
	437376	AA749400	Hs.257890	ESTs	2.22	2.44
30	450712	AI732130	Hs.270496	ESTs, Wealdy similar to ALUB_HUMAN !!!!	2.22	1.62
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	2.22	2.36
	445183	AB007877	Hs.12385	KIAAQ417 gene product	2.20	1.84
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.20	1.76
25	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.19	1.59
35	414900	AW452420	Hs.248678	ESTs	2.18	1.89
	427704	AW971063	Hs.292882	ESTs	2.17	1.86
	404942	A140471C4	Un 100041	splicing factor, arginine/serine-rich 9	2.17	1.86
	448019 459254	AW947164 AA694386	Hs.195641 Hs.290914	ESTs, Moderately similar to 138022 hypot ESTs	2.17	1.64
40	418965	A1002238	Hs.11482	splicing factor, arginine/serine-rich 11	2.16 2.16	1.61 1.79
	443357	AW016773	1402	fow molecular mass ubiquinone-binding pr	2.16	2.32
	412432	AA126311	Hs.9879	ESTs	2.15	2.73
	449567	AJ990790	Hs.188614	ESTs	2.08	2.85
	433179	AW362945	Hs.162459	ESTs	2.07	4.77
45	408243	Y00787	Hs.624	interleukin 8	2.05	3.12
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.97	2.89
	449656	AA002008	Hs.188633	ESTs	1.94	3.60
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.93	2.76
50	445162 419356	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	1.93	2.66
20	424263	A1656166 M77640	Hs.7331 Hs.1757	hypothetical protein FLJ22316	1.92 1.89	3.39
	414694	NM_015362	Hs.76907	L1 cell adhesion molecule (hydrocephalus HSPC002 protein	1.88	3.10 4.25
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	1.87	2.66
	409105	AW467539	Hs.255877	ESTs	1.87	2.96
55	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	1.85	2.80
	404149			C6002509*:gij5031885[ref]NP_005568.1] ii	1.84	2.93
	406387			Target Exon	1.82	2.96
	420871	AA702972	Hs.65300	ESTs	1.76	3.12
60	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.75	3.12
oo	418751 412347	BE389014 AW970026	Hs.73818	phosphoinositide-3-kinase, regulatory su	1.70	3.20
	413211	AW967107	Hs.109274	ubiquinol-cytochrome c reductase hinge p hypothetical protein MGC4365	1.67 1.66	3.65
	459317	BRCA1b	113.103214	Eos Control	1.61	2.89 7.34
	425525	AA358883	Hs.23871	ESTs	1.59	2.67
65	436823	AW749865	Hs.117077	ESTs, Weakly similar to 138022 hypotheti	1.56	2.76
	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.55	2.76
	424389	AA339786		lymphocyte-specific protein 1	1.53	2.95
	426672	AW270555	Hs.171774	hypothetical protein	1.51	3.39
70	415977	AL037622	Hs.78935	methionine aminopeptidase; elF-2-associa	1.47	2.65
70	404780			Target Exon	1.43	2.77
	436476	AA326108	, Hs.33829	bHLH protein DEC2	1.41	3.04
	428284	AA535762 AA486794	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.38	2.94
	448571		Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	1.37	2.80
75	428156 447752	BE269388 M73700	Hs.182698 He 105938	mitochondrial ribosomal protein L20	1.36	3.29
	447455	H38335	Hs.105938 Hs.6750	lactotransferrin Homo sapiens mRNA for FLJ00058 protein,	1.35	2.70 3.03
	453281	W46280	Hs.55940	ESTs, Weakly similar to A25704 synapsin	1.35 1.34	3.03 2.69
	413142	M81740	Hs.75212	omithine decarboxytase 1	1.33	2.09
••	407194	AA621644		gb:af54a01.s1 Soares_total_fetus_Nb2HF8_	1.32	2.70
80	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.26	3.27
	406797	AI432224		ribosomal protein L6	1.26	2.72
	406711	N25514	Hs.77385	myosin, light polypeptide 6, atkati, smo	1.25	7.10
	414608	BE396215	Hs.76572	ATP synthase, H transporting, mitochondr	1.24	2.72



	401846			NM_000988*:Homo sapiens ribosomat protei	1.24	2.82		
	432982	AA531058	Hs.182248	truncated calcium binding protein	1.23	3.10 2.74		
	428578	BE391797	Hs.343588	ribosomal protein \$12	1.23			
_	400199			Eas Control	1.21	3.58		
5	400079			Eos Control	1.20	2.99		
	412623	R28898	Hs.74170	metaflothionein 1E (functional)	1.19	263		
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.19	4.15		
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	4.75		
10	442492	AA528489	Hs.234518	ribosomal protein L23	1,17	274		
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.17	3.15		
	435398	H87136	Hs.5174	ribosomal protein S17	1.16	3.22		
	432205	AI806583	Hs.125291	ESTs	1.15	2.76		
	406859	AI581134	Hs.181357	taminin receptor 1 (67kD, ribosomal prot	1.09	2.66		
	401254			Target Exon	1.00	3.08		
15	405752			Target Exon	1.00	2.87		
	445772	AI733941	Hs.145493	ESTs, Wealthy similar to ALU7_HUMAN ALU S	1.00	2.70		
	452916	AA642831	Hs.31016	putative DNA binding protein	1.00	2.62		
	451411	AA017492	Hs.135655	EST	1.00	2.64		
20	415658	BE501921	Hs.270471	ESTs	1.00	2.82		
20	448610	NM_006157	Hs.21602	nel (chicken)-like 1	1.00	<b>3.30</b> · ·		
		TABLE S4B:						
		Pixey: Unique Eos probeset identifier number						
25	CAT numb		ne cluster number					
25	25 Accession: Genbank accession numbers							
	Pkey		r Accession			1004440 ALECTICE ALTOHASO AAGCATTO AAGCOCC ALTESDAD		
	412262	4362_1	AK056051 AI971	258 A1681134 AU146134 A1803300 AA917325 AA9236	903 BF 890U08 A	U304442 A1167464 A1284188 AA054272 AA829262 A1351910		
20			T90930 AJ886230	U70056 AU119916 BF446537 BE503207 BE502849	A10981U2 AA25	8553 AV718529 AV719917 BF724133 BI438668 AI804000		
30		BE349103 AI912294 BE645117 AA227954 AA446520 AA879147 AA281770 AW136872 AA807907 AI435989 AI339626 AI383274 AA418512 BE771804						
		BF894509 AA455093 A1379061 A1150855 BF769906 R17298 AU138740 BF808607 BE674633 AV700132 AA227789 AA253099 AW975199 AA935418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810 R42784 R44804 R41278						
					00/06 AA 10132	[] K41205 H14412 WYS22044 W24010 K45104 K44004 K41510		
	409760	865166_1	AA302840 T9301	6 T92950 AU184997 AA077551		FORKERWA OKONTO A STROOMS CONTOURS AND ASSESSMENT		
25	453912	32562_3	BM472224 B1966	849 BI966735 AW973032 BI962894 BI963048 AA548	765 AI9205U4 A	AD41551 AW043754 AI086702 AW008105 AA974849 AW614893		
35				6996 AW262982 AI580991 BF726843 AV693312 W353	325 AAU39927 I	BG460936 AW388482 AW388420 BF374777 W01360 N94710		
			H87967			**************************************		
	456629	207_22	AW891965 AW6	04749 BE080872 R15559 BE177623 AW883520 AW94	15343 AIZ4616	7 T07082 AW805679 W96278 AA135796 W32615 AW995418		
			AW801688 BE00	3837 AW801621 AW385721 AW385742 AW385714 A	W604757 W8/	109 AW604738 AW385757 AW580796 AW801247 BE003239		
40			BE003183 AA84	7112 AW580975 AW604760 AW385727 BE164590 BE	003090 AW362	791 AW604759 AW866589 AW604758 N44337 AI378548		
40			AW890438 AA07	7172 AI288683 AA229639 AA091945 AW945454 AAU	63629 AA/U25	04 AW861938 AW894816 AW580841 AA094372 T06399		
			AW885686 BE244086 BE005035 AW851913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE08742 BE067470 AW894935 BE082529 AI248811 BE178917 BE002200					
			AA248197 AW38	11373 AW177325 AW806879 AA935217 BE067498 BE	083742 BE067	470 AW894935 BE082529 AI248811 BE179917 BE002200		
			AWENTER AWS	02880 AWROASEN AWRR13EN AIQNA206 AWRE3533 CX	00609 AW38 13	LS RE085230 WM888150 RE012353 WM285139 WM001450		
			AI695314 BE083	790 AW858568 AW945550 BE177153 AW970506 BE	350419 Al9069	19 AW360794 AI906917 AW885979 AW794240 AW945566		
45			AI688683 AI688	694 AW009660 AW601421 AW360793 BE066524 BE0	83901 AW3698	47 AW381871 AW935435 AW664582 AW877775 AW838449		
•			DE 180AES AWR	BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717				
			BE011715 BE16	7842 BE011718 BE011724 AW363639 AW878658 AV	/878662 AW89	1887 BE082356 AW389211 AW804286 AW610312 Al904717		
			AW610318 AW9	96909 AW610296 AW901923 AW880003 AI762171 A	W062582 AW31	8713 AW062593 AW176663 AW842064 AW842089 AW842095		
			A1243049 AW90	2074 AW062592 AW176664 AW751692 BE087703 A!	907439 BE0098	86 BE172115 BE077030 AW608556 AW835577 AI909628		
50			BE077029 AW1	BE077029 AW176241 BE077552 BE 160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 A1907484 BE172821				
			AW606768 AW9	AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999878 A1124870				
			BE163472 AW8	BE163472 AWR41823 AW379762 AW893237 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008 BE178350 BE178214 BE063291 AW820236 AW999663 BE089486 BE173126 BE171775 BE185787 AA558280 A1174840 AW999112 BE218391				
			BE178350 BE17	8214 BE063291 AW820236 AW999653 BE089486 BE	173126 BE171	775 BE 185787 AA558280 AI174840 AW999112 BE 216391		
			BE172734 BE17	18021 BE172738 BE173324 AW603494 AL036722 R3	3192 R60905 H	53721 H41052 AL037917 R37795 AW998972 AA767189		
55			AW044272 H50	689 AA768399 AA767764 A1087888 H44202 BE22279	2 N90597 W81	396 N90615 AI935353 BE501168 F10945 AW118215 AI970480		
			Al627641 AW23	16081 AA574090 A1627652 A1681913 A1759983 N6959	1 N69276 BE46	77722 AW392780 BE172467 H92861 AI524921 F02989 Z39328		
			F02705 F01414	T88678 AJ215165 H87220 AW374781	<b></b>	****** ******* BEGINSTO A 10004FO A 1007097 & 100FDCO		
	436280	36296_1	AK026215 Al20	1248 BE671206 AA860436 AA730787 AA834507 D79	304 079806 AV	/961628 AI017068 BE044373 AA322458 AA987927 AA385869		
					W707819 A169	0734 R79189 AI535900 AW589301 AI128434 BE838011 BE837891		
60			BF894555 H954					
	442793	417820_2	BG741247 BG7	41022 AI017798 AI953594 AW445065 AI245087				
	411690	53926_1	AK027091 BF5	14593 8F768430 BI037830 BE175161 BG000114 BG8	19/1/1 AA/453	91 AA669569 AA669253 BI049453 BE304449 BG010136		
				91358 BF762561 T56173 BC003629 BF091330 BE697	323 BF091340	RE042220 WAI 44 IOU WAI 4041 I 4450510 DI031031		
	439195	21979_1	AF086037 H893					
65	413645	1234345_1	1 AA 130992 AW9	69537 AA503835				
	413204	1494523_1	BEO/1616 BEO	71613 BE071603 BE071587 BE071607 BE071615 BE				
	443357			54600 AI052778 BG057892 AW016773 AI452937 AW	085293			
	455797	1511159_	1 BE091833 BE0	91874 BE091871	1744E00 AMAE	0447 AA843698 AW188066 AW007171 AW007027 AI075008		
			REFORMAL REL	59368 AI937311 AU151256 AW341542 AW <i>214</i> 231 AV	とうきょうひつろ ヤイトカラ	D441 WVD47030 W44 (00000 W4100) 11 1 W44001051 W012000		
70	418751	21393_1	01 000111 001		OFO4F A 467704	NO ANNATOCIO ANTOCCON AARTOCON AINOADIG AINOSIRR AADSEGGR		
70		21393_1	AI 520351 AAR	neggo awusuray aarootri aloosasa aliinssii aab	05946 AA67789	99 AW473512 AW296620 AA8/2699 AlU94216 AlU25168 AA250930		
70		21393_1	AL520351 AA6 AI539154 AI50	08992 AW151842 AA622181 AI273454 AI005661 AA2 0192 AI289493 AI040740 BE167841 AW151374 BE16	05946 AA67789 7754 BF036108	19 AW473512 AW296620 AA872899 A1094216 A1025188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697		
70	418751	_	AL520351 AA6 AI539154 AI50 WG6050 P5130	08992 AW151842 AA622181 A1273454 A1005661 AA2 0192 A1289493 A1040740 BE167841 AW151374 BE16 13 R09158 R59113 T48473 T59023 AA122066 AW606	05946 AA67785 7754 BF036108 643 R38386 R0	19 AW473512 AW296620 AA872899 A1094216 A1025168 AA250999   AA299181 N23237 T62967 W96060 AA574412 AW606697   6567		
70		_	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW	08992 AW151842 AA622181 A1273454 A1005661 AA2 080620 A1289493 A1040740 BE167841 AW151374 BE16 08 R09158 R59113 T48473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BG	05946 AA6778: 7754 BF036108 643 R38386 R0 :181820 BE716	99 ANN 73512 ANY 79620 AABY 2899 AUD 42 16 AUG 5188 AAG 5999 1 AAG 99181 NG 3737 T62967 W96060 AA5 74412 AW 606697 5567 719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786		
	418751 424389	1059_4	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW BE838286 BE8	08992 AW151842 AA622181 AI273454 A1005661 AA2 0192 A1289493 A1040740 BE167841 AW151374 BE16 10 R09158 R59113 T48473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BE 033282 BE716636 AA777158 W34063 BE716628 BE71	05946 AA6778 7754 BF036108 643 R38386 R0 1181820 BE716 16625 BE83837	99 AWA73512 AW29620 AA872899 AU94216 AU25188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697   S567   719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786   1 BF371044 BE716631 BE716402		
70 75	418751	1059_4	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW BE838286 BE8	08992 AW151842 AA622181 A1273454 A1005661 AA2 080620 A1289493 A1040740 BE167841 AW151374 BE16 08 R09158 R59113 T48473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BG	05946 AA6778 7754 BF036108 643 R38386 R0 1181820 BE716 16625 BE83837	99 AWA73512 AW29620 AA872899 AU94216 AU25188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697   S567   719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786   1 BF371044 BE716631 BE716402		
	418751 424389 406797	1059_4	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW BE838286 BE8	08992 AW151842 AA622181 AI273454 A1005661 AA2 0192 A1289493 A1040740 BE167841 AW151374 BE16 10 R09158 R59113 T48473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BE 033282 BE716636 AA777158 W34063 BE716628 BE71	05946 AA6778 7754 BF036108 643 R38386 R0 1181820 BE716 16625 BE83837	99 AWA73512 AW29620 AA872899 AU94216 AU25188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697   S567   719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786   1 BF371044 BE716631 BE716402		
	418751 424389 406797 TABLE	1059_4 0_0 54C:	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW BE838286 BE8 AI432224 AW2	08992 AW151842 AA622181 A1273454 A1005661 AX 0192 A1289433 A1040740 BE167841 AW151374 BE16 13 R09158 R59113 T48473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BC 38282 BE716636 AA777158 W34063 BE716628 BE7 76890 A1499346 AA937014 AA653573 A1318525 A124	05946 AA6778 7754 BF036108 643 R38386 R0 1181820 BE716 16625 BE83837	99 AWA73512 AW29620 AA872899 AU94216 AU25188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697   S567   719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786   1 BF371044 BE716631 BE716402		
	418751 424389 406797 TABLE Pkey:	1059_4 ' 0_0 54C:	AL520351 AA6 AI539154 AI50 W96059 R5130 BG190758 AW BE838286 BE8 AI432224 AW2	08992 AW151842 AA622181 A1273454 A1005661 AA2 0192 A1289493 A1040740 BE167841 AW151374 BE16 03 R09158 R59113 148473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BC 032828 BE716636 AA777158 W94063 BE716628 BE71 76890 A1499346 AA937014 AA653573 A1318525 A124	05946 AA67781 7754 BF036108 643 R38386 R0 6181820 BE716 16625 BE83837 6219 AA961591	99 AW373512 AW236620 AA872899 AUG4216 AUG5168 AA236996   AA239181 N23237 T62967 W96060 AA574412 AW606697   6567   719 AU32483 AU61017 W73951 AU350771 AA912611 AA339786   1 BF371044 BE716631 BE716402   AUZ70640		
75	418751 424389 406797 TABLE	1059_4 : 0_0 54C:	AL520351 AA6 AI539154 AI50 W96059 R5130 BG199758 AW BE838286 BE8 AI432224 AW2 Mique number corres sequence source. Th	18992 AW151842 AA622181 A1273454 A1005661 AA2 19192 A1289493 A1040740 BE167841 AW151374 BE16 13 R09158 R59113 148473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BC 33282 BE716636 AA777158 W94063 BE716628 BE71 76890 A1499346 AA937014 AA653573 A1318525 A124 1900ding to an Eos probese! a 7 digit numbers in this column are Genbank Identifier	05946 AA6778: 7754 BF036108 643 R38386 R3 181820 BE716 16625 BE83837 6219 AA96159:	99 AWA73512 AW29620 AA872899 AU94216 AU25188 AA256996   AA299181 N23237 T62967 W96060 AA574412 AW606697   S567   719 A1125483 A1161017 W73951 A1250771 AA912611 AA339786   1 BF371044 BE716631 BE716402		
	418751 424389 406797 TABLE Pkey: Ref:	1059_4 0_0 54C: U	AL520351 AA6 AI539154 AI50 W96059 R5133 BG190758 AW BE838286 BE8 AI432224 AW2  Inique number comes sequence source. The	18992 AW151842 AA622181 AZ73454 A1005661 AA2 1912 A1289493 A1040740 BE167841 AW151374 BE16 13 R09158 R59113 748473 7159023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BC 33282 BE716636 AA777158 W34063 BE716628 BE71 76890 A1499346 AA937014 AA653573 A1318525 A124  Leponding to an Eos probeset 10 7 digit numbers in this column are Genbank Identifier Tromosome 22' Durham, et al. (1999) Nature 402-489-	05946 AA6778: 7754 BF036108 643 R38386 R3 181820 BE716 16625 BE83837 6219 AA96159:	99 AW373512 AW236620 AA872899 AUG4216 AUG5168 AA236996   AA239181 N23237 T62967 W96060 AA574412 AW606697   6567   719 AU32483 AU61017 W73951 AU350771 AA912611 AA339786   1 BF371044 BE716631 BE716402   AUZ70640		
75	418751 424389 406797 TABLE Pkey:	1059_4 0_0 54C: U S S	AL520351 AA6 AI539154 AI50 W96059 R5133 BG190758 AW BE838286 BE8 AI432224 AW2 Anique number corressequence source. The equence of human ci	18992 AW151842 AA622181 A1273454 A1005661 AA2 19192 A1289493 A1040740 BE167841 AW151374 BE16 13 R09158 R59113 148473 T59023 AA122066 AW606 961118 W77994 AA339877 AW845121 AW845129 BC 33282 BE716636 AA777158 W94063 BE716628 BE71 76890 A1499346 AA937014 AA653573 A1318525 A124 1900ding to an Eos probese! a 7 digit numbers in this column are Genbank Identifier	05946 AA6778: 7754 BF036108 643 R38386 R3 181820 BE716 16625 BE83837 6219 AA96159:	99 AW373512 AW236620 AA872899 AUG4216 AUG5168 AA236996   AA239181 N23237 T62967 W96060 AA574412 AW606697   6567   719 AU32483 AU61017 W73951 AU350771 AA912611 AA339786   1 BF371044 BE716631 BE716402   AUZ70640		

	Pkey	Ref	Strand	N1_position
	405885	7677703	Minus	42574-42998
	403752	7678857	Plus	33704-33828
_	404489	8113772	Plus	98183-98480
5	404942	7382153	Plus	92095-92252
	404149	7534008	Plus	121831-121951,124044-124150
	406387	9256180	Plus	116229-116371,117512-117651
	404780	9887810	Minus	175708-175871
	401846	7712190	Minus	82775-82823,82912-83022
10	401254	9796309	Plus	152209-152383
	405752	9212305	Plus	91392-91528

TABLE 55A: ABOUT 201 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT DID NOT METASTASIZE RELATIVE TO PRIMARY MELANOMAS THAT LATER METASTASIZED 15

LATER METASTASIZEU
Table 55A lists about 201 genes upregulated in primary melanomas from tumors that did not metastasize relative to primary melanomas that metastasized later. Genes were selected from 59880 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative lavel of mRNA expression.

Pkey:
Unique Eos probeset identifier number
ExAcon:
Exemplar Accession number, Genbank accession number
Unique Dr. Unique Eos probeset identifier number

20

UnigeneID: Unigene Tide:

R1: R2:

Unigene number
Unigene gene fite
Unigene gene fite
Unigene gene fite
Sun percentile of Als for primary melanomas that did not metastasize divided by the 90th percentile of Als from primary melanomas that metastasized later
Sun percentile of Als for primary melanomas that did not metastasize divided by the 90th percentile of Als from primary melanomas that metastasized later,
where the 15th percentile of normal fissue Als was subtracted from both the numerator and denominator

25

	Pkey 413554	ExAcon AA319146	UnigenelD Hs.75426	Unigene Title secretogranin II (chromogranin C)	R1 8.08	R2 5.48
	404854			Target Exon	5.18	8.18
30	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	4.89	4.95
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	4.83	4.86
	408471	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	4.71	4.70
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.71	3.85
·	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	3.98	4.01
35	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	3.92	3.35 2.78
	400417	X72475		Target	3.83 3.67	2.70
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.62	3.68
	409190	AU076536	Hs.50984	sarcoma amplified sequence	3.62 3.61	3.89
40	408692	AL040127	Hs.34074	dipeptidytpeptidase VI	3.56	3.61
40	423619	T48591	Hs.249159	adrenergic, alpha-2A-, receptor ESTs; hypothetical protein for IMAGE:447	3.55	2.85
	442117	AW664964 AB007924	Hs.128899 Hs.13245	KIAA0455 gene product	3.38	2.55
	445745 406663	U24683	rts.13243	immunoglobulin heavy constant mu	3.34	6.16
	414522	AW518944	Hs.76325	Immunoglobulin J chain	3.32	2.75
45	419235	AW470411	Hs.288433	Uentopiumiu .	3.32	2.74
45	441598	AI733219	Hs.58262	ESTs	3.31	3.71
	402294	74100210	10.0000	Target Exon	3.24	2.35
	402737			Target Exon	3.22	2.87
	414135	NM 004419	Hs.2128	dual specificity phosphatase 5	3.20	3.04
50	410268	AA3161B1	Hs.61635	six transmembrane epithelial antigen of	3.18	2.81
	427335	AA448542	Hs.251677	G antigen 7B	3.17	4.62
	404995			ENSP00000251890*:Monocytic leukemia zinc	3.13	2.34
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	3.12	2.21
	430015	AW768399		ESTs	3.12	1.93
55	414340	A1022656	Hs.296272	ESTs	3.09	2.87 3.16
	400072			Eas Control	3.08 3.06	2.73
	422567	AF111178	Hs.118407	glypican 6	3.06	2.73
	401284			Target Exon ab:MR0-HT0208-101299-202-a04 HT0208 Homo	3.02	2.76
60	455839	BE145814	Un 21522		3.00	3.15
UU	454027	R40192	Hs.21527 Hs.174104	Human DNA sequence from clone GS1-115M3 ESTs	2.99	2.44
	437258 445612	AL041243 N94126	Hs.12969	hypothetical protein	2.98	2.40
	445012	AI823763	Hs.7055	ESTs, Wealthy similar to 178885 serine/th	2.97	2.13
	437723	AJ672731	Hs.13256	ESTs	2.95	2.46
65	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	2.95	2.77
05	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.94	2.68
	424761	AA534528	Hs.152944	loss of heterozygosity, 11, chromosomal	2.92	3.81
	405757			Target Exon	2.92	3.00
	406621	X57809	Hs.8997	immunoglobulin tambda locus	2.92	6.71
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	2.86	2.16
	431712	R26584	Hs.267993	hypothetical protein FLJ10143	2.82	2.50
	413441	AJ929374	Hs.75367	Src-like-adapter	2.82	2.48
	452651	AJ218918	Hs.30209	KIAA0854 protein	2.82	1.13
26	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.78	2.77
75	439778	AL109729	Hs.99364	putative transmembrane protein	2.77 2.75	1.92 2.89
	434293	NM_004445	Hs.3796	Eph86	2.75 2.70	2.03
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.69	2.67
	406638	M13861	11- 93-4000	gb:Human T-cell receptor active beta-cha	2.68	3.08
80	432331	W37862	Hs.274368	MSTP032 protein	2.68	2.58
90	408989	AW361666	Hs.49500	KIAA0746 protein NM_017990*:Homo sapiens hypothetical pro	2.68	2.53
	401731 401979			C17000767:gi]11990770]emb[CAC19651.1] (A	2.68	3.42
	401979		Hs.72472	BMP-R18	2.68	2.51
	413333		113.12412	- · · · ·	=:==	
				550		

						2.12
	425032		Hs.154276	BTB and CNC homology 1, basic leucine zi	2.67 2.66	2.13 3.25
	406837 422550	R70292 BE297626	Hs.156110 Hs.296049	immunoglobulin kappa constant microfibrillar-associated protein 4	2.66	2.74
	425100	AF051850	Hs.154567	supervillin	2.65	2.80
5	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	2.65	2.63
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.64	1.84 2.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.63 2.62	2.00
	425580 450680	L11144 AF131784	Hs.1907 Hs.25318	galanin Homo sapiens clone 25194 mRNA sequence	261	1.80
10	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	2.61	1.82
	433470	AW960564		transmembrane 4 superfamily member 1	2.60	2.44
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	2.60	2.47
	401112			NM_024997*:Homo sapiens hypothetical pro	2.60 2.59	2.58 2.32
15	411802 407856	AA733204 AA045281	Hs.266175	nuclear transcription factor Y, gamma phosphoprotein associated with GEMs	2.59	1.88
13	425209	AL049761	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.58	2.81
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.56	2.10
	442560	AA365042	Hs.325531	ESTs, Wealthy similar to 2004399A chromos	2.55	3.97
20	408491	AI088063	Hs.7882	ESTs	· 2.54 2.54	2.74 2.02
20	420223	N27807	Hs.143844	ribosomal protein L4 ESTs	2.54	2.59
	444467 436729	AI150368 BE621807	rs.143044	transmembrane 4 superfamily member 1	2.53	2.29
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	2.53	1.80
	453507	AF083217	Hs.33085	WD repeat domain 3	2.52	1.99
25	420315	NM_006299	Hs.96448	zinc finger protein 193	2.52 2.50	2.50 2.35
	443060 453500	D78874 AJ478427	Hs.8944 Hs.43125	procollagen C-endopeptidase enhancer 2 esophageal cancer related gene 4 protein	2.50	2.44
	402692	M410421	NS.43123	Target Exon	2.50	1.73
	427792	M63928	Hs.180841	turnor necrosis factor receptor superfami	2.50	4.55
30	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.49	2.95
	420568	F09247	Hs.247735	protocadherin alpha 10	2.49 2.49	3.55 2.52
	444115	AW954585	Hs.271920	ESTs, Wealthy similar to Z195_HUMAN ZINC NM_018937*:Homo sapiens protocadherin be	2.48	2.52
	404049 417694	R09486	Hs.193118	ESTs	2.48	2.09
35	420600	BE011657	Hs.165695	ESTs, Weakly similar to unnamed protein	2.48	2.00
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.47	2.01
	404752			NM_024778:Homo sapiens hypothetical prol	2.47 2.47	3.07 2.46
	421429	MM_014922 AJ227874	Hs.104305 Hs.99244	death effector filament-forming Ced-4-fi ESTs	2.46	1.88
40	436378 429852	ABQ10445	Hs.225948	small inducible cytokine subfamily A (Cy	2.44	2.98
	431190	AL134172	Hs.120852	ESTs	2.44	2.48
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.44	2.96
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.44 2.43	3.16 3.33
45	445547 443030	D85181 R68048	Hs.273 Hs.9238	galactosylceramidase (Krabbe disease) hypothetical protein FLJ23516	2.43	2.07
43	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	2.43	3.36
	406782	AA430373	10.00121	gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.40	3.38
	407250	L09095		gb:Homo sapiens mRNA fragment.	2.38	3.78
50	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.36 2.34	3.56 2.84
30	431365 414555	AA504080 N98569	Hs.191958 Hs.76422	immunoglobulin superfamity receptor tran phospholipase A2, group IIA (platelets,	2.33	3.21
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.31	2.94
	403632			Target Exon	2.27	2.80
<i></i>	434232	AW297064	Hs.131862	ESTs	2.24	2.98 2.81
55	428114	AJ821548	Hs.98363	ESTs, Wealthy similar to I38022 hypotheti	2.23 2.19	2.81
	403294 429249	X81479	Hs.2375	Target Exon egf-like module containing, mucin-like,	2.16	3.13
	403295	70.410		Target Exon	2.15	2.95
	427817	AA503373	Hs.186678	ESTs	2.13	2.80
60	425154	NM_001851		collagen, type IX, alpha 1	2.08 _. 2.04	3.28 3.50
	443176 401770	AI696081	Hs.223770	ESTs C17001739*:gi 2327052 gb AAC48759.1  (U9	2.04	5.39
	407124	R08160		gb:yf18a07.s1 Soares fetal liver spleen	2.03	2.95
	456060		Hs.45184	Homo sapiens cDNA FLI12284 fis, clone MA	2.03	2.97
65	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA1399 pro	2.01 2.01	3.42 3.05
	426653		Hs.171695	dual specificity phosphatase 1	2.01	3.58
	410677 401673		Hs.65424	tetranectin (plasminogen-binding protein C16001416*:gi 12743112 ref XP_010131.2	1.99	4.99
	420983		Hs.100764	catheosin G	1.95	5.47
70	413624		Hs.75445	SPARC-like 1 (mast9, hevin)	1.94	4.58
	433554		Hs.8108	disabled (Drosophila) homolog 1	1.93	2.82
	405121		11-040400	mitogen-activated protein kinase 8 inter G protein-coupled receptor 24	1.92 1.92	2.82 2.80
	436456 450852		Hs.248122 Hs.7740	oxysteral binding protein-like 1	1.91	5.08
75	432902		15.7740	histone deacetylase 3	1.90	2.84
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	1.89	3.04
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.87 1.85	2.85 3.71
	424398		Hs.146393	homocysteine-inducible, endoplasmic reti CD79A antigen (immunoglobulin-associated	1.85	3.38
80	416714 433465		Hs.79630 Hs.3314	selenoprotein P, plasma, 1	1.85	3.57
55	447990		Hs.20144	small inducible cytokine subfamily A (Cy	1.82	6.17
	421563	3 NM_00643	3 Hs.105806	granutysin	1.80	3.50
	453804	1 AA300204	Hs.35276	KIAA0852 protein	1,78	2.87



						•	
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.78	3.54	
	437866	AA156781		metallothionein 1E (functional)	1.77 1.75	2.97 6.89	
	427751	AF000152		conserved gene amplified in osteosarcoma	1.74	3.60	
5	400442	ANA 004020	Un 155507	DKFZP586G1722 protein	1.74	3.45	
,	456898 414477	NM_001928 U41635	Hs.155597 Hs.76228	D component of complement (adipsin) amplified in osteosarcoma	1.71	4.99	
	432870	AW974124	115.70220	gb:EST386227 MAGE resequences, MAGM Homo	1.68	2.86	
	456642	AW451623	Hs.109752	outative c-Myc-responsive	1.68	3.09	
	456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone H	1.66	2.83	
10	430449	AA352723	Hs.241471	RNB6	1.65	2.84	
	401029			v-myc avian myelocytomatosis viral relat	1.65	2.88	
	402742			NM_002508:Homo sapiens nidogen (enactin)	1.64	3.37	
	402559			Rho GTPase activating protein 1	1.63	3.07	
	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	1.62	311	
15	406851	AA609784		major histocompatibility complex, class	1.62	2.86	
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.60	3.94	
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (I	1.60 1.59	3.75 2.96	
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDN	1.58	2.95	
20	452950	AA428123	Hs.302766	tyrosine 3-monooxygenase/tryptophan 5-mo	1.58	4,11	
20	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.57	2.98	
	444182	AW160432	Hs.296460	craniofacial development protein 1 hypothetical protein FLJ20277	1.57	3.88	
	407815	AW373860	Hs.183860 Hs.107253	hypothetical protein OKFZp761F241	1.56	2.88	
	452887 416819	A1702223 U77735	Hs.80205	pim-2 oncogene	1.56	3.59	
25	414583	AA362907	Hs.76494	proline arginine-rich end leucine-rich r	1.56	4.38	
23	426104	AI204418	Hs.190080	ESTs	1.55	3.47	
	441591	AF055992	Hs.183	Duffy blood group	1.52	4.28	
	446406	AI553681	14.100	Ang/Abt-interacting protein ArgBP2	1,49	2.87	
	427343	AJ880044	Hs.176977	protein kinase C binding protein 2	1.49	2.88	
30	415550	L13720	Hs.78501	growth arrest-specific 6	1.47	4.82	
••	411961	AJ478432	Hs.72956	hypermethylated in cancer 1	1.46	3.48	
	406213			ENSP00000246202*:DJ63M2.2 (similar to AC	1.42	3.19	
	400847			NM_003105*:Homo sapiens sortitin-related	1.41	2.97	
	404642			NM_021965*:Homo sapiens phosphoglucomuta	1.40	3.02	
35	452650	AW270150	Hs.254516	ESTs	1.40	2.86	
	432894	AW167668	Hs.279772	brain specific protein	1.37	5.52	
	404030			NM_015669°:Homo sapiens protocadherin be	1.37	3.03	
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	1.35	3.15	
40	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.34	3.09	
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.32	3.29	
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.32	2.89	
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.31	2.89	
	423959	AA333025		gb:EST37122 Embryo, 8 week I Homo sapien	1.31	2.88	
45	408135	AA317248	Hs.42957	methyltransferase-like 1	1.29	3.81	
45	427523	8E242779	Hs.179526	upregulated by 1,25-dihydroxyvilamin D-3	1.29	3.25 2.85	
	415512	Y16270	Hs.78482	paralemmin	1.29 1.28	3.06	
	413531	AL036958	Hs.75416	DAZ associated protein 2	1.27	2.80	
	419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	1.26	2.90	
50	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.25	3.41	
20	422934 450935	BE244189 BE514743	Hs.122492	hypothetical protein tumor suppressor deleted in oral cancer-	1.25	3.63	
	416630	H69392	Hs.174051	small nuclear ribonucleoprotein 70kD pol	1.24	2.93	<i>‡</i>
	416950	AL049798	Hs.80552	dermalopontin	1.22	2.81	
	412558	AW962019	113.00332	gb:EST374092 MAGE resequences, MAGG Homo	1,21	3.02	
55	419593	W73092	Hs.58282	ESTs	1.19	2.84	
•••	403470			Target Exon	1.14	2.82	
	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	1.12	2.96	
	400559			Target Exon	1.00	2.90	
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	1.00	2.84	
60	427072	H38046	Hs.293981	ESTs	1.00	2.89	
	430439	AL133561		DKFZP434B061 protein	1.00	3.09	
	418183	NM_00177	2 Hs.83731	CD33 antigen (gp67)	1.00	2.93	
65	TABLE						
65	Pkey:	_		t identifier number			
	CAT nu		ene cluster numbe				
	Accessi	on: G	enbank accession	numbers			
	Ohau	CAT Numb	er Accession				
70	Pkey 406636			83 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L	12062   12080		
70	430540		RC017171 R	CO12105 NM 007126 AF100752 AL 137377 770768 RM47486	55 RG754806 AU124376	BG757203 BG7	64420 BG775028 BG824418
	430540	113_2	DMM/CR10 A	11120207 P.C 770238 P.CEREZAN P.CQ13323 RI759980 P.C3959	998 RMM48875 REBRIO	70 RF313689 BEI	879144 BM309834 AWZ45647
			A1770171 RE	196861 BE856897 AA463876 AI375927 AA648810 AA94819	3 AA490916 AI459893 A	1458188 AI24040	08 Al191843 Al131029 AW768399
			AIRESTON AV	V337984 AWN26150 RE456591 RE674599 AI818438 AA77215	97 AI651927 AW151143	B1198825 BG81	19083 RW428/64 RE903201
75			DC733715 D	MANAZONO RERONDOS RERONDOS REZISTAR RESPONZA RG875.	384 RF996406 BF98893	10 BM475542 AW	V246215 BE501897 BE903610
, ,			DE561530 B	ESCAST REGATER RETTO A FIZZANT RIZOTOM RG761305 RF2626	42 8F391848 BF382475	5 BG008258 BI54	17991 B1459099 BE391391 BE259420
			DC208100 A	W245422 A1423847 AIQ14618 HRD534 RF301004 AI 531791 A	AI435581 BF793112 AL!	577303 AA37326	55 BE746965 BF743630 BE879296
			AIRSOAGR RI	MN 18598 MB89260 AWN 72450 F20201 AW 151405 AW 517572	2 AA773468 BG259694	BE391 163 BG62	1529 AM21728 BG/6/231 BM462953
			RC3/INS3/A V	V52648 AA 113434 RE785431 RID41981 RG832385 BG253168	8 BG759470 BF369329 I	BF981332 BE259	9418 BE785738 BI091658 N72512
80			W59777 W9	5600 BC958989 AI205206 H19721 W17051 W77958 RI26201	IO AAB44319 W74143 W	/72214 N85194 B	3E734033 BG164099 AA931069
			F13645 R41	394 AK025758 BG180977 BE349455 AAB12018 AA740241 A	1027722 AI150356 AABE	16395 AW977627	7 BE220225 AA884082 AW518114
			AI243844 A	A809493 AA481029 AA825718 AI347866 AI431670 AA814436	5 AJ251109 R07704 AA7	65606 AA724593	3 AI918399 AI537550 AA491103



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5	430015	713_2	AW008188 R07703 AAS89120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134994 BF104082 H80591 BC017761 BC012195 NM, 007126 AF100752 AL137377 Z70768 BM474655 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM05810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AD375927 AA648810 AA948193 AA490916 AI459893 A458188 AJ24008 A191843 AL131029 AW768399 AJ365196 AW337984 AW0261510 BE4668591 BE674599 A8181438 AR772197 AK651143 B1198825 BG819033 BM458764 BE903567 BE7321715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875388 BF998406 BF988930 BM475542 AW246215 BE501897 BE903610
10			BES51530 BES60537 BES03782 BET72947 BIZ27204 BG761305 BEZ62642 BE331848 BE382475 BG008258 BIS47991 BH59099 BE391331 BE259420 BE28109 AW245422 AH23847 A1914618 H80534 BE301004 AL531791 AH35581 BF793112 AL577303 AA37265 BE746985 BF743330 BE879296 AW245422 AH23847 A1914618 H80534 BE301004 AL531791 AH35581 BF793112 AL577303 AA37265 BE746985 BF743330 BE879296 AW245492 BW072450 F20201 AW8151055 AW517572 AA772468 BC329569 BE391163 BG621529 AH21728 BE67672731 BW462953 BG340524 W52648 AA113434 BE785431 BID41981 BG632385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W58590 BG298989 AI205206 H19721 W17051 W77558 BI262010 AA844319 W74143 W72214 N58194 BE734033 BG164099 AA31069 F13648 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI170336 AA86395 AW977627 BE270225 AA884002 AW518114 AI2433844 AA805493 AA481025 AA4826718 AI347866 AH31670 AA814436 AI251109 R07704 AA765606 AA724593 A1918399 AI537550 AA491103
15	455839 406642	1518842_1 0_0	AVV006188 R07703 AA389120 AA746235 AW028983 AA789102 AU165751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE007760 BC746251 BE962912 BM454584 AL134894 BF104082 H80591 BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 AJ245210 AJ245212 AJ245211 AJ245213
20	406638 433470	0_0 6624_1	M13881 X7584 AL573167 A445461 A453743 AJ983655 AL564644 AA977180 AL694111 AL591358 AW071625 AL678712 AL720939 AJ927769 BE439796 AJ963432 AA292956 AW192593 AL865838 AL696905 AJ424384 A1161312 AJ911921 AL597801 BL94959 AJ240988 AL492554 AW367737 BE044033 AW008570 AW629505 BL94958 AA088439 AA706057 BF222820 BF533608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AJ799814 AA129575 AL671727 AJ470033 BE646195 AW779725 AA903050 AA147228 AA404570 AJ075878 W38161 AJ872739
25			AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AB90245 AA662517 132487 AB20108 A333170 A05319395067 AW275048 AA182640 AA478328 A129835 AW058153 AW471421 AW103470 AW003456 AW19197 A1823466 A4962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061065 H80983 R79933 A1950693 A1245632 A134330 AA148284 A1788502 AA487893 A1621320 AW194272 C06365 AA953883 BE85829 A18918523 A8172628 A192717 A1453453 A1496956 AM278678 A1678536 A1678578 BE477736 A1073569 A197599 A19855837 278771 A1553829 A16933030 AA603566 BE7773488 AW339301
30			BE773469 BE773469 BE773495 A650338 BE773499 A745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811382 BE773491 BE773494 BE773485 BE773473 BE773473 BE773470 BE773470 BE773470 BE773479 BE773
35			BF843900 AW806193 AAS02832 AA649494 AL568520 AL547960 BE706937 BE811350 BE773498 BE811401 BE773494 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AJ377595 C06111 AW088968 BE811404 BE811472 AI855912 AI925607 AI871950 AI033510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773483 AI567995 W60075 BF941183 AJ38844 BE811458 BE773481 AJ252300 A948565 BE706942 BE156350 T65026 AW742958 AW1979554 BE905184 AA722206 AJ344943 AJ348877 AJ334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BC482895 AA182734 AA877242
40			AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259321 BG741786 BI868522 AU135866 BIS52770 BI259310 BI259529 BI255959 BG485098 BI258228 BG498501 BM044512 AU133984 AL556858 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BIS51761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224133 BG400746 BG478065 BE790436 AW981686 BG771056 BE908365 BE546656 BG541235 AW583735 BG528290 BI250895
45	411802	609_6	AW651691 BM048978 BM043805 BG142185 AA315188 A1446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BF345917 AL549635 BB040919 AA733204 AA232382 T34425 T32000 BF906697 Z42382 BI544863 AL548378 AW816536 AW816719 BE152340
50	420223 436729	191648_1 6624_1	BF375392 AW816716 BE152336 BF375367 N27807 AA256634 BE276324 X77808 AL573167 AM45461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AIG62422 AB 202056 AW162503 AIR65938 AIG63648 AA977180 AI61312 AI911921 AI597801 BI494959 AI240988 AI49254 AW262737 BE044033
55			AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA129575 AI671727 A1470033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06122 BF057147 AA627686 AA167944 A1990245 AA662817 T32487 AI800106 A1333170 AI859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 AI892846 A1061065 H80983 R79933 A1950693 AI245632 A1343939 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE858936 A1918523 AI872628 A1927217 A1453453
60			A189366 AW339678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 228771 A1363829 A1893030 AA603586 BE773498 AW339301 BE773489 BE773496 BE773495 A1650338 BE773499 A1745719 BE811476 DE811446 BE811418 BE811410 BE811409 BE811338 BE811352 BE773501 BE773494 BE773496 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BC055071 AW675302 BF003068 A4719173 BE811348 A1592462 A1686240 BE773500 A1244845 A1565439 A1918453 A1472507 AM6740 A033576 AA191414 AW674346 COST89 A1690246 D57559 A168707 A163703 A469867 R21757 BE702457 A488907 AL574600 AL574070 AL574707 AL574525
65			AL578810 BCJ98381 M3/28364 BEG79732 AAA79834 AA479712 C17732 BM091258 BF843901 AW82022 C174/6 BEJ2740 AA12304 AA79804 BF843900 AW806193 AA502812 AA649494 AL568520 AL547980 BE70537 BF81330 BE773498 BE811401 BE77348 BE811473 FEB11380 BE73417 BF757734 BE92807 AB717596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811433 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AT744233 AW984527 C17506 BF843883 A1248307 BE773483 AI567995 BF601437 BF6014787 AI787884 BE811478 BF773481 AI567307 AA498558 BF7064978 F1553050 AW782586 AW794258 AW197954 BE905184 AA772200
70			A1344943 AJ34897 AI334850 BE621857 BE156280 AA454099 AA037722 BF643897 AW805183 AA043218 BG482894 AA182734 AA817247 AA81
75			BE790436 AW080238 AU137549 BG42986 BE392486 AW961886 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895 AW651691 BM048974 BM043805 BG142185 AA315188 A446615 C06300 BC497644 AA088544 AW815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 056120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 B1870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BC088925 BE088854 AA921353 R21800 AA011222 T97525
80	406782 432902		AAA30373 AA968771 U75697 AJ362269 AW375181 AL035820 AF039703 NM_003883 U56914 BE513355 BE302938 BE302936 BE302936 BE303018 AA094475 F08725 R98879 R18769 BE019412 AA045846 AL120913 BE168807 BE168812 R21136 BE168915 H71247 N59055 AA533007 AW938705 BE260952 BE313803 AA307436 AW951917 AW951926 AW277164 A439049 AW581905 A1744899 AW804572 BE004443 AA335928 AA486355 AA115468 AA312123 R77086 AA595186 AW166991 A1952071 AW593311 AW571813 A1749734 A1674761 A1560970 A1480266 AA534470 AA737815 BE300597 AW022818
			560

			8E300599'A	A911621 A1074678 BE300694 A1187018 R98969 AA456572 A1032111 A1830414 AA045874 AA932352 A1871262 T78896 AA714518
			AWMM02772 T	17250 R76914 AW317029 H71248 AA331900 AA282808 Al032140 Al208512 Al244759 Al420456 Al208085 Al283758 Al369297 R46731 9348 AW273644 Al559914 Al220114 AW615802 AA887531 AA810217 AA832227 Al567776 Al918324 AA862566 AA831038 AW246807
_			W79118 R43	inga 741762 AW135694 AW263376 AA115046 T34171 T34077 N53974 W79902 BE514017 BE513761 H79778 AW878598
5	437866	34267_1	1552054 ALS	B1000 AA 156850 AW293839 B1335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 W966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481
			AV755539 A	W468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AI536733
			BM144850 A	4471883 AA040926 BF507639 AA043777 AW874142 BEB32523 BE163972 BK022546 BK021204 W751975 W39241 BF808798 W22600 BF082190 AA031290 R42801 H98235 H17925 AK631236 AK933786 H42736 AF000152 AU123911
10	427751	15028_1	AW410526 F	RU354207 REROM92 RM142340 RE019322 AL597008 AW327818 BID41915 AW504825 AW504941 BE987969 NM_005730 U81556
			AM22831 AI	1154008 AA147822 AA873109 A1089244 A1360868 AW168024 A1819848 AA811327 A1355616 AA281629 A1880578 A1274316 AW014622
			ALZGOGGR N	270283 AA171981 A1349410 AA402469 A1421985 A1004864 A1423497 A1361503 A1363096 AW805345 A1.539979 AA553967 AW502264 22420 A1281054 A1500699 AW342095 C75122 AW504577 A1130811 A1423567 R79086 A1860451 BE 222885 A1697830 A1279575 BF438693
			AW576277 1	RE218210 AI952376 AA506609 AI147566 AI391690 AA991622 AI696368 AI784664 AA741555 AI002681 AW474554 AW474508 D25623
15			AJ493929 A	A179800 W73566 AW411368 AA147971 AA088581 BF804510 AU145809 AU148108 AA223219 AU157840 AW169757 AI537862 N42341 W327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 AI906211 BF802713 N40338
			AA249397 F	16752039 RE250441 H64761 RFR53011 H81877 H96088 AL576453 W73585 H39990 AW438965 BH899684 Al040299 AL561879 AA293821
			H27760 BCI BE091011 A	018922 AL533396 BE513580 BF432649 AIBR4985 AA404264 AW024396 AW167863 AW027036 AI302177 A1660487 AW026086 BF432564 U193156 AA744623 AIB59510 BI063081 BI061541 AA777036 BG058486 BI063555 AI349411 BF874521 AW139801 AI268585 AA401267
20			AI905209 R	64276 N72043 AF022231 BI256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697
			A1857745 A1	W192840 AW410527 AIB97435 AW006631 AW504124 AL048926 A085476 AW327855 AA459344 AW207516 AW204875 BM142514 Kag60980 AW242609 Bio12363 AW837102 BE703126 BE814612 BE837981 BE703141 BF343101 R47375 AA031413 N40264 BG027363
			BES36360 F	16301363 AA2R0192 RE294042 RE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603
25			BE857292 /	NT 1933 AU 155418 BG770385 AA339673 BG337748 H42694 BEB34346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280 BF304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629
23	432870	1238170_1	AW974124	AA572989 AA569080
	406851 417739	0_0 2145372_1	AA6097841 R12357.R3	197304 4740 Z43995
20	446406	11004_1	RC105015	RASRZA AIRS9S33 AWIIZZ9SZ RM312713 C04108 AU159507 AWZ90967 AWZ35078 AWZ71693 AA999835 AL134290 AWZ35ZZZ BM312405
30			AI480093 A RE769194 I	1469044 A1308242 A1274858 A1824850 A1933881 BE857254 AW235980 A1985474 A1540755 W17232 D56716 BE835412 AA091594 BE769189 BE765413 BE766491 BF154895 BE765626 BF372247 BE769079 BE769122 BF154873 BF154880 226986 BE768478 BF372008
			T34949 BE	768476 BE768462 BF370113 BE835323 BE769217 BE769113 AA093838 BE769188 N88480 AA093969 AA092843
	423959 450935	887999_1 4469_1	BE273069	BC002850 BC016704 NM 005851 AF089814 AK001498 AL537879 BG754157 Al129659 Al261895 BG397540 BF663515 AW517226
35			BG677982	AI435188 AI453123 AI198380 AA524481 8G981512 AW269638 AI348113 AI095743 AA457108 AW044584 AU151602 AI744572 AI078741
			A1350340 A	N089613 AIS68618 BF109806 AW440972 AA401965 AI027227 A1127506 AA434027 BF732901 AW264768 AA833667 AL038554 AI568161 NA402084 BE677778 AA933621 BF663514 BG763563 AL574521 BG177226 BG759860 BE906329 AW161323 AI879350 BF946477
			BF766208	aa633194 al537880 al038553 bg468205 bg761617 bi762655 bg436637 n49458 bi834722 bg397879 bi258799 aw004930 aa902847 W167549 aa743167 aa848017 aa365434 ai819503 aa767866 ai582000 n33615 ai950146 aa444029 aa227130 aa041525 aw339842
40			A1832036 A AA865972	AA838006 AW157822 AI890994 BI771150 BI821666 BE279491
	412558	1227364_1	AW962019	BE389091 Aw984393 Aw984439 Aw984451 Aw984367 Aw984371 Aw984349 Aw984356 Aw984444 Aw984443 Aw984449
	412695 430439	1243394_1 6750_2		AL117481 AL122069 AW439292 AI968826 AL041090
45	TABLE 5	sc.		ı
.,	Pkey:	t to	ique number co	xresponding to an Eos probeset
	Ret:	Ser sec	quence source quence of hum:	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA an chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
50	Strand:	ind	icates DNA str	and from which exons were predicted.
30	NI_positi	on: Ind	licates nucleou	de positions of predicted exons.
	Pkey	Ref	Strand	Nt_position
	404854 402294	7143420 2282012	Plus Minus	14260-14537 2575-3000
55	402737	9212184	Minus	13358-13552
	404995 401284	6006247 9800819	Minus Minus	154015-154123 101307-101421
	405757	3334694	Minus	66825-70466
60	40,1731 401979	9690317 2828778	Plus Minus	43830-43963,44787-44935,45698-45810,4741 75693-75851,76977-77112
•	401112	9966198	Minus	60628-61041
	402692 404049	8468956 3688074	Plus Minus	124606-125387 75765-78155
45	404752	7109522	Minus	120168-120326
65	403632 403294	8572864 8096496	Minus Plus	35197-35358 41565-41881
	403295	8096528	Plus	22386-22708
	401770 401673		Ptus Minus	183424-183576 122587-122705,122765-123047
70	405121	8102330	Minus	35816-36004,36587-36684
	400442 401029		Plus Plus	59362-59574 41999-42172
	402742	9212200	Minus	23487-23613
75	402559 406213		Plus Plus	33539-33715 25921-26612,34539-35161
	400847	9188605	Plus	44643-44835
	404642 404030		Plus Plus	102999-103145 149362-151749
80	403470	9929739	Minus	8376-8552
٥٥	402230 400559		Minus Plus	29782-29932 75483-75584

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TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI
Table 56A lists about 277 genes upregulated in metanoma metastases relative to benign nevi. Genes were selected from 59680 probesels on the Eos/Aflymetrix Hu03 Genechip
array. Gene expression data for each probesel obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA
expression.

expression.
Pkey:
ExAcon:
UnigeneID:
Unigene Title:
R1: 5

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number

Unigene gene title
Title percentile of metanoma metastasis Als divided by the maximum of benign nevi Als
Title percentile of metanoma metastasis Als divided by the maximum of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both
the numerator and denominator 10 R2:

		0.0				
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	422424	Al186431	Hs.296638	prostate differentiation factor	13.73	17.18
15	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11.67 9.35	13.25 8.75
	407846	AA426202	Hs.40403	Obp/p300-interacting transactivator, wit	8.63	6.22
	444381 417880	BE387335 BE241595	Hs.283713 Hs.82848	ESTs, Weakly similar to S64054 hypotheti selectin L (hymphocyte adhesion molecule	8.21	8.65
	424321	W74048	Hs.1765	tymphocyte-specific protein tyrosine kin	7.13	5.04
20	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	6.79	7.12
20	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	5.94
	429500	X78565	Hs.289114	hexabraction (tenascin C, cytotactin)	6.43	3.46
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.43	5.44
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.31	6.08
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	6.20	6.04 4.72
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	6.03 6.01	7.07
	417308	H50720	Hs.81892	KIAA0101 gene product	5.99	8.88
	448569 439310	BE382657 AF086120	Hs.21486 Hs.102793	signal transducer and activator of trans ESTs	5.95	6.63
30	452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.95	3.77
50	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.76	6.37
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	5.76	3.14
	409274	NM_003930	Hs.52644	SKAP55 homologue	5.65	5.01
	442739	NM_007274	Hs.8679	cytosotic acyl coenzyme A thioester hydr	5.58	3.50
35	442711	AF151073	Hs.8645	hypothetical protein	5.45	5.84 5.75
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42 5.35	5.75 4.94
	412918	BE563957	11- 400030	activated RNA polymerase II transcriptio	5.33 5.33	5.34
	428125	AA393071	Hs.182579	leucine aminopeptidase small inducible cytokine subfamily A (Cy	5.33	4.98
40	446921 431183	AB012113 NM_006855	Hs.16530 Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.25
70	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.33
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.05	8.77
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	5.03	5.17
	436701	AW959032		ESTs, Moderately similar to 178885 serin	5.03	4.17
45	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.99	5.08
	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	4.98	4.71 4.08
	418299	AA279530	Hs.83968	integrin, bata 2 (antigen CD18 (p95), ly	4.98 4.97	4.00
	432469	AL080084		CGI-100 protein	4.85	4.07
50	404854 415701	NM_003878	Hs.78619	Target Exon gamma-ghutamyt hydrotase (conjugase, fol	4.82	4.90
50	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	3.45
	408958	T99607	Hs.49346	signal recognition particle 54kD	4.78	2.34
	453949	AU077146	Hs.36927	heat shock 105kD	4.78	6.32
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	6.57
55	440245	AK001913	Hs.7100	hypothetical protein	4.74	3.83
	412228	AW503785	Hs.73792	comptement component (3d/Epstein Barr vi	4.74 4.73	5.53 4.35
	417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.67	4.60
	451003	AF058696 BE379766	Hs.25812	Nijmegen breakage syndrome 1 (nibrin) polymerase (RNA) II (DNA directed) polyp	4.62	3.50
60	424571 434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.61	5.67
00	452268	NM_003512		H2A histone family, member L	4.60	3.79
	421311	N71848	Hs.283609		4.60	3.58
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.68
	425706	AW406678	Hs.122559		4.59	3.83
65	450293	N36754	Hs.171118		4.57	5.40
	406836	AW514501	Hs.156110		4.57 4.53	6.33 4.77
	413441	AI929374	Hs.75367	Src-like-adapter	4.48	4.89
	431129 418506	AL137751 AA084248	Hs.263671 Hs.85339	Homo sapiens mRNA; cDNA DKFZp43410812 (f G protein-coupled receptor 39	4.47	4.17
70	411060	NM_006074			4.47	4.33
, ,	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	4.45	3.32
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.43	4.43
	448883	BE614989	Hs.7503	hypothetical protein FLJ14153	4.42	3.91
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	4.41	4.09
75	419285	D31887	Hs.89868	KIAA0062 protein	4.40	3.56
	418321	D63477	Hs.84087	KIAA0143 protein	4.38	3.00 4.26
	430154		Hs.234726		4,37 4.36	4.20 4.90
	428450				4.36	3.57
80	428297 447232		Hs.183583 Hs.327	3 serine (or cysteine) proteinase inhibito interleukin 10 receptor, alpha	4.36	4.07
00	409598			mitochondrial ribosomal protein S28	4.35	3.29
	442432		Hs.38178	hypothetical protein FLJ23468	4.34	5.80
	407047			gb:H.sapiens SOD-2 gene for manganese su	4.33	3.51
	-			564		

	443991	NM_002250		potassium intermediate/small conductance	4.33	4.23
	452322	BE566343		glutaredoxin (thiottransferase)	4.32	2.68
	420991	AW504814		Homo sapiens mRNA for FLJ00111 protein,	4.32	4.54
-	449722	BE280074		cyclin B1	4.31	3.73 5.74
5	408380	AF123050		diubiquitin	4.30 4.28	4.80
	427127	AW802282		pyruvate dehydrogenase phosphatase	4.28	3.59
	417933	X02308	Hs.82962	thymidylate synthetase chondroitin 4-sulfotransferase	4.25	4.15
	432828 450306	AB042326 AL080080	Hs.287402 Hs.24766	Choredoxin domain-containing	4.24	3.15
10	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.23	4.12
10	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.22	4.64
	427337	Z46223	Hs.176663	Fc fragment of tgG, low affinity IIIb, r	4.20	4.62
	408989	AW361666	Hs.49500	KIAA0746 protein	4.20	4.92
	449626	AA774247	Hs.301637	zinc finger protein 258	4.19	3.17
15	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	4.18	8.91
	415726	T89844	Hs.78712	aminolevulinate, delta-, synthase 1	4,16	4.21
	444207	A1565004		cathepsin D (lysosomal aspartyl protease	4.16	1.89
	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	4.14	3.30
	438718	ALD40058	Hs.6375	uncharacterized hypothalamus protein HTO	4.14	3.04
20	437802	A1475995	Hs.122910	ESTs	4.12	5.13
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	4.12	3.87
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.11	4.96
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	4.11	6.37
25	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	4.10	4.16 2.35
25	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 fis, clone PL	4.10	4.50
	452882	AW972990	Hs.196270	folate transporter/carrier	4.10 4.09	6.07
	414522	AW518944	Hs.76325	Immunoglobulin J chain	4.09	5.03
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.08	3.71
30	405506	414/402402	U= 02212	Target Exon	4.07	8.61
30	417497	AW402482 AW851121	Hs.82212 Hs.75497	CD53 antigen Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	4.05
	413715		Hs.105115	absent in melanoma 2	4.05	4.61
	421508 445701	NM_004833 AF055581	Hs.13131	lymphocyte adaptor protein	4.02	4.56
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	4.00	8.91
35	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.15
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.58
•	450515	AW304226	14,200	biphenyl hydrolase-like (serine hydrolas	3.85	4.26
	446506	Al123118	Hs.15159	chemokine-like factor, alternatively spl	3.81	4.06
	410668	BE379794	Hs.159651	hypothetical protein	3.80	6.84
40	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.46
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	6.44
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	4.00
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.76	4.67
	454080	Al199711	Hs.576	fucosidase, alpha-L- 1, tissue	3.74	6.22
45	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.36
	428398	A1249368	Hs.98558	ESTs	3.68	5.18
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	3.67	4.12
	414829	AA321568	Hs.77435	pleckstrin	3.65	4.45 4.84
50	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63 3.59	4.49
20	433867	AK000596	Hs.3618	hippocalcin-like 1	3.54	5.31
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.49	4.57
	418310	AA814100	Hs.86693 Hs.300697	ESTs immunoglobulin heavy constant gamma 3 (G	3.48	4.33
	406868 438746	AAS05445 AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.87
55	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.44	10.42
"	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	3.41	4.60
	432606	NM_002104		granzyme K (serine protease, granzyme 3;	3.40	4.50
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	3.40	4.22
	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	5.03
60	422545	X02761	Hs.287820	fibronectin 1	3.39	7.32
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.36	4.47
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.34	5.02
	416975	NM_004131		granzyme B (granzyme 2, cytotoxic T-lymp	3.34	4.24
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.33	4.29
65	432642		Hs.3069	heat shock 70kD protein 9B (mortalin-2)	3.32	4.48
	425234	AW152225	Hs.165909		3.24	4.64 13.58
	443623		Hs.9641	complement component 1, q subcomponent.	3.23 3.23	4.20
	426490				3.16	5.05
70	443958		Hs.10029	cathepsin C	3.15	4.04
70	407862		Hs.337988		3.14	5.32
	412577		Hs.74076 6 Hs.75724	CD163 antigen coatomer protein complex, subunit beta 2	3.13	4.65
	414050				3.13	4.34
	442904 421633		Hs.106260		3.12	4.99
75	421033		Hs. 29768		3.11	5.47
,,	428797		Hs.193700		3.10	4.30
	408515		Hs.29988		3.10	4.03
	409442		Hs.16924		3.07	4.00
	456373		Hs.89751		3.04	4.38
80	430413				3.04	5.53
	418526			solute carrier family 16 (monocarboxylic	3.03	4.97
	452139		Hs.16331		3.01	4.87
	430478				2.98	4.44

	439237	AW408158		ESTs, Weakly similar to A47582 B-cell gr	2.95	7.45
	406782 450455	AA430373 AL117424		gb:zw20111.s1 Soares ovary tumor NbHOT H chloride intraceffular channel 4	2.93 2.90	8.49 5.08
	422530	AW972300		bone marrow stromal cell antigen 2	2.87	7.07
5	429490	AI971131		ESTs, Wealthy similar to ALU7_HUMAN ALU S	2.87	4.29
	410231 419956	AA314163 AL137939	Hs.61153 Hs.40096	proteasome (prosome, macropain) 26S subu cadherin 19, type 2	2.82 2.80	5.53 4.26
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.79	5.55
••	421712	AK000140	Hs.107139	hypothetical protein	2.79	6.29
10	429732 448517	U20158 AA082750	Hs.2488 Hs.42194	lymphocyte cytosolic protein 2 (SH2 doma hypothetical protein FLJ22649 similar to	2.78 . 2.78	4.74 4.69
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	2.77	5.18
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.90
15	422173	BE385828	Hs.250619 Hs.17914	phorbolin-like protein MDS019 (CEM15) membrane-spanning 4-domains, subfamily A	2.75 2.72	4.33 4.19
13	446566 429402	H95741 AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72	5.15
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-8	2.71	4.82
	425762	BE244076	Hs.159578 Hs.2407	AT-hook transcription factor AKNA	2.71 2.69	4.61 4.45
20	429412 409202	NM_006235 AA236881	Hs.51043	POU domain, class 2, associating factor hexosaminidase 8 (beta polypeptide)	2.68	4.89
	426124	A1268389	Hs.250697	phosphatidylinositol glycan, class F	2.68	4.25
	422672	X12784	Hs.119129	collagen, type IV, atpha 1	2.67 2.65	5.00 9.54
	417389 445784	BE260964 AI253155	Hs.82045 Hs.146065	midkine (neurite growth-promoting factor ESTs	265	4.11
25	410341	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	4.50
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.63	4.17 5.80
	424687 410016	J05070 AA297977	Hs.151738 Hs.57907	matrix metalloproteinase 9 (gelatinase 8 small inducible cytokine subfamily A (Cy	2.62 2.61	5.57
	424779	AL046851	Hs.153053	CD37 antigen	2.60	5.72
30	420224	M84371	Hs.96023	CD19 antigen	2.60	4.02
	421924 426143	BE514514 BE379836	Hs.109606	coronin, actin-binding protein, 1A proteasome (prosome, macropain) subunit,	2.57 2.56	4.83 4.50
	421563	NM_006433	Hs.105806	granulysin	2.56	5.35
25	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	2.55	4.32
35	428169 417022	AI928984 NM 014737	Hs.182793 Hs.80905	golgi phosphoprotein 2 Ras association (RalGDS/AF-6) domain fam	2.54 2.54	5.78 4.09
	414646	AA353776	Hs.901	CD48 antigen (B-celt membrane protein)	253	4,41
	429800	AA333375	Hs.223014	antizyme inhibitor	2.50	5.68
40	407241	M34516 AB004550	Hs.107526	gb:Human omega light chain protein 14.1 UDP-Gat:betaGlcNAc beta 1,4- galactosylt	2.50 2.45	4.69 4.35
40	421739 412819	T25829	Hs.24048	FK506 binding protein precursor	2.45	4.66
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.91
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.41 2.41	4.80 4.00
45	420340 449296	NM_000734 AL137257	Hs.97087 Hs.23458	CD3Z antigen, zeta polypeptide (TiT3 com Homo sapiens cDNA: FLJ23015 fis, clone L	2.41	4.77
	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase	2.41	4.04
	400223	ALIATZAGE	Hs.265827	Eos Control	2.39 2.38	5.47 7.67
	431629 414622	AU077025 A1752666	Hs.76669	interferon, atpha-inducible protein (clo nicotinamide N-methyltransferase	2.38	5.32
50	415149	X12451	Hs.78056	cathepsin L	2.37	8.07
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37 2.35	5.23 4.57
	454390 427407	AB020713 BE268649	Hs.56966 Hs.177766	KIAA0906 protein ADP-ribosyltransferase (NAD; poly (ADP-r	2.31	5.48
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	2.24	4.08
55	438956	W00847	Hs.135056 Hs.1652	Human DNA sequence from clone RP5-850E9 chemokine (C-C motif) receptor 7	2.23 2.23	4.02 4.90
	423397 416232	NM_001838 AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.18	4.97
	436692	AW243158	Hs.5297	DKFZP564A2416 protein	2.17	4.13
60	420842	A1083668 AA321649	Hs.50601 Hs.2248	hypothetical protein MGC10986 small inducible cytokine subfamily B (Cy	2.14 2.13	5.14 4.43
00	428227 429642	X68264	Hs.211579		2.11	5.42
	416448	L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10	6.36
	416714 409220	AF283770 BE243323	Hs.79630 Hs.51233	CD79A antigen (immunoglobulin-associated tumor necrosis factor receptor superfami	2.10 2.09	4.06 4.67
65	414045	NM_002951		ribophorin II	2.07	4.32
_	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.24
	441211	AW946155 H06586	Hs.7750 Hs.94	hypothetical protein AL133206 DnaJ (Hsp40) homolog, subfamily A, membe	2.06 2.05	4.64 4.33
	434692 452363	A1582743	Hs.94953	Homo sapiens. Similar to complement comp	2.04	13.36
70	438393	AA351815	Hs.50740	Homo sapiens cDNA: FLJ22272 fis, clone H	2.03	4.52
	413313				2.02 2.00	4.11 4.04
	452700 406621		Hs.288940 Hs.8997	) five-span transmembrane protein M83 immmootobulin tambda locus	1.99	4.35
~-	424415	NM_001975	5 Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.52
75	429451		Hs.202833		1.95 1.95	5.60 5.38
	416967 414945		Hs.80645 Hs.77667	interferon regulatory factor 1 lymphocyte antigen 6 comptex, locus E	1.93 1.93	4.69
	418917		Hs.1217	adenosine deaminase	1.91	4.32
80	445411		Hs.12646	hypothetical protein FLJ22693	1.91 1.90	4.48 6.03
80	413945 429119		1 Hs.75627 Hs.19643	CD14 antigen 7 hypothetical protein FLJ10788	1,90 1,90	4.08
	413317		Hs.75283	sorting nexin 1	1.89	4.06
	427239	BE270447		ubiquitin carrier protein	1.67	5.98

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	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.87	6.33	
	413142	M81740	Hs.75212	omithine decarboxylase 1	1.85	4.21	
	447131 430040	NM_004585 AW503115	Hs.17466 Hs.227823	retinoic acid receptor responder (lazaro pMS protein	1.84 1.83	5.07 5.57	
5	416819	U77735	Hs.80205	pim-2 oncogene	1.83	4.12	
	425356	BE244879	Hs.155939	inositol polyphosphate-5-phosphatase, 14	1.82	5.71	
	414570	Y00285	Hs.76473	insufin-like growth factor 2 receptor	1.81	4.73	
	443639 418707	8E269042 U97502	Hs.9661 Hs.87497	proteasome (prosome, macropain) subunit, butyrophilin, subfamily 3, member A2	1.80 1.78	4.71 5.16	
10	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.78	7.00	
	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	5.10	
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.15	
	424825 428385	AF207069 AF112213	Hs.153357 Hs.184062	procollagen-lysine, 2-oxoglutarate 5-dio putative Rab5-interacting protein	1.70 1.69	4.43 4.06	
15	427378	BE515037	Hs.177556	metanoma antigen, family D, 1	1.67	5.68	
	413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.56	
	442414	BE408758	Hs.8297	nbonuclease 6 precursor	1.65	4.40	
	410129 452472	BE244074 AW957300	Hs.58831 Hs.294142	regulator of Fas-induced apoptosis ESTs, Wealthy similar to C55663 oligodend	1.64 1.63	4.02 4.49	
20	445143	BE245342	Hs.306079	sec61 homolog	1.62	4.73	
	413511	AI627178	Hs.75412	arginine-rich, mutated in early stage tu	1.60	4.19	
	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.61	
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	1.59 1.56	4.26 4.10	
25	410068 419489	AI633888 AW411280	Hs.58435 Hs.90693	FYN-binding protein (FYB-120/130) replication initiation region protein (6	1.55	4.30	
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.54	
	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	1.53	4.00	
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.53 1.51	4.79 4.12 .	
30	426059 418879	BE292842 AW162087	Hs.166120 Hs.5437	interferon regulatory factor 7 Tax I (human T-cell leukernia virus type I	1.50	4.93	
50	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (HV	1.45	4.15	
	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.45	4.03	
	432805	X94630	Hs.3107	CD97 antigen	1.43	4.11	
35	447150	AI439011	Hs.86386	myeloid cell teukernia sequence 1 (BCL2-r	1.43 1.41	4.08 4.36	
رر	421975 427458	AW961017 BE208364	Hs.6459 Hs.29283	hypothetical protein FLJ11856 ESTs, Wealdy similar to UKHU proteoglyca	1.41	4.10	
	412968	AW500508	Hs.75102	alanyi-tRNA synthetase	1.40	4.25	
	428511	AA019912	Hs.184693		1.38	4.91	
40	413825	BE299181	Hs.75564	CD151 entigen	1.37	4.45	
40	427496 407143	D21260 C14076	Hs.178710 Hs.332329		1.30 1.29	4.04 4.37	
			113.502.52	201			
	TABLE 5		ua Ess sents	set identifier number			
45	Pkey: CAT num		ie cluster numb				
	Accessio		bank accessio				
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	Pkey 412918	2764_3	r Accession RETRASES	AL519009 AV755430 AV756363 AV711927 BI523	434 A1521453 AA846815 AWO	24829 AW949702 BG21892	6 AA626658 A1445621 A1452815
50	412310	2,00	AA946555	AA723580 AA612925 BG105326 BG532618 AW5	13994 AW602165 AI373448 A	4907901 AW135104 BG186	662 W69205 BG219754
- •			BE774875	BG190378 AA483698 BE066066 BE066067 BE06	6062 AW304207 BE939361 A	N795569 BG210592 AW795	644 BE939358 AW102886
				BG182971 H97042 O58090 BI046351 H81248 AI7		8287 D57835 AA935095 BF	700910 BG215802 BG195459
	426204	20142 4	AW368467	7 BG495535 BG533177 B1087962 BE541579 BF13 A210833 BM353155 A1473754 A1147901 A1803109	0753 AARA220G AAA18025 AIA7851	S AMADONS AIRSONNA C	8828 AW301673 RF218952
55	436701	28142_1	209892 AF	8F433234 AA394157 BF378047 BE467036 AA319	724 AW290940 AI222671 AI3	17724 AW001711 AI028652	AA398130 AI470582 AI915936
55			AA908929	C75102 N36920 H50440 AI919034 AI004399 AI3	33862 AI123606 AA648518 AA	516258 AI865321 N22865 A	A848101 AI589792 AA758196
			AA214630	Al373911 AW194733 AA213447 Al290291 BF437	165 AA757592 BF086904 AW	95 <b>9032</b> AW992466 BF44686	38 A1936337 BE938849
			AW149064	4 AI701629 N90021			
60	432469	58644_1					
oo		30044_1	BC016556	BC016365 NM_016040 AF151858 BI561037 AW1	966873 AW967497 BE219482	BE018650 AW770511 AW4	59095 AW470133 BM150181 1 BEAAGRE2 AL 597A35 RE000262
		3004-1	BM193977	7 AI824135 AI632346 AI129838 BM147664 AI2921	12 BE244667 AA251084 AW5	D3659 BM193866 BM19448	1 BF446862 AL597435 BF000262
		3004_1	BM193977 AI824386	7 A1824135 A1632346 A1129838 BM147664 A12921 A1990100 AW087624 AA668793 AL080084 B13351	12 BE244667 AA251084 AWS 366 B1820940 BG779242 BM0	03659 BM193866 BM19448 39854 AA282620 AA256771	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335
		3004-1	BM193977 AI824386 AW37039 BM144854	7 A1824135 A1632346 A1129838 BM147664 A12921 A1990100 AW087624 AA668793 AL080084 B13351 9 AW954201 BM145846 BG111760 A1750065 BG6 9 A1184602 A1343932 AW136586 AW029464 A170	12 BE244667 AA251084 AW5 866 B1820940 BG779242 BM0 155794 AA564086 BG494071 B 8651 AA824243 BM145917 AA	03659 BM193866 BM19448 9854 AA282620 AA256771 9M069606 A1675331 BE302 662210 AA825708 A133585	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335 224 AI476466 AI625980 8 AI273704 AA662171 N48971
65		JUM_1	BM193977 AI824386 AW37039 BM144854 AA976614	r a1824135 a1632346 a1129838 BM147664 a12921 A1990100 awd87624 aa668793 a1080084 b1335 9 aw954201 BM145846 BG111760 a1750065 BGG 8 a1184602 a1343932 aw136586 aw029464 a170 1 a1344537 aa609603 a1873901 a1859995 aa833	12 BE244667 AA251084 AW5 866 B1820940 BG779242 BM0 855794 AA564086 BG494071 B 8651 AA824243 BM145917 AA 89 AA765811 A1150322 A1926	03559 BM193866 BM19448 69854 AA282620 AA256771 8M069606 AI675331 BE302 662210 AA825708 AI33585 816 BM148634 N98862 AA	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335 224 AI476466 AI625980 8 AI273704 AA662171 N48971 D19347 AA897062 AA831100
65		30M_1	BM193977 AI824386 AW370399 BM144854 AA976614 N69889 B	r ar24135 ar532346 a1729838 bm147664 a17291 a1990100 awdb7624 aa668793 al080084 bi3358 9 aw954201 bm145846 bc111760 a1750055 bgg 8 a1184602 a1343932 aw135586 aw029464 a170 a a1344537 aa609603 arb73901 arb59995 aa8338 25243155 aa822179 aa831098 aa112676 a17024	12 BE244667 AA251084 AW5 166 BI820940 BG779242 BM0 155794 AA564086 BC494071 B 3651 AA824243 BM145917 AA 189 AA765811 A1150322 A1926 17 BG621752 BE006492 AA35	03659 BM193866 BM19448 19854 AA282620 AA256771 18066966 A1675331 BE302 662210 AA825708 A133585 816 BM148634 N98862 AA 3202 BG674256 N46921 BI	1 BF446862 AL597435 BF000262 AW564511 AA451623 H00335 224 A1476466 A1625980 8 A1273704 AA662171 N48971 D19347 AA897062 AA831100 048774 AW300233 BF739890
65		3004_1	BM193977 AI824386 AW370399 BM14485 AA976614 N69889 B AW96687	r arzalisa arsazara alipbasa bimatoga alipbasa Alipbatoo awdrig2a aaggapasa alorooga biosas 9 awgsazoi bimasbag bc111760 ait50055 bcg 1 alibagoz alia3932 aw136586 aw029464 ait00 Alibagoz alia3932 aw136586 aw029464 ait00 Alibagoz arbasasasa arbasasasasasasasasasasasasasasasasasasa	12 BE244667 AA251084 AWS 166 BIR20940 BG779242 BM0 155794 AA564086 BG494071 E 8651 AA824243 BM145917 AA 189 AA765811 A150322 A1926 17 BG621752 BE006492 AA35 178 AA287713 BE348728 BG6	03659 BM193866 BM19448 19854 AA282620 AA256771 186059606 AI675331 BE302 18605210 AA825708 A133585 816 BM148634 N98862 AA 13202 BGG74256 N46921 BI 116446 AL599953 AL59995	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335 224 A1476466 AI625980 8 A1273704 AA662171 N48971 D19347 AA697062 AA631100 D19347 AAW300233 BF739890 BF381073 AW5005056 AA094735
65		3004_1	BM193977 AI824386 AW370399 BM144854 AA976614 N69889 B AW96687 H03613 A BG171509	P AB24135 AB32346 A1729838 BM147664 A17291 A1990100 AW087624 AA668793 AL080084 B13351 9 AW954201 BM145846 BC111760 A1750065 BGG 8 A1184602 A1343932 AW136586 AW029464 A170 A1344537 AA609603 A1873901 A1859995 AA8335 E243185 AA282179 AA831098 AA112676 A17024 9 AA393405 BF115146 AA910851 AA013099 N28 A287714 H27168 R54718 BF792697 AV693803 A 8 BFS71997 AA490239 AW388161 BE842126 BG'	12 BE24467 AA251084 AWS 166 BI820940 BG779242 BND 155794 AA564088 BG99407 I 1661 AA824243 BMI 45917 AA 189 AA765811 A1150322 A1926 177 BG621752 BE006492 AA3 1878 AA287713 BE348728 BG6 17685883 BG6 19956 BF54150 165309 N71903 A1955397 A153	33559 BM193866 BM19448 59854 AA282620 AA256771 BM069606 A1675331 BE332 662210 AA825708 A133585 816 BM148534 N98862 AA 3202 BG674255 N46921 B1 16446 AL599953 AL599952 BF216789 AA319751 BM6 6898 BE242040 F09718 AA	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335 224 Al476466 Al625980 8 AIZ73704 AA662171 N48971 019347 AA897062 AA831100 048774 AW300233 BF739990 BF381073 AW505056 AA094735 52652 BF335838 AA280397 7772421 AA450218 M78543
		J. J	BM193977 AI824386 AW370399 BM144854 AA976614 N69889 B AW96687 H03613 A BG171509 BE241414	7 AI24135 AI632346 A1729838 BM147664 A17291 9 AW954201 BM145846 BC111760 A1750055 BC6 9 AW954201 BM145846 BC111760 A1750055 BC6 1 A184602 A1343932 AW136586 AW029464 A170 1 A1344537 AA609603 A1873901 A1859995 AA6333 5243155 AA5282179 AA831098 AA112676 A17024 9 AA393405 BF115145 AA910851 AA013099 N28 A287714 HZ7168 R54718 BF792697 AV693603 A 8 BF571997 AA490239 AW388161 BE842126 BG ² 1 AA013038 H00297 AW576477 AW150918 AW59	12 BE244667 AA251084 AWS 166 BI820940 BG779242 BND 155794 AA564088 BG99407 16 1655794 AA564088 BG99407 16 16551 AA824243 BM145917 AA 189 AA765811 A1150322 A1926 179 BG621752 BE006492 AA3 1878 AA287713 BE348728 BG6 1765309 N1903 A1955397 A153 1371 A1382711 N71926 H7245	33559 BM193866 BM19448 59854 AA282620 AA256771 BM069606 A1675331 BE332 662210 AA825708 A133585 816 BM148534 N98862 AA 3202 BG674255 N46921 B1 16446 AL599953 AL599952 BF216789 AA319751 BM6 6898 BE242040 F09718 AA	1 BF446862 AL597435 BF000262 AW964511 AA451623 H00335 224 Al476466 Al625980 8 AIZ73704 AA662171 N48971 019347 AA897062 AA831100 048774 AW300233 BF739990 BF381073 AW505056 AA094735 52652 BF335838 AA280397 7772421 AA450218 M78543
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			AA903144 BF	38083 BF984258 AV657996	AI749532 BE768614 BE857252 B	E932516 BE7685/3 AV65	7993 AV657777 AV752631 BE774974 T55847			
	450515	13638_2	BEODORNE AIS	1511 BE/10/93 BE180119    RORTO AARATSQR AMTO1221	BG617338 H45942 T55897 AV657	7718 BG383437 435800 A1394207 A170817	1 AW025415 Al079409 AW008420 AW304226			
5	430313	13000_2	N34543 AW60	3578 AA526961 AA983631 N	199134 AA626645 R45023 AA9024	117 AW672925 AA449985	AA953982 AW6/54/1 AA010062 N80194			
•			H14620 H284	75 H26247 BF333581 AW842	2369 H06848 H05608 H81745 H15	016 R51905 AA860423 AI	850904 AA876023			
		0_0	AA430373 AA	968771		AIE03760 AI00774 5 D1407	207 AMONAG AWICE207 DE020010 AA222202			
	426143	3806_1	BUUU5265 BG	1767ZU AWUUDUZ7 BM35ZU 222RQ2 AAAQA2NR AARSARQ0	54 AWUZOJ 16 ALGJOGZZ ALGGUOGA 1 ALGGROGS AWORGOSK AAKROJOJ	A1092748 AA993184 AI126	2387 A1400449 AW166297 BF939910 AA232282 5077 A1081758 A1240686 A1261863 A1378423			
10			AA465237 AL3	76096 AA035579 AI087306	AA448162 AA129977 A1090903 A10	080686 AI288939 N33004	AI801240 AW021546 AI370773 AI086064			
			A4669528 AI2	50053 AIR70113 AAR53181	AA858014 BG055562 BG939559 A	.W080765 AA032283 AW4	67587 H40506 D00762 NM_002788 AA641134			
			AI582295 AI4	17525 Al563975 Al093566 Al	707743 AI290741 AW073417 BE8	75418 BM264076 BG8768	84 AI680535 AW854219 BE774635 AW854212			
						19 BGB/0231 BGB/0430 M	W819099 AI908570 AA449871 AU135228			
15	400223	2368_1	BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599							
			AL521812 BG	705730 BI495545 BI495546	BF 112248 BM023182 BM023123 A	V1075173 AW051799 BF05	8224 BI324885 BF436008 AA398446 BG822375			
			BM019558 BM	A023382 BG164174 N56909	81467064 BM023464 AI207475 BN	A311415 BG758430 BG75 300403 A1355580 A1336A3	8807 AI934826 N90351 8G422026 BE910312			
			ANU27778 ANU AAGE 2774 AA	611730 ALSOUGGO BANDUG 113 / .631734 RCQ40967 RE79108	N 191829 BG/3909/ AIT36/20 AA 7 AA573315 WR16R5 AA393525 B	G944103 Al3339125 Al149	7 AA868702 AA393660 AA025127 BG027630 864 AA977655 N90314 BE612839 BG491847			
20			A1129091 AA	161234 AA781198 AA759256	AABBR954 AA975B44 AI184099 A	J018025 AA398363 AJ003	331 AJ 193380 AA626020 AJ 244476 AJ 601 1 1 4			
			AW135664 A	206607 AW263599 AA81321	19 A1684453 AA878626 AA772222 I	A1085496 A1630226 BG94	0966 AID22010 AA770649 AA887624 AA491739			
	427220	20450 2	AA974295 BC	S530040 AA037091 AA01991	2 BI160457 H64512 BG503896	2 AWN71374 AI345565 AI3	07208 BE138953 8E049086 AI334881			
	427239	20459_2	AWN75006 A	W075191 AA464019 AW302	733 AMO75100 AWO73433 AI8028!	54 AL334909 AJB02853 AJ3	145036 A1348921 A1340734 A1307478 A1251289			
25			AW302327 A	W072520 AJ312145 AW0736	56 AW072513 AW071289 Al30755	9 AA876186 T29587 AI3U	7493 AI255068 AI252868 AI252839 AWU/4809			
			AI252926 AI2	52160 Al251662 Al251262 A	1610913 A1270787 A1270156 A1252	2075 AW073469 AW07290	11 AW072496 AW071420 AL305762 AL254764			
			AI802837 AI2	51264 AW073049 AW07131 190711 RE130228 AWA70476	1 AIJ4064J BE138965 BE138502 A 1 AW271039 AW302085 RF041872	AVVU73430 ALSSA733 ALVS AL254494 AL271496 AL25	4335 BE139260 AI054302 AI054060 AI054057 2427 BF718773 BF718645 AW074866 BE857822			
			NUSSIZZ NZ	03111 02 133220 11410410	ANTEN IGOS ANTOQUOS DESTROIL					
30	TABLE 560									
	Pkey:	Uniqu	se number com	esponding to an Eos probese	l Conbook Montifier (CI) for	mhors "Dunham et al " m	efers to the publication entitled "The DNA			
	Ref:	Sequ	ence source. : ence of human	ne / ciga numbers in inis coi chromosome 22° Dumbaro e	umn are Genbank identifia (Gi) no 1 al. (1999) <u>Nature</u> 402:489-495.	muers. Duman, et al. 16	CCS III die publicadori chados 11-0 010 1			
	Strand:			d from which exons were pre-						
35	Nt_position	n: Indica	ates nucleotide	positions of predicted exons.						
	Diam.	Ref	Channel	All excition						
	Pkey 404854	7143420	Strand Plus	Nt_position 14260-14537						
40	405506	6466489	Plus	80014-80401,80593-81125						
40	402474	7547175	Minus	53526-53628,55755-55920,	57530-57757					
	<del></del>	4. 400UT 204		CLU ATER IN MET ANOMA A	CTACTACEC DEL ATRIC TO MODI	MAI CYIN				
	Toble 57A	lists shout 304	oenes uncernal	ated in melanoma metastases	AETASTASES RELATIVE TO NOR relative to normal skin. Genes we	re selected from 59680 pro	obesets on the Eos/Affymetrix Hu03 Genechip			
45	алтау. Се	ne expression d	ata for each pro	obeset obtained from this ana	dysis was expressed as average int	tensity (AI), a normalized v	atue reflecting the relative level of mRNA			
	expression	1.								
	Pkey: ExAcon:			et identifier number n number, Genbank accessio	a aumhae					
	Unigenel C		ene number	I number, Ochobra boccasio	ii iigiia.Çi					
50	Unigene T	ide: Unig	ene gene title							
	R1:	90th	percentile of m	elanoma metastasis Als divid	led by the 90th percentile of normal	lskin Als Lekin Ale where the 15th r	percentile of normal tissue Als was subtracted from			
	R2:			ielanoma metastasis als divid and denominator	en by the Such percentile of normal	1 2 Kill 1412' MINSE AIG 15111 F	ACCEPTAGE OF FAMILIES 6330C 743 HID 3000 00000 IV.			
			41C 110111C10101	and octionistics						
55	Pkey	ExAcon	UnigenelD			R1 18.94	R2 25.00			
	422424 438549	AI186431 BE386801	Hs.296638 Hs.21858	<ul> <li>prostate differentiati</li> <li>trinucleotide repeat</li> </ul>		18.94	18.47			
	417880	BE241595	Hs.82848		te adhesion molecule	14.05	11.15			
	452838	U65011	Hs.30743	preferentially expres	ised antigen in mela	13.91	15.41			
60	446619	AU076643	Hs.313		otein 1 (osteopontin,	13.41 12.24	9.73 7.33			
	426555 439310	NM_000372 AF086120	Hs.2053 Hs.10279		aneous albinism IA)	10.12	10.80			
	414020	NM_002984	Hs.75703		kine A4 (homologous	9.74	10.16			
	447210	AF035269	Hs.17752	phosphalidylserine-	specific phosphotipas	9.43	11.69			
65	414812	X72755	Hs.77367		y gamma interferon	9.28	10.97 7.06			
	430377 426600	NM_001922 NM_003378			nerase (dopachrome della	9.07 9.06	7.96 19.93			
	453857	AL080235	Hs.35861			8.66	5.87			
70	418310	AAB14100	Hs.86693	ESTs		8.65	6.62			
70	433447	U29195	Hs.3281 Hs.23786	neuronal pentraxin		8.27 8.01	4.68 6.37			
	430280 430822	AA361258 AJ005371	Hs.24801		or hosphate dehydrogenase	7.80	6.10			
	456373	8E247706	Hs.89751		g 4-domains, subfamily A	7.78	7.60			
25	415752	BE314524	Hs.78776	putative transmemt	orane protein	7.68	5.41 9.06			
75	419628	H67546	Hs.49768		then D	7.66 7.56	8.96 4.59			
	417355 424321	D13168 W74048	Hs.82002 Hs.1765		r type is c protein tyrosine kin	7.48	5.77			
	412228	AW503785	Hs.73792	complement compo	onent (3d/Epstein Barr vi	7.43	4.93			
80	436485	X59135	Hs.15611			7.35 6.97	7.98 5.06			
٥U	414646 422241	AA353776 Y00062	Hs.901 Hs.17012		ell membrane protein) Osphatase, receptor t	6.83	5.20			
	429170	NM_001394		dual specificity pho	sphatase 4	6.67	3.77			
	417542	J04129	Hs.82269		rialed endometrial prole	6.67	15.22			
					560					

						• • •
	428398 408989	A1249368	Hs.98558	ESTs	6.57	3.60
	417022	AW361666	Hs.49500	KIAA0746 protein	6.48	4.93 3.65
	449644	NM_014737 AW960707	Hs.80905 Hs.148324	Ras association (RatGDS/AF-6) domain fam ESTs	6.38 6.35	5.84
5	412326	R07566	Hs.73817	small inducible cytokine A3 (hornologous	6.30	7.18
_	457211	AW972565	Hs.32399	ESTs, Wealthy similar to S51797 vasodilat	6.25	7.21
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	6.25	5.36
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	6.18	6.01
	432828	AB042326	Hs.287402	chondroitin 4-sulfutransferase	6.12	6.51
10	449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
	436856	A1469355	Hs.127310	ESTs	6.00	5.54
	43365B	L03678	Hs.156110	immunoglobulin kappa constant	5.92	7.18
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.89	4.07
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	5.86	6.07
15	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	5.74	6.03
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	5.92
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.69	3.22
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	5.17
20	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	5.68	3.35
20	436315	BE390513	Hs.27935	hypothetical protein MGC4837	5.67	4.56
	452973	H88409	Hs.40527	ESTs	5.63	5.50
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	5.62	3.09
	406663	U24583	11: 4004	immunoglobulin heavy constant mu	5.54	9.68
25	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.52	6.42
23	408380	AF123050	Hs.44532	diubiquitin	5.51	4.49
	418299 429500	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.43	4.50
	446341	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	5.42	3.54
	425234	AL040763 AW152225	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	5.41	5.29
30	434203	BE262677	Hs. 165909 Hs. 283558	ESTs, Weakly similar to I38022 hypotheti	5.40 5.38	4.35 4.16
50	420338	AA825595	Hs.88269	hypothetical protein PRO1855 Homo sapiens, clone MGC:17339, mRNA, com	5.37	5.77
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	5.32
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.29	4.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	5.29	3.61
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.27	5.35
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.26	6.00
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.26	5.04
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	5.23	3.60
	400750			Target Exon	5.18	3.62
40	417933	X02308	Hs.82962	thymidylate synthetase	5.14	3.33
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.12	5.36
	445784	AI253155	Hs.146065	ESTs	5.12	4.06
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	5.06	7.68
AC	421508	NM_004833	Hs.105115	absent in melanoma 2	5.03	5.59
45	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.96	6.25
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	4.95	5.13
	400417	X72475		Target	4.90	3.93
	420137	AA306478	Hs.95327	CO3D antigen, delta polypeptide (TiT3 co	4.88	6.81
50	409264	NM_014937	Hs.52463	KIAA0966 protein	4.88	3.18
30	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	4.87	4.20
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.85	5.86
	409142 425088	AL136877 AA663372	Hs.50758	SMC4 (structural maintenance of chromoso	4.83	5.94
	405506	144003372	Hs.169395	hypothetical protein FLJ12015 Target Exon	4.82 4.74	5.19 4.09
55	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.74	3.72
-	430838	N46664	Hs.169395	hypothetical protein FLJ12015	4.73	3.50
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.72	3.66
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.71	5.16
	447217	BE465754	Hs.17778	neuropilin 2	4.70	4.52
60	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxytic	4.69	3.51
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.68	3.69
	419956	AL137939	Hs.40096	cadherin 19, type 2	4.68	5.83
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	5.29
15	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.66	3.84
65	449722	BE280074	Hs.23960	cyclin B1	4.64	4.29
	424006	AF054815	Hs.137548	CD84 antigen (feukocyte antigen)	4.62	4.54
	407845	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.62	6.78
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59	5.81
70	406673	M34996	Hs.198253	major histocompatibility complex, class	4.57	5.60
70	431620	AA126109	Hs.264981	2-5-ofgoadenylate synthetase 2 (69-71	4.56	4.44
	441224	AU076964	Hs.7753	Calumenin	4.56	3.75
	442739 444371	NM_007274	Hs.8679	cytosofic acyl coenzyme A thioester hydr	4.56	3.22
	448719	BE540274 AA033627	Hs.239	forkhead box M1	4.53	5.28
75	420301	AA767526	Hs.21858 Hs.22030	trinucleotide repeat containing 3 paired box gene 5 (8-cell lineage specif	4.48 4.47	9.08
, ,	430294	AA787326 AI538226	Hs.32976	paired box gene 5 (6-cet) tineage spect guanine nucleotide binding protein 4	4.47 4.43	5.61 4.11
	428513	8E220806	Hs. 184697	Homo sapiens clone 23785 mRNA sequence	4.43 4.41	4,43
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.39	3.99
_	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	4.38	5.50
80	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.37	3.25
-	421633	AF121860	Hs.106260	sorting nexin 10	4.36	6.23
	414829	AA321568	Hs.77436	pleckstrin	4.35	2.91
	417166	AA431323	Hs.42146	ESTs	4.35	4.08

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	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	4.34	5.35
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	4.34	3.72
	411305	BE241596	Hs.69547	myelin basic protein	4.32	4.18 2.44
5	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	4.28 4.27	4.48
,	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2 heat shock 70kD protein 98 (mortafin-2)	4.25	2.69
	432642	BE297635	Hs.3069	apolipoprotein L	4.25	3.75
	422282 433867	AF019225 AK000596	Hs.114309 Hs.3618	hippocatcin-like 1	4.23	5.13
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	4.20	2.15
10	438619	AB032773	110.10001	TU12B1-TY protein	4,19	3.32
	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.14
	420208	BE276055	Hs.95972	silver (mouse homolog) like	4.16	5.08
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	4.16	2.38
	430770	AA765694	Hs.123296	ESTs	4.15	3.67
15	424541	AW392551	Hs.180559	ESTs, Wealdy similar to A56194 thromboxa	4.15	3.98
	427337	Z46223	Hs.176663	Fc tragment of tgG, low affinity IIIb, r	4.14	3.51
	456760	AW961251	Hs.127828	guanine nucleotide binding pretein (G pr	4.14	4.42
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.13	5.07
20	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.12	6.43
20	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	4.11	8.73 4.48
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	4,11 4,10	4.78
	444863	AW384082	Hs.104879	serina (or cysteina) proteinase inhibito hypothetical protein FLJ14428	4.07	2.76
	435080 442711	AJ831760 AF151073	Hs.155111 Hs.8645	hypothetical protein	4.06	3.49
25	423605	AF047826	Hs.129887	cadherin 19, type 2	4.06	2.42
23	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.05	3.26
	421712	AK000140	Hs.107139	hypothetical protein	4.02	7.60
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	4.00	3.87
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	4.00	5.87
30	412719	AW016610	Hs.816	ESTs	3.99	5.46
	437179	AA393508		serologically defined colon cancer antig	3.96	4.51
	420319	AW406289	Hs.96593	hypothetical protein	3.95	5.47
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.91	4.58
25	418064	BE387287	Hs.83384	\$100 calcium-binding protein, beta (neur	3.84	4.42
35	420286	A1796395	Hs.111377	ESTs	3.83	4.56 5.70
	410600	AW575742	11- 47550	ESTs, Moderately similar to S65657 alpha	3.80 3.76	4.86
	410326	Al368909	Hs.47650	ESTs CD27 autions	3.70	8.72
	424779 452194	AL046851 Al694413	Hs.153053	CD37 antigen Ubiquitin-like protein FAT10??? - diubiq	3.69	6.38
40	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.65	5.40
40	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.65	4.48
	424153	AA451737	Hs.141496	MAGE-like 2	3.64	5.62
	421666	AL035250	Hs.1408	endothelin 3	3.64	5.52
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60	5.56
45	422173	BE385828	Hs.250619	phorbotin-like protein MDS019 (CEM15)	3.59	4.35
	421563	NM_006433	Hs.105806	granulysin	3.49	7.38
	453837	AL138387	Hs.256126	bacutoviral IAP repeat-containing 7 (liv	3.49	6.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protesse, decysln	3.48	4.23
50	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	3.47	5.38
50	408838	AI669535	Hs.40369	ESTs	3.45	4.59 5.01
	402829	V03034	11- 00470	C1002500:gij6754254 ref NP_034610.1  hea	3.42 3.42	8.14
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	3.40	4.35
	430594 429714	AK000790 BE561801	Hs.246885 Hs.2484	hypothetical protein FLJ20783 T-cell teukemia/hymphoma 1A	3.36	4.84
55	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.35	4.45
23	421958	AA357185	Hs.109918	ras homolog gene family, member H	3.35	4.28
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.34	5.18
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31	8.00
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.29	4.50
60	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.28	5.42
	404854			Target Exon	3.28	4.28
	400860			Target Exon	3.26	4.41
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.24	5.65
65	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.24	4.35
65	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.24	4.90
	440065	W03476	Hs.266331	hypothetical protein MGC4595	3.20	6.21 4.72
	440704		Hs.162	insulin-like growth factor binding prote	3.20 3.18	4.20
	411088		Hs.145053	ESTs	3.18	4.68
70	447513		Hs.313500 Hs.40368	ESTs, Moderatety similar to ALU7_HUMAN A adaptor-related protein complex 1, sigma	3.15	4.27
70	413190 430017		Hs.35	protein tyrosine phosphatase, non-recept	3.15	4.28
	406837		Hs.156110	immunoglobulin kappa constant	3.12	4.09
	409103		Hs.112208	XAGE-1 protein	3.04	4.04
	425706		Hs.122559	hypothetical protein FLJ22570	3.04	4.28
75	447656			src kinase-associated phosphoprotein of	3.03	4,30
	427792		Hs.180841	tumor necrosis factor receptor superfami	3.01	4.82
	402994			NM_002463*:Homo sapiens myxovirus (influ	2.99	5.74
	434276		Hs.93605	leucine zipper, putative tumor suppresso	2.97	5.07
	449523	NM_000579		chemokine (C-C motif) receptor 5	2.96	4.15
80	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	2.96	5.81
	406621		Hs.8997	immunoglobulin lambda locus	2.93	7.88
	447131			retinoic acid receptor responder (tazaro	2.91	13.22
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.90	8.37



	448275	BE514434	Hs.20830	tinesin-like 2	2.87	4.15
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.86	5.53
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	281	4.60
5	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.80 2.78	5.89 4.90
3	412819 432886	T25829 BE159028	Hs.24048 Hs.279704	FK506 binding protein precursor chromatin accessibility complex 1	2.76	4.21
	428380	NM_004271	Hs.184018	MD-1, RP105-associated	2.76	5.15
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.76	4.30
10	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.75	4.13
10	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.74 2.73	5.05 9.20
	428746 453953	AW503820 AW408337	Hs.192861 Hs.36972	Spi-B transcription factor (Spi-1/PU.1 r CD7 antigen (p41)	2.72	4.38
	407241	M34516		gb:Human omega light chain protein 14.1	2.68	4.07
1.5	437669	AI358105	Hs.123164	ESTs. Wealthy similar to match to ESTs AA	2.66	4.71
15	453779	N35187	Hs.43388	28kD interferon responsive protein	2.65 2.64	4.31 4.15
	432874 410129	W94322 BE244074	Hs.279651 Hs.58831	metanoma inhibitory activity regulator of Fas-induced apoptosis	2.62	7.36
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.62	4.43
20	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.61	5.42
20	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.60 2.60	9.69 5.17
	417370 411358	T28651 R47479	Hs.82030 Hs.94761	tryptophanyl-IRNA synthelase KIAA1691 protein	2.59	4.01
	425367	8E271188	Hs.155975	protein tyrosine phosphalase, receptor t	2.58	13.24
25	426470	AA528794	Hs.128644	ESTs	2.54	4.52
25	425535	AB007937	Hs.158287	KIAA0468 gene product	2.52 2.50	11.31 7.80
	431629 425722	AU077025 A1659076	Hs.265827 Hs.97031	interferon, alpha-inducible protein (clo hypothetical protein MGC13047	2.49	4.25
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	2.49	4.04
20	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fs, clone PL	2.48	4.08
30	441859	AW194364	Hs.94814	ESTs, Wealdy similar to FIG1 MOUSE FIG-1	2.48 2.48	5.25 4.88
	416714 431186	AF283770 NM_012249	Hs.79630 Hs.250697	CD79A antigen (immunoglobulin-associated ras-like protein	2.46	6.04
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.45	5.34
25	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.43	6.57
35	428437	AV656017	Hs.184325	CGI-76 prolein	2.42 2.39	4.96 8.46
•	427634 420842	Al399745 Al083668	Hs.18449 Hs.50601	hypothetical protein MGC10820 hypothetical protein MGC10986	2.38	5.90
	428289	M26301	Hs.2253	complement component 2	2.38	5.32
40	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.37	6.99
40	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.34 2.34	9.69 4.81
	433671 432403	AW138797 AA550815	Hs.132906 Hs.124840	19A24 protein ESTs	2.34	4.99
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.32	4.56
4.5	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.30	4.22
45	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	2.30 2.29	6.18 7.01
	401591 451708	A1306536	Hs.60975	Target Exon ESTs	2.26	4.50
	452700	AJ859390	Hs.288940	five-span transmembrane protein M83	2.24	4.90
50	424618	L29472	Hs.1802	major histocompatibility complex, class	2.22	5.40
50	409208	Y00093	Hs.248122	integrin, alpha X (antigen CD11C (p150),	2.21 2.19	4.74 4.61
	436456 419741	AW292677 NM_007019	Hs.93002	G protein-coupled receptor 24 ubiquitin carrier protein E2-C	2.17	7.43
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.16	5.58
5.5	438555	A1222089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	2.13	4.26 4.00
55	407260 448243	L09095 AW369771		gb:Homo sapiens mRNA fragment. integrin, beta 8	2.13 2.10	4.03
	437938	A1950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.07	4.45
	425262	D87119	Hs.155418	GS3955 protein	2.06	4.36
60	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.05 2.04	4.66 4.22
OU	400261 432468	AW402155	Hs.3003	Eos Control CD3E antigen, epsilon polypeptide (TiT3	2.02	4.23
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.99	4.45
	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	1.98	4.42
65	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.98 1.96	4.55 4.54
UJ	452923 452244	BE276018 N33530	Hs.288940 Hs.176674	five-span transmembrane protein M83 ESTs	1.95	4.23
	427239		113.110074	ubiquitin carrier protein	1.94	4.93
	418678	NM_001327		cancer/testis antigen (NY-ESO-1)	1.94	5.28
70	431836		Hs.271411	beta-site APP-cleaving enzyme 2	1.93 1.93	4.17 5.06
70	444090 404067		Hs.10306	natural killer cell group 7 sequence Target Exon	1.92	6.16
	426890		Hs.41294	ESTs	1.91	4.23
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	1.91	4.10
75	401914			Target Exon	1.87	4.76
75	448499 439627		Hs.77550 Hs.29076	hypothetical protein MGC1780 hypothetical protein FLJ21841	1.87 1.85	5.17 6.59
	439027			phosphoinositide-3-kinase, catalytic, de	1.85	4.03
	416819		Hs.80205	pim-2 oncogene	1.84	4.57
00	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.84	6.40
80	430378		Hs.2556	tumor necrosis factor receptor superfami	1.78 1.76	4.02 5.26
	435968 410423		Hs.111577 Hs.63489	integral membrane protein 3 protein tyrosine phosphatase, non-recept	1.75	4.30
	434224		Hs.84	interleukin 2 receptor, garrama (severe co	1.74	4.91



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	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.71	6.00	
	430148	BE387620	Hs.234489	tactate dehydrogenase B	1.70	4.34	
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.69	4.04	
_	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.66	5.95	
5	423984	AF 163825	Hs.136713	pre-8 lymphocyte gene 3	1.64	6.26	
	426666	AW500131	Hs.171763	CD22 antigen	1.63	4.33	
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.62	7.19	
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.61	4.33	
	421859	AA356620	Hs.108947	KIAA0050 gene product	1.59	4.30	
10	415198	AW009480	Hs.943	natural killer cell transcript 4	1.56	4.12	
	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.55	4.29	
	413969	X14034	Hs.75648	phosphotipase C, gamma 2 (phosphatidylin	1.53	4.63	
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.52	4.11	
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEX	1.52	4.36	
15	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.50	8.67	
	406885	D28423		gb:Human mRNA for pre-mRNA splicing fact	1.49	5.07	
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.48	4.50	
	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.48	4.91	
	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.43	4.26	
20	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.43	4.74	
	417287	A1831678	Hs.285714	KIAA1599 protein	1.41	4.01	
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.38	4.07	
	403043			Target Exon	1.36	4.89	
	407239	AA076350	Hs.67846	teukocyte immunoglobulin-like receptor,	1.32	4.57	
25	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.30	4.00	
	422934	BE244189	Hs.122492	hypothetical protein	1.30	4.37	
	442680	BE270707	Hs.8583	similar to APOSEC1	1.26	4,48	
	***2000	555.5.5.	1 4.5555				
	TABLE 57	rR·					
30	Pkey:		ique Eos probeset	identifier number			
50	CAT numi		ene cluster number				
	Accession		enbank accession				
	700000						
	Pkey	CAT Numb	er Accession				
35	438619	35124_1	NM 016575	AB032773 A1765521 BF593742 A1497757 A1761233 AW467	938 BF000670 AJ818496 N	24761 AL043306 BF476	138 BF593836 AA132787
	400015	00.12.	A1147248 A10	86795 AA151317 T95298 AW083548 AA058371 N27951 A	769860 AI784548 AW2055	06 AI800679 AI041733 A	AI459902 BE327641
			AIR65829 AI2	54736 Al302433 Al744176 Al241825 AA027842 AL524933	AL524932 BF947764 BF34	0737 BF948700 BG996	395 N53455 N21027
			A1127616 N3	5901 AA682443 AA678249 AA719371 AA132582 T15981 H	99958 N40717 AW959402	AI267251 BF909329 AI1	42035 T95379 H29420
			DS0532 H173	318 H17331 H29327 R40829 R43395 R59573 A1749561 R5	599 H16755 Al694500 AA	027907	
40	437179	12239_1	AKNEETIN DE	019085 AA 187684 BG656226 BM023227 AI932311 AW26	4381 AA398371 RMD21483	AI432433 AI375777 AI1	29580 AW262782
70	43/1/9	12235_1	AA 134107 DI	W023515 AA977504 AIB59222 AI348454 R69725 AA975268	RM021207 AL080074 AA1	29218 AW207842 N905	81 AA771919 AI092259
			MA 139 IU/ DI	074114 BG656536 BE501677 AW193419 AA917040 W9043	A A1342084 A1378057 A1 A3	16486 AW020068 RI491	093 RF476021 R41226
			AIU204 ID AIU	174114 BG030330 BE3U1077 ATT133413 AA317040 T1437	0 10342304 10301 10301 11000	W-00 /1102000 D1101	35 21 77 402 77 77 72 7
	*****	******	1059631 FU41	25 C02343 AA115589 R56480 AI400988 R54266 R31422	20042 DE462447 AARRE17	D DE5/0623 A1335R24 A	W408712 RM149172
15	410600	497855_1	BF 34 / 859 A	N499616 AA191322 AW499617 AL601010 AW575742 AA7	29043 BE403441 MADOUIT:	D ANNETOLO ANNOLO A	4 T70755 AAQRRAA3
45	452194	90339_1	AI594413 AV	v994700 Al912946 N73548 Al082035 AW271652 W24189 V	424162 AIT 19716 AAU2403	D WAAD IO 150 WAAD 1272-	4 179733 70300043
			A1709339				
	406782	0_0	AA430373 A	A968771	44 1103403 4141004063 000	2250C AMP22CENE AMN	01021 AA766843 DM144372
	409208	10117_2	AK074047 A	144342 AW014280 BM145128 N28267 AW206231 AA9890	41 H9319/ AW594063 BG	230290 AVI 230000 AVIU	0 103 1 AA703043 BM144372
50			AA989341 A	1824838 A1963970 A1637671 AW196330 BG427526 BM148	/89 BF893644 BF881946	*********	EAGE202 DE227660
50	448243	13061_2		A479726 BE622314 AL 134913 BE006305 BE006312 BE00	5298 AA044582 AW994956	AA234175 AAU43900 B	SEU00303 BF327009
			BE006317 B	F326759 BF541959		0 12407004 A10C1E30 TO	, roo4 NEO202 DO2228
	437938	66997_1	U71456 AA4	82911 W78802 AW856538 BF737212 N36809 N35320 AA2	82915 AW505512 Alb5383	2 W8/831 ABG1530 18	3304 N33331 N31210
			W01059 AI8	20532 T82391 AI820501 T63226 R66056 R67840 AW96110	11 AA337499 W37181 AA16	90009 AWZU5862 AA988	5/// AA6309/3 BF (/243/
			BG751124 A	1741346 A1950344 A1689062 A1872193 AW102898 AW1735	86 AI763273 AI890387 AW	150329 AI/62668 AA48	8892 ALIGOSHA ARGUSTE
55			AA642789 A	1950087 BF589902 N70208 AA283144 AA488964 H60052 F	197040 BF886630 AW9676	77 AW971573 AW9676	/1 AI3U8119 AA2518/5
			AA908598 A	1819225 A1564269 AA908741 AA293273 AA969759 AW276	905 AA044209 H83488 192	(48/	
	400261	23110_1	BC006097 X	03066 NM_002120 M26040 AW469119 AW469127 AI2997	72 AW518149 AJ144456 AV	V628070 A1629032 A135	8810 A1680433 A1440472
			A1357070 A1	865365 AWD14799 AI767973 AW518041 AA909398 AW768	3606		
	427239	20459_2	AL532360 B	E794750 AA582906 AI015067 AW271034 BG271636 AW07	5177 AW071374 AI345565	A1307208 BE138953 B	E049086 A1334881
60			AW075006 /	AW075181 AA464019 AW302733 AW075100 AW073433 AI	802854 Al334909 Al802853	3 A1345036 A1348921 AL	340734 AJ307478 AJ251289
			AW302327	AW072520 AI312145 AW073656 AW072513 AW071289 AI3	107559 AA876186 T29587 <i>F</i>	N307493 AI255068 AI25	52868 AI252839 AW074809
			A1252926 AI	252160 A1251662 A1251262 A1610913 A1270787 A1270156 :	A1252075 AW073459 AW07	72901 AWU72496 AWU7	142U ALSUS/62 ALZS4/64
			AIRO2R37 AI	251264 AW073049 AW071311 AI340643 RF 138965 RF 138	502 AW073456 Al334733 <i>F</i>	41054335 BE139260 A10	54302 A1054060 A1054057
			AI053722 AI	289711 BE 139228 AW470478 AW271039 AW302085 BEO4	11872 A1254494 A1271496 A	N252427 BF718773 BF7	718645 AW074866 BE857822
65	406827	0_0	AA971409				
	432665	27095_3	BG165971 E	3E143233 AL577712 AI400326 AA769318 AA427866 AW08	8714 AL150755 AL924874 A	u186243 AAB04195 AA7	768972 AW574769
			AW341643	AW204520 AA235326 AIDOSO76 RE826687 AW004816 AW	007235 BE826639 BE82661	34 BF222941 BE826631	BE826643 AA292639
			AW514133	A1690331 A1673409 AA627727 A1923685 AA931499 A12497	83 AIB 10663 AA548622 AA	.702095 AA832395 BI25	9508 AA262993 AW075840
			AA810885				
70							
	TABLE S	57C:					
	Pkey:		Unique number cos	responding to an Eos probeset			_
	Ref.		Sequence source	The 7 digit numbers in this column are Genbank Identifier (	Gi) numbers. "Dunham, et a	al." refers to the publicati	on entitled "The DNA
	74611		sequence of huma	n chromosome 22" Dunham, et al. (1999) Nature 402:489-49	<b>35</b> .	•	
75	Strand:			nd from which exons were predicted.			
	Nt_posi			e positions of predicted exons.			
	**CP-00**						
	Pkey	Ref	Strand	NL position			
	400750			198991-199168.199316-199548			
80	402474			53526-53628,55755-55920,57530-57757			
50	405506			80014-80401,80593-81125			
	402829			101532-101852,102006-102263			
	404854			14260-14537			
	404004		. 103	11900 11001			

	400860	9757499	Minus	151830-152104,152649-152744
	402994	2996643	Minus	4727-4969
	401591	9966977	Minus	55410-55835
	404067	3282162	Ptus	1415-2071
5	401914	9369520	Plus	62537-62945,63155-63308
•	403043	7768753	Minus	314423-316252

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TABLE SBA: ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE
Table SBA fists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease.

Cenes were selected from 59680 probesets on the Eos/Aflymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (A), a normalized value reflecting the relative level of mRNA expression.

Prey:

Linique Eos probeset identifier number

Exacon:

Unique Eos probeset identifier number

Exacon:

Unique Formative Accession number, Genbank accession number

Uniquenel Title:

Uniquene Title:

Uniquene gene title

90th percentile of Als for metastases from patients with firrited disease divided by 90th percentile of Als for metastases from patients with progressive disease where the 15th percentile of normal fissue Als was subtracted from both the numerator and denominator

15

20

	Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	12.74	12.92
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.66	5.88
25	412659	AW753865	Hs.74376	offactomedin related ER localized protei	7.23	5.76
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	6.91	14.26
	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	6.86	7.10
	436485	X59135	Hs.156110	immunoglobulin kappa constant	6.85	6.81
	426600	NM 003378	Hs.171014	VGF nerve growth factor inducible	6.73	11.21
30	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.53	4.63
50	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	5.48	7.08
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	5.27	5.94
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.78	3.07
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	4.68	3.27
35	413916	N49813	Hs.75615	apolipoprotein C-II	4.62	4.82
33	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.55	3.12
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.31	4.15
	409060	AI815867	Hs.50130	necdin (mouse) homolog	4.23	3.44
	401941	M013007	115.30130	Target Exon	3.89	3.19
40		AF039843	Hs. 18676	sprouty (Orosophila) homolog 2	3.88	2.43
40	447471			ESTs	3.66	4.16
	419628	H67546	Hs.49768	ral guanine nucleotide dissociation stim	3.63	2.81
	414863	AW131473	Hs.106185		3.47	3.06
	423416	NM_004920	Hs.128316	apoptosis-associated tyrosine kinase	3.47	3.43
A.E	400275			NM_006513*:Homo sapiens seryl-IRNA synth	3.42	1.96
45	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	3.41	2.89
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.37	6.31
	411763	AW862589		gb:QV0-CT0387-180300-167-a07 CT0387 Homo	3.34	3.74
	402007			C18000503*:gi[8922165 ref]NP_060080.1] h	3.30	2.00
50	424775	AB014540	Hs.153026	SWAP-70 protein	3.30	3.16
50	424036	AA770688		H2A histone family, member L		
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	3.30	5.58 3.23
	401739			NM_005622*:Homo sapiens SA (rat hyperten	3.30	
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.27	2.47
	413398	D21262	Hs.75337	nucleolar and coiled-body phosphprolein	3.26	2.61
55	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	3.26	2.58
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.14	4.04
	436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	3.13	2.38
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.13	2.47
	404405			Target Exon	3.11	4.69
60	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.11	2.10
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.10	2.26
	400417	X72475		Target	3.08	2.32
	401512			NM_014080:Homo sapiens dual oxidase-like	3.07	2.87
	423242	AL039402	Hs.125783	DEME-6 protein	3.06	2.78
65	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	3.06	2.81
	451952	AL120173	Hs.301663	ESTs	3.05	2.65
	427419	NM_000200	Hs.177888	histatin 3	3.05	4.24
	406663	U24583		immunoglobulin heavy constant mu	3.05	4.55
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.03	1.90
70	451993	AA765776	Hs.122983	ESTs	3.02	1.71
	421097	A1280112	Hs.125232	Homo sapiens cDNA FLI13266 fis, clone OV	3.01	3.11
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	3.00	3.47
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	3.00	2.22
	400237			NM_001087*:Homo sapiens angio-associated	2.98	3.43
75	414063	H26904	Hs.75736	apolipoproteln D	2.97	5.76
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.94	2.38
	414781	D50917	Hs.77293	KIAA0127 gene product	2.94	2.88
	445823	AI478563	Hs.145519	FKSG87 protein	2.92	1.98
	404439			ENSP00000067222":Mitochondrial 28S ribos	2.92	2.57
80	421218	NM_000499	Hs.72912	cytochrome P450, subtamily I (aromatic c	2.90	2.47
	420350	AW406896	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	2.90	3.87
	424855	AW204725	Hs.25560	ESTs	2.89	2.61
	436700	A1693690	Hs.301406	hypothetical protein PP3501	2.88	3.63

	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.87	2.92
	427157	U51166	Hs.173824	thymine-DNA glycosylase	2.87	2.11 2.48
	402273		11-0400	Target Exon	2.87 2.83	3.09
5	414135 430643	NM_004419 AW970065	Hs.2128 Hs.287425	dual specificity phosphatase 5 MEGF10 protein	2.83	3.04
,	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX).	2.82	2.12
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.81	2.88
	407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	2.81	3.43
10	405441			Target Exon	2.80 2.80	3.15 2.48
10	450816	BE271927 AA694099	Hs.87385 Hs.266820	ESTs ESTs	2.78	2.70
	435675 426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	2.78	2.53
	441623	AA315805	. 4.24	desmoglein 2	2.78	2.27
	413336	AI569938	Hs.296178	hypothetical protein FLJ22637	2.76	3.18
15	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.76 2.76	1.92 1.88
	437740	AA810265	Hs.122915 Hs.2012	ESTs transcobalamin I (vitamin B12 binding pr	2.75	8.06
	426322 411852	J05068 AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.74	3.30
	428422	AI557280	Hs.184270	capping protein (actin filament) muscle	2.73 .	231
20	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.72	2.19
	401454			NM_014226*:Homo sapiens renal tumor anti	2.72 2.72	1.99 2.89
	436825 407705	AW341123 AB023139	Hs.120275 Hs.37892	ESTs KIAA0922 protein	2.72	2.48
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.72	2.63
25	449151	AI632331	Hs.196038	ESTs	2.72	2.99
	433464	N92481		gb:zb12g02.s1 Soares_fetal_fung_NbHL19W	2.69	3.17
	401009	45400000	14- 202000	Target Exon	2.69 2.68	3.28 2.02
	427227 · 405268	AF103803	Hs.283690	hypothetical protein ENSP0000223174*:KIAA0783 PROTEIN.	2.67	2.18
30	410295	AA741357		nidogen (enactin)	2.65	2.06
	435905	AW997484	Hs.5003	KIAA0456 protein	2.65	2.12
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	2.65	2.52
	457423	AK000642	Hs.265018	hypothetical protein FLJ 20635	2.64 2.63	2.51 2.20
35	448752 414931	AA593867 AK000342	Hs.300842 Hs.77646	KIAA1608 protein Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.63	1.83
. 33	441283	AA927670	Hs.131704	ESTs	2.62	1.92
•	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.60	2.21
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.60	3.06
40	406678	U77534	15- 140007	gb:Human clone 1A11 immunoglobulin varia	2.54 2.49	3.06 3.44
40	430278 425970	AI673074 AK001500	Hs.116567 Hs.165186	ESTs, Weakly similar to T22914 hypotheti hypothetical protein FLJ13852	2.47	3.46
	407363	AF035032	Hs.8997	gb:Homo saplens clone MCA1L myosin-react	2.45	3.45
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.44	3.52
45	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, member	2.44	6.15
45	418635	L11329	Hs.1183	dual specificity phosphatase 2	2.42 2.41	3.92 3.08
	451558 430354	NM_001089 AA954810	Hs.26630 Hs.239784	ATP-binding cassette, sub-family A (ABC1 human homolog of Orosophila Scribble	2.36	3.99
	405701	74054010	13.255.04	ENSP0000004954*:Adseverin (Scinderin).	2.33	4.25
	433427	AI816449	Hs.171889	cholinephosphotransferase 1	2.30	3.30
50	401965			CGI-148 protein	2.29	3.45
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1 carboxypeptidase N, polypeptide 1, 50kD	2.23 2.19	4.07 3.17
	428142 422103	NM_001308 AA984330	Hs.2246 Hs.111676	protein kinase H11; small stress protein	2.18	4.18
	425746	NM_001701		bile acid Coenzyme A: amino acid N-acylt	2.12	3.48
55	404835	-		NM_018943":Homo sapiens tubulin, alpha-1	2.09	5.72
	401127			Target Exon	2.09 2.08	4.38 3.22
	406161 421654	AW163267	Hs.106469	Target Exon suppressor of var1 (S.cerevisiae) 3-like	2.08	3.03
	406632	AB006838	113.100103	gb:Homo sapiens mRNA for HRV Fab N31-VH.	2.07	3.25
60	447940	D86982	Hs.20060	KIAA0229 protein	2.05	4.80
	411773	NM_006799		protease, serine, 21 (testisIn)	2.05	5.33
	413211	AW967107	Hs.109274	hypothetical protein MGC4365 hypothetical protein MGC13047	2.02 2.01	4,74 3.76
	425722 437044	A1659076 AL035864	Hs.97031 Hs.69517	differentially expressed in Fanconi's an	1.96	5.27
65	436420	AA443966	Hs.31595	ESTs	1.94	3.68
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	1.92	3.88
	423420		Hs.128382	Homo sapiens mRNA; cDNA DKFZp7o111224 (f	1.90	3.63 3.04
	427923 406652			hypothetical protein PP3501 major histocompatibility complex, class	1.90 1.88	3.00
70	435624		Hs.24889	formin 2	1.88	3.54
. •	436552			HSPC028 protein	1.86	3.29
	408204		Hs.43666	protein tyrosine phosphatase type IVA, m	1.86	3.78
	402728		15 44667	C1002541*:git4758590fref[NP_004249.1] im	1.86 1.84	3.14 4.72
75	420932 458559			ESTs, Wealdy similar to T21697 hypotheti ESTs	1.78	3.06
,,	400278		1 10.2030 14	ENSP00000243264: Dolichyl-diphosphooligos	1.76	3.55
	425751		Hs.1940	crystallin, alpha B	1.76	5.31
	420737		Hs.99899	CD70; tumor necrosis factor (figand) s	1.74	3.00
80	410005			eukaryotic translation initiation factor hypothetical protein PP3501	1.74 1.73	3.79 3.57
00	454429 426321		Hs.301406 Hs.180677	zinc linger protein 162	1.72	3.27
	402897			NM_023068*:Homo sapiens sialoadhesin (SN	1.69	3.81
	423639		Hs.130411	KIAA1405 protein	1.67	3.31
				574		



	448848	AF131851	Hs.22241	hypothetical protein	1.65 1.60	4.27 3.02
	414420	AA043424	Hs.76095	immediate early response 3	1.56	3.28
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H mesenchymal stem cell protein DSCD75	1.55	3.73
5	450635 400252	AW403954	Hs.25237	NM_004651*:Homo sapiens ubiquitin specif	1.55	3.26
,	411825	AK000334		hypothetical protein FLJ20327	1.55	3.18
	414328	Z21666	Hs.300463	aconitase 2, mitochondrial	1.52	4.03
	400263			Eos Control	1.51	3.42
	421552	AF026692	Hs.105700	secreted trizzled-related protein 4	1.50	3.19
10	436673	AF201931	Hs.5268	hypothetical protein FLJ10479	1.49	3.33
	404739			Target Exon	1.49	3.10
	438344	8E387726	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.46	3.42 3.15
	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA sequence	1.44 1.44	3.04
15	425240	AA306495	Hs.1869 Hs.73165	phosphoglucomutase 1 interleukin 12 receptor, beta 2	1.43	171
13	412099 434642	U64198 W25739	105.73103	chromobox homolog 5 (Drosophila HP1 alph	1.42	3.07
	404406	W23733		Target Exon	1.42	3.87
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.41	3.80
	447697	W52125		tubulin alpha 1	1.40	4.45
20	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.40	3.28
	447216	R75812	Hs.169248	p75NTR-associated cell death executor, o	1.39	3.77
	401772			NM_014520:Homo sapiens MYB binding prote	1.39	3.67
	413031	BE515051	Hs.75160	phosphofructokinase, muscle	1.38 1.37	3.31 3.17
25	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	1.37	3.05
25	428011	8E387514	Hs.181418 Hs.12912	KIAA0152 gene product skb1 (S. pombe) homolog	1.35	3.11
	445580 436703	AF167572 AW880614	Hs.146381	RNA binding motif protein, X chromosome	1.34	3.05
	438277	AL022326	Hs.6139	synaptogyrin 1	1.34	3.09
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.32	3.23 .
30	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	1.31	3.01
	412968	AW500508	Hs.75102	atanyl-IRNA synthetase	1.28	3.58
	452378	AA025855	Hs.19597	KIAA1694 protein	1.25	3.08
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 protein,	1.24	3.45
25	402212			KIAA0430 gene product	1.21	3.03 3.20
35	428773	BE256238	Hs.193163	bridging integrator 1	1.20 1.18	3.03
	430067 418289	U79458 AW403103	Hs.231840 Hs.83951	WW domain binding protein 2 Hermansky-Pudlak syndrome	1.17	3.32
	405752	A11403103	115.03331	Target Exon	1.00	3.40
	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropportin	1.00	3.00
40	422000	74200.000	110.10 1000	rece among aparts process represent		
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40	TABLE 5	BB:				
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40	Pkey: CAT num	Unix iber: Ger	e cluster number			
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	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number bank accession nu	umbers	55 AU120415 AU14	1179 AU121081 BE409287 AU141397 AU122238
	Pkey: CAT num Accessio	Unix aber: Ger n: Ger	e cluster number bank accession number Accession NM 006513 BC	umbers 2009:3390 X91257 BC000716 BM450041 BI771139 AV7109	55 AU120415 AU14 235 BE545230 AU1	1179 AU121081 BE409287 AU141397 AU122238 13414 AV761720 AU129842 AU143343 BE270064
	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number bank accession number Accession NM_006513 B0 B1256788 BE38	umbers 2009390 X91257 BC000716 BM450041 BI771139 AV71099 2017 AU143368 AU133780 AU139704 BG531086 BE2687 200813 RI772360 RE617354 AU140124 BE777005 BC7467	235 BE545230 AU14 716 BEB14960 AW1	13414 AV761720 AU129842 AU143343 BE270064 61287 AV762084 BG898985 AW674875 AA313975
	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number shank accession number Accession NM_006513 BC BI256788 BE38 BG473378 BE38 AV740016 AA3	umbers C009390 X91257 BC000716 BM450041 BI771139 AV7109: 85217 AU143368 AU133780 AU139704 BG531086 BE268: 938813 BI772360 BE617354 AU140124 BE277050 187279 BM011248 AU190426 AW73888 B7630091 BC38	235 BE545230 AU14 716 BEB14960 AW1 14599 AW410037 AA	13414 AV761720 AU129842 AU143343 BE270064 61287 AV762084 BG898985 AW674875 AA313975 1378483 D49914 AL573323 AL549819 AL572282
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number bank accession number Accession NM_006513 BC BI256788 BE38 BC473378 BE2 AV749916 AA3 AV 572871 AL5	umbers C009390 X91257 BC000716 BM450041 BI771139 AV71093 86217 AU143368 AU133780 AU139704 BG531086 BE2682 898813 BI772360 BE617354 AU140124 BE277005 BG7461 874328 BM011248 AU098465 AW238888 BG940091 BG28 86117 AL571945 AL547790 AL581217 AL514559 AL57329	235 8E545230 AU14 716 BE814960 AW1 14599 AW410037 AA 26 AL540816 AW411	13414 AV761720 AU129842 AU143343 BE:27UB4 61287 AV762084 BG898985 AW674875 AA313975 1378483 D49914 AL573323 AL54819 AL572282 1038 B1262249 BG284713 A1659394 A1093582 AW965846
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number ibank accession number Accession NM_006513 BC BI256788 BE38 BG473378 BE3 AV749916 AA3 AL572871 AL6	umbers 20093390 X91257 BC000716 BM450041 BI771139 AV71093 36217 AU143368 AU133780 AU139704 BGS31086 BE2682 298813 BI772360 BE617354 AU140124 BE277005 BC7461 174328 BM011248 AU098465 AW238888 BG940091 BG28 68117 A L571945 AL158790 AL581217 AL514639 AL57392 88117 AL571945 AU146879 AW77347 AW157115 AW571	235 8E545230 AU14 716 BE814960 AW1 14599 AW410037 AA 26 AL540816 AW411 4750 BG683509 AW	13414 AV761720 AU125842 AU143343 BEZZUDA 61287 AV762088 BG898983 ANBTA875 AA313975 1378483 D49914 AL573323 AL549819 AL572282 1887824 AU8162249 BG244713 AI655334 AU033582 AW965846 1887824 AU818522 AA703770 BES42873 AA515504
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number ibank accession number Accession NM_006513 BG BI256788 BE33 BG473378 BE3 AV749916 AA3 AL572871 AA5 AA652206 AI6I AU154982 AAI	umbers  C009390 X91257 BC000716 BM450041 BI771139 AV7109: 86217 AU143368 AU133780 AU139704 BGS31086 BE268: 298813 BI772360 BE617354 AU140124 BE277005 BG7461 74328 BM011248 AU099465 AW23888 BG940091 BG28 68117 AL571945 AL547790 AL581217 AL514559 AL57392 86014 AA654357 AU146982 AW273447 AW157715 AW57- 38014 AA654357 AU146982 AW273447 AW157715 AW57- 381254 AA856251 AU086802 AA845654 AA708889 BF0658	235 BE545230 AU14 716 BE814950 AW1 14599 AW410037 AA 26 AL540816 AW411 4750 BG683509 AW 316 AA464944 BG26	13414 A7761720 AU173842 AU143343 BE27/UDA 61287 AV762084 BG898983 AW674875 AA313975 1378483 D49914 AL573323 AL549819 AL572282 1038 BL62249 BG284713 AL559394 AL033882 AW965846 1887824 AL818522 AA703770 BE542873 AA515504 11335 AL003384 BG402820 AA932098 W68695 AW182900
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number ibank accession number Accession NM_006513 BC BI256788 BE38 BC473378 BE2 AV749916 AA3 AL572871 AL5 AA652206 Al6i AU154988 AA6 W33334 AI073	umbers  2009390 X91257 BC000716 BM450041 BI771139 AV71093 8217 AU143368 AU133780 AU139704 BGS31086 BE2682 8298813 BI772360 BE617354 AU140124 BE277005 BG7461 874328 BM011248 AU998465 AW238888 BG930091 BG28 86117 AL571945 AL547790 AL581217 AL514659 AL57392 86014 AA654357 AU146982 AW273447 AW157715 AW57- 831254 AA828821 A0186982 AW273447 AW157715 AW57- 831254 AA828821 A0186982 AW273447 AW157715 AW57- 831254 AA828821 A0186981 AR5154399 BG319570 BF76628	235 BE545230 AU14 716 BE814960 AW1 14599 AW410037 AA 26 AL540816 AW411 4750 BG683509 AW 316 AA464944 BG26 64242 BF764209 AH	13414 A7761720 AU173842 AU143343 BE27/UDA 61287 AV762084 BG898985 AW674875 AA313975 1378483 D49914 AL673323 AL549819 AL672282 0038 B1262249 BG284713 A1559394 AU093582 AW965846 887824 AU318522 AA703770 BE542873 AA515504 1335 AU003584 BG402820 AA932098 W68695 AW182900 520320 T66029 BF447193 F59285 AL548949 B1333775
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e cluster number bank accession number Accession NM_006513 Bt BI256788 BE38 BG473378 BE2 AV749916 AA3 AL572871 AA AA652206 AI6 AU154982 AA6 W37334 AI073 BF743802 RF6	umbers  2009390 X91257 BC000716 BM450041 BI771139 AV71093 86217 AU143368 AU133780 AU1339704 BGS31086 BE2686 298813 BI772360 BE617354 AU140124 BE277005 BG7461 74328 BM011248 AU998465 AW23888 BG940091 BG28 68117 AL571945 AL547790 AL581217 AL514559 AL57392 88014 AA654357 AU146982 AW273447 AW157715 AW373 831254 AA628521 AU868602 AA854654 AA190869 BF0628 864 C17924 C18528 AU29318 BF153493 BG3174381 AA659 180730 RF2684138 BF5054718 BG774381 AA659	235 BE545230 AU14 716 BEB14950 AW1 14599 AW410037 AA 256 AL540816 AW411 4750 BG683509 AW 816 AA464944 BG26 64242 BF764209 AW 833 AA297649 AA0	13414 AV761720 AU173942 AU143343 BE27UDA 61287 AV762088 BG899935 AW674875 AA313975 1378483 D49914 AL573323 AL549819 AL572282 1887824 AB18522 AA703770 BE542873 AA515504 11335 AID03584 BG402820 AA332098 W68695 AW182900 220320 T06029 BF447133 F29285 AL548949 B1333775 10945 BG105512 BE268206 T32623 BG015679 AL518518
45	Pkey: CAT num Accessio Pkey	Unix iber: Ger n: Ger CAT Numbe	e duster number bank accession nu r Accession NM_006513 Bt B1256788 BE33 BG473378 BE3 AV749916 AA3 AL572871 AL5 AA652206 Al61 AU154982 AA6 W37334 A1073 BE743602 BE6	umbers  C009390 X91257 BC000716 BM450041 BI771139 AV7109: 86217 AU143388 AU133780 AU139704 BGS31086 BE2682 89813 BI772506 BE617354 AU140124 BE277005 BG7461 74328 BM011248 AU098465 AW23888 BG940091 BG38 68117 AL571945 AL547790 AL581217 AL514599 AL57392 88014 AA654357 AU146982 AW273447 AW157715 AW57- 331254 AA654357 AU146982 AW273447 AW157715 AW57- 331254 AA628521 AU088602 AA854654 AA798689 BF0658 864 C17924 C18528 AL29318 BF154399 BG319570 BF76 5182309 BE268139 BF038434 BE552718 BG774381 AA659	235 BE545230 AU1* 716 BEB14950 AW1 14599 AW410037 AA 26 AL540816 AW41 4750 BG683509 AW 116 AA464944 BG26 64242 BF764209 AN 18833 AA297649 AA0 1 AJ963016 BG05764	13414 A7761720 AU173942 AU143343 BE27UDA 61287 AV762084 BG899935 AW674875 AA313975 1378483 D49914 AL573323 AL549819 AL572282 10038 BL62249 BG284713 AL559394 AL033582 AW965846 1887824 AL818522 AA703770 BE542873 AA515504 11305 AL003584 BG402820 AA932098 W68695 AW182900 520320 T06029 BF447193 F29285 AL548949 BI333775 10945 BG105512 BE269205 T32623 BG015679 AL518518 103 AJ720256 AA844560 AA055570 BE619806 C17428
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•			H02874 AW97	5323 R16904 AA328030 AA054671 R79546 BF832310 A1249109
	406678	0_0	U77534 U775	
	406632	0_0	ADDOCESS AR	NOCRET ARRINGRES ARRINGREA ARRINGRES
	400278	170_1	Y00281 NM_0	02950 BC010839 BC007995 BC675232 BM468552 AL555484 BG831516 BF035300 BC677277 BF852972 BE314901 BF850656
10			AI371816 AA2	92474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BIZZ3401 BE856245 AW821164 BF914775 BF914761
			AU125835 B12	22678 B1091137 BF340536 BM462798 B1224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283
			BI013120 BF8	18845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T95891 BF981330 AW936510 AA478169 H04587 BG166574
			BI869342 BES	62482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 Al520674 BF435417 AW245648 A952404 T29534 AU153459
1.5			AU152168 AV	V591591 AU146918 AU393187 AA478013 AU148143 AU24471 AIG40728 AIB71537 AW264752 N93787 AU89357 AV756134 AU471659
15			AU147466 AA	779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 A1799771 F04407 A1285530 A1914643 AW068751 AA513325 639285 AA569644 T96892 A1923594 BF439180 B1770936 BF032438 AU154884 AA682793 AW072992 AU158815 A1884444 AL048031
			AA16462/ AA	1152546 AL695187 AL048033 AIZ45650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354
			AU 130322 AU	290705 AU 159092 AU 982693 AU 817553 AA 236729 AU 687858 BG 163767 AU 524675 AU 678155 AA 127100 AU 762661 AU 159718 AU 469720
			AAAB3637 AV	V131696 R26868 A1199885 AW875614 AW938694 AW578974 B1763988 BG819168 BE874767 BG978292 BE162948 AL555483
20			AW120719 T	56783 AID18819 AI476552 BI492837 AI824440 BC996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153
20			AW120549 A1	676567 AIRGG759 RC987935
	400252	2656_2	1144R39 NM (	narsi ronnasa riasrata autit7940 BG759024 BG749694 BE799505 BG831537 Al816335 AA325352 AL547005 AW157038 Al859331
	10000	2000_2	AURTETRE ALI	1507FS A1 043549 AW162880 A11159233 A1143169 T03478 BE727648 AA764725 BE206603 A1369814 A1984369 AW157545 BE221480
			MOODIE ALITE	CONSE ANTAINGE AMDRESSE RESULTION AATMITISE AASTRISES AMTISES AMTISES AMISSISSE AAGUZZAS HIG/73U3 BEDASSISSE
25			VISEOUST MO.	2868 D62600 D62600 D64715 TD6015 RF222174 AI954706 D53218 D53787 R59889 W86896 AI497670 K70771 BF309414 BE020147
			RC010507 AV	AGRAGER DERRECTO AL 579715 HERELD DESGER RIDAADGY AL 555239 RF220278 AAD81991 AL819544 AW001573 AW131600 AL656/64
			D52367 W22	034 BGB18979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267
			VV21941 AA 7	28817
20	411825	7891_1	AK000695 A)	CO00489 BC001688 BG235988 AW006329 AI887644 AI207230 AI148213 AI304333 AI634653 AW662636 AI281247 AA946921 AA424487
30			BE272330 AI	830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 BI906631 AW083424 AA625199 NM_017767
			AK000334 BI	984048 AW815634 AL573992 AA430612 AA928390 AA46447 AW340827 AA424290 AI927759 BG951502 AW881353 BI765535
	400263	18977_1	Z11692 X514	66 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 1560409 AL562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486
			BMU16525 A	1500019 AL502666 AI903176 BF649536 AA377735 BF050641 BF727175 BC000347 BG733 320 AC503260 B127176 BF6486 BI011828 AI313235 BC831724 BF65882 BC998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719
35			00070497 A	W498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758
23			DMAS2445 A	1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385
			RE772007 R	199487 RE761700 RID61519 RE944452 RE898506 AI038390 BMD44934 AW381142 BG743518 BE769206 BE893973 BI015047 BE806479
			BE761350 BI	2769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503
			RC674499 R	G77A17A RIN150RA
40	434642	15461_1	AF147443 B	M471094 AA948055 AA973157 AA284289 W25739 BI021926 BF898367 W02720 BF798341 BF378312 AA427766 BG955568 BF899591
			RFRR4215	
	447697	MH497_6	BE742621 A	L528391 AA328484 W52125 AA321596 AA022458 AW971024 AI052029 AI761638 AA628498 BE619513 AA412069 AI027538 AW514954
		_	AI884599 AI	097362 AI499259 AI419408 AW469200 AI992152 AI142045 AI066572 AI275439 AA581877 AI347308 AI016726 AI127541 AW002064
4.5			AI141785 AV	V051842 AI355329 AI198198 AI347858 AI027870 AI039163 AA576695 AI183286 AI362001 AI361994 AA594668 AA459257 AA745778
45			A1139667 F2	0651 AI201510 AA832171 BM464599 BM464574 AI972621 AI183887 AW131911 AW771584 BE619828 AA492218 AA025767 AA977354
				45137 W73596 A1864400 A1200026 A1270963 F18139 W46301 H55825 A1039867 A1457570 A1928639 A1824685 A1083898 AW024570
			AA285299 A	W381097 AW582409 BE964181
	TABLE 5	۰۰.		
50	Pkey:		taiana anatar caa	responding to an Eos probeset
30	Ref:		Samence course	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	1401.	,	sequence of human	chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:			nd from which exons were predicted.
	Nt_positi			positions of predicted exons.
55				
	Pkey	Ref	Strand	NL position
	401941	4982556	Plus	112022-112204
	402007	7381786	Plus	143964-144081
<b>CO</b>	401739	2982169		132194-132404
60	404405	7272262		83251-83415
	401512	7622346		136399-136557
	404439	7139680		55316-55585
	402273	2979528		28990-29203,32299-32402,32474-32668 100952-101283
65	405441	7408124 9186923		114659-114832
05	401454	8117391		83179-83304
	401009 405268	4156151		24404-24521
	405701	4263751		93243-93364
	401985	3126781		18239-18389,19921-20076
70	404835	6970743		85462-85584,88139-88287,90338-91018,9482
. •	401127	8699701		88327-88458,96150-96266
	406161	7144954		16666-16836
	402728	9211639		3192-3569,4267-4728
	402897	8570339		61939-62241,64304-64615,65140-65391
75	404739			42742-43571
	404406			47543-47928
	401772			183917-184042
	402212			69382-69936
80	405752	9212305	Plus	91392-91528
30				

TABLE 59A: ABOUT 201 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE



Table 59A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease.

Genes were selected from 59680 probesets on the Eos/Afrymetrix Hur03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pitey:

Unique Eos probeset identifier number

Exacon:

Unique Eos probeset identifier number

Exemplar Accession number, Genbantk accession number

Uniquene Title:

Uniquene gene title

R1:

90th percentitle of Als for metastases from patients with progressive disease divided by the 90th percentitle of Als for metastases from patients with limited disease.

R2:

90th percentitle of Als for metastases from patients with progressive disease divided by the 90th percentitle of Als for metastases from patients with limited disease, where the 15th percentitle of normal tissue Als was subtracted from both the numerator and denominator

5

10

	OL-	ExAccri	Disease	Unigene Title	R1	R2
	Pkey 422168	AA586894	UnigenelD Hs.112408	S100 calcium-binding protein A7 (psorias	8.58	13.77
15	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.43	5.91
1.5	440099	AL080058	Hs.6909	DKFZP564G202 protein	7.07	4.56
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.91	3.51
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.90	6.44
	418067	Al127958	Hs.83393	cystatin E/M	6.62	10.34
20	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.47	13.26
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.25	3.41
	401780			NM_005557*:Homo sapiens keratin 16 (foca	6.10	4.24
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	5.97	6.60
26	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	5.89	3.57
25	412636	NM_004415		desmoptakin (DPI, DPII)	5.82	3.51 3.16
	417124	BE122762	Hs.25338	ESTs	5.16	3.10
•	430686	NM_001942	Hs.2633 Hs.1420	desmoglein 1	5.03 4,84	4.15
	421733	AL119671 AA305159	Hs.113019	fibroblast growth factor receptor 3 (ach fis485	4.79	4.59
30	422192 407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial segu	4.33	2.37
50	429493	AL134708	Hs.145998	ESTs	4.28	4.79
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23	4.82
	409010	AI648675	141.10000	Homo sapiens, Similar to RIKEN cDNA 1700	4.23	3.69
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	4,11	2.33
35	409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	4.06	3.65
	424670	W61215	Hs.116651	epithelial V-like antigen 1	4.02	4.07
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	3.97	4.71
	418663	AK001100	Hs.41690	desmocollin 3	3.95	5.08
	402075			ENSP0000251056*:Plasma membrane calcium	3.93	5.85
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.90	3.19
	427809	M26380	Hs.180878	lipoprotein lipase	3.87	3.21
	413859	AW992356	Hs.8354	Homo sapiens pyruvate dehydrogenase kina	3.85	5.75
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	3.60	3.10
45	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	3.79	3.36
45	421485	AA243499	Hs. 104800	hypothetical protein FLJ10134	3.67	3.35
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.65	4.14
	418686	Z36830	Hs.87268	annexin AB	3.65 3.64	3.62 3.18
	448429	D17408	Hs.21223	catponin 1, basic, smooth muscle	3.60	4.10
50	422963 428874	M79141	Hs. 13234 Hs. 194366	ESTs transthyretin (prealbumin, armyloidosis t	3.58	3.97
30	428674 401785	W32133	rts. 194300	NM 002275":Homo sapiens keratin 15 (KRT1	3.58	5.05
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.56	1.92
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	3.54	5.62
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.53	4.70
55	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.52	8.33
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.51	2.32
	454229	AW957744	Hs.278469 .	lacrimal proline rich protein	3.50	3.12
	401781			Target Exon	3.45	3.57
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kO)	3.45	5.07
60	431567	N51357	Hs.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	3.44	5.03
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.42	7.72
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	3.41	2.65
	442315	AA173992	Hs.7956	ESTs, Moderately similar to 2N91_HUMAN Z	3.41 3.32	5.03 2.86
65	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.32	3.18
0.5	410883 418026	D43767 BE379727	Hs.66742 Hs.83213	CCL17 chemokine (TARC) (SCYA17) fatly acid binding protein 4, adipocyte	3.26	3.10
	453309	AI791809	Hs.32949	defensin, beta 1	3.24	3.64
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.21	3.64
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.19	4.37
70	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.16	5.48
. •	452101	T60298	Hs.10844	Homo sapiens cDNA FLJ14476 fis, clone MA	3.15	3.60
	412633	AF001691	Hs.74304	periptakin	3.15	3.98
	407839	AA045144	Hs.161566	ESTs	3.15	4,11
	427318	AF186081	Hs.175783	zinc transporter	3.11	3.58
75	427899	AAB29286	Hs.332053	serum amyloid A1	3.10	3.53
	421948	L42583	Hs.334309	keratin 6A	3.08	2.75
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.05	2.99
	410001	AB041036	Hs.57771	katlikrein 11	3.04	3.02
0.0	413435		Hs.75360	carboxypeptidase E	3.00	2.40
80	428500		Hs.184641	fatty acid desaturase 2	2.98	5.22
	410099			KIAA0036 gene product	2.97 2.93	2.05 3.45
	437679			inositol(myo)-1(or 4)-monophosphatase 2	2.93	3.45 4.78
	413835	A1272727	Hs.249163	fatty acid hydroxylase	2.33	4.10

	446058	AL049801	Hs.13649	Novel human gene mapping to chomosome 13	2.89	2.93
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.88	3.14
	428398	A1249368	Hs.98558	ESTs	2.88	2.05
-	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.86	2.12
5	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.84	2.98
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.83	2.82
	428695	A1355647	Hs.189999	purinergic receptor (family A group 5)	2.83	2.37
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	2.73
• •	428471	X57348	Hs.184510	stratifin	2.79	3.31
10	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	2.79	3.72
	433147	AF091434	Hs.43080	platelet derived growth factor C	2.77	1.70
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.76	2.18
	425787	AA363867	Hs.155029	ESTs	2.75	2.42
1.5	450172	NM_005864	Hs.24587	signal transduction protein (SH3 contain	2.75	2.36
15	421773	W69233	Hs.112457	ESTs	2.73	5.59
	408536	AW381532	Hs.135188	ESTs	2.73	5.17
	437143	AW204056	Hs.8917	EST\$	2.72	1.84
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metalio	2.70	1.82
20	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	2.69	4.62
20	410325	AB023154	Hs.62264	KIAA0937 protein	2.69	2.32
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.69	3.74
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.67	2.36
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	2.65	1.78
05	420876	AA918425	Hs.177744	ESTs	2.64	7.26
25	426105	A1678765	Hs.21812	ESTs :	2.64	2.51
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	2.64	2.66
	409509	AL036923	Hs.322710	EST ₈	2.62	2.09
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	2.62	2.68
20	432503	AA551196	Hs.188952	ESTs	2.62	4.64
30	409341	AJ963376	Hs.12532	chromosome 1 open reading frame 21	2.62	1.74
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.62	2.90
	456247	R09746		gb:yf27d10.r1 Soares fetal liver spleen	2.61	3.43
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.60	3.84
26	439706	AW872527	Hs.59761	ESTs, Wealty similar to DAP1_HUMAN DEATH	2.58	3.49
35	440659	AF134160	Hs.7327	claudin 1	2,57	3.97
	459710	AI701596	Hs.121592	ESTs	2.57	3.59
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.56	3.35
	433882	U90441	Hs.3622	procollagen-profine, 2-oxoglutarate 4-di	· 2.51	3.75
40	427666	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.51	3.02
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	2.47	3.53
	449550	AA353125	Hs.184721	ESTs	2.43	4.22
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.40	6.22
	442000	H38671	Hs.8071	KIAA0735 gene product; synaptic vesicle	2.38	3.14
AC	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	2.36	3.59
45	420039	NM_004605	Hs.94581	sufforansferase family, cytosofic, 28,	2.36	2.91
	412477	AA150864		microsomal glutathione S-transferase 1	2.34	4.15
	450693	AW450461	Hs.203965	ESTs _	2.32	3.93
	406433			Target Exon	2.29	3.20
50	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	2.24	4.40
50	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.23	4.87
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	2.23	4.22
	422083	NM_001141	Hs.111256	erachidonate 15-lipoxygenase, second typ	2.22	5.71
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.21	4.86
55	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.19	3.90
55	442572	Al001922	Hs.135121	hypothetical protein FLJ22415	2.16	2.87
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.13	3.27
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	2.09	5.28
	428899	AA744610	Hs.194431	palladin	2.08	3.76
60	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.06	3.09
oo	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.05	2.88
	450423	AA486735	Hs.31869	sialoadhesin	2.02	3.04
	444105	AW189097	11-013033	ESTs	2.01	3.05
	430410	AF099144	Hs.347933	tryptase beta 1	2.01	3.71
65	409453	AI885516	Hs.95612	ESTs	2.01	4.34
UJ	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.00	5.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.99	3.59
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.92	4.16
	451541	BE279383	Hs.26557	plakophilin 3	1.89	3.90
70	425206	NM_002153		hydroxysteroid (17-beta) dehydrogenase 2	1.89	3.29
70	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.64	3.04
	401760	44300443	44- 430000	Target Exon	1.84	3.32
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	1.83	4.69
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.83	2.96
75	452208	AA024792	Hs.31895	hypothetical protein MGC4093	1.82	3.70
75	420074	AA253425	Hs.190074	ESTs	1.81	2.90
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.79	3.65
	427540	R12014	Hs.20976	ESTs	1,77	2.92
	429259	AA420450	Hs.292911	Plakophilin	1.76	3.65
80	422106	D84239	Hs.111732	Fc fragment of tgG binding protein	1.75	4.06
OU	453556	AA425414	Hs.33287	nuclear factor I/B	1,74	3.07
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.73	3.22
	406851	AA609784		major histocompatibility complex, class	1.73	3.96
	444726	NM_006147		interferon regulatory factor 6	1.71	3.65

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	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.71	4.13
	446051	BE048061	Hs.37054	ephrin-A3	1.68	3.61 3.00
	408522	AJ541214	Hs.46320	Small proline-rich protein SPRK (human,	1.67 1.66	3.11
5	450835	BE262773	Hs.25584	hypothetical protein FLJ10767 placental growth factor, vascular endoth	1.66	3.23
3	432004 431179	BE018302 AJ338644	Hs.2894 Hs.195432	aldehyde dehydrogenase 2 family (mitocho	1.64	3.29
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.57	3.94
	423184	NM_004428	Hs.1624	eptrin-A1	1.56	2.88
	414694	NM_015362	Hs.76907	HSPC002 protein	1.56	2.92
10	458746	AI380797	Hs.158992	ESTs	1.56	2.92
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.55	3.75
	438367	N79688	Hs.204354	ras homolog gene family, member 8	1.54	4.56
	403903			C5001632 gi]10645308 gb AAG21430.1 AC00	1.53 1.52	3.99 3.16
15	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.50	4.25
15	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth gap junction protein, beta 5 (connexin 3	1.50	3.35
	429211	AF052693 AF001548	Hs.198249 Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.49	3.21
	415274 418226	AA424202	Hs.83834	cytochrome b-5	1.49	3.90
	454194	BE141599	113.0000	gb:QV2-HT0083-071299-018-h01 HT0083 Homo	1.48	29(:
20	434879	M34572	Hs.159263	collagen, type VI, alpha 2	1.46	3.26
	418400	BE243026	Hs.301989	KIAA0246 protein	1.46	4.00
	409178	BE393948	Hs.50915	kallikrein 5	1.45	2.94
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.44	3.18
0.5	429002	AW248439	Hs.2340	junction plakoglobin	1.43 1.40	3.07 4.61
25	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.38	3.11
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.37	4.32
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.37	2.99
	427929 425184	BE613835 BE278288	Hs.181159 Hs.155048	Lutheran blood group (Auberger b antigen	1.36	3.17 .
30	407143	C14076	Hs.332329	EST	1.36	2.99
50	416950	AL049798	Hs.80552	dermatopontin	1.35	3.39
	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	1.34	3.17
	442599	AF078037	Hs.324051	RetA-associated inhibitor	1.33	3.30
	413659	BE155647		gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.32	2.89
35	454478	AW805749		superoxide dismutase 2, mitochondrial	1.30	3.50 3.57
	404467			Target Exon	1.29 1.28	3.00
	452516	AA058630	Hs.29759	RNĂ POLYMERASE I AND TRANSCRIPT RELEASE hypothetical protein FLJ23153	1.27	3.05
	412524	AA417813	Hs.44208 Hs.1516	insulin-like growth factor-binding prote	1.24	2.86
40	422354 406711	U20982 N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.24	3.29
70	450796	NM_001988		envoplakin	1.23	3.21
	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.23	3.65
	452791	AA227581	Hs.30634	hypothetical protein FLJ20509	1.22	2.90
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	1.19	3.47
45	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	2.91
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.10	3.50
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.00	2.99 2.91
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	1.00	2.31
50	TABLE	·00-				
30	TABLE 5		ique Eos probeset id	entifier number		,
	Pkey: CAT nun	_	na cluster number	CHARGE FOR THE CO.		·
	Accessio		nbank accession nu	mbers		
	7.00000					
55	Pkey	CAT Number	er Accession			
	412635	1438_1	M77830 NM_00	4415 AF139065 BG681115 BG740377 BI712964 BG000656	AA128470 BI430	1324 H274UB BE93103U BE107 103 AW37U027 AW37U013
			J05211 BG6988	65 BG740734 BG680618 BG739778 B1765807 BM353403 B	M35J248 AW 17	FOR DECISION REPORTED AND STATE BY STATE OF THE STATE OF
			BF149266 BE94	10187 B1060445 B1060444 BF350983 BE720095 BE720069 ( 70253 BE160433 B1039775 AW886475 BM462504 BE93173	DE / 13139 DEVO	M0777 RE381183 RC621737 A11127260 AW364859
۲۸			BE713548 AW1	70253 BE160433 B1039775 AW666475 B10462504 BE55175 23489 BE819009 BF381184 BE715956 R58704 AA852212 A	WISERSER RIDGE	358 RE087707 RE819046 RE819005 AA377127 RE073467
60			DE0100E0 DE0	10049 RIO36306 RC000973 RIO40954 RF919911 AU140155	A1951766 A14345	18 VM804P14 RF (25303 8593)/003 95353959 BL (43503
			AVAIDDEE 16 DEG	14.43C4 01020703 ALI14RAD7 DE 144343 RE709863 RE98564	2 RF001923 HF9	2351D AW265328 BG436319 BE 162100 MW303173
			A14/047CQQ DCQ	140200 AW177022 DER73670 AW178000 RE082526 RE4768	KK RFORK994 BF	78XX/P RE08X201 RE08X314 RE08X303 RL013033
			AVAINCEDS AN AVAI	0.47678 BERNA153 AW365157 RFR13930 RF002030 AW365	153 BE 184941 B	F/49421 BE184920 BF039302 BE104933 BF042234
65			DECDOATA DEG	210AR DEGGGRAG RE368816 RE184924 RE159646 RE71463	2 BE 184948 BG9	8P842 99131158 99033931 4433400 CO41 12 DLA20154
			OCOCETAL AND	100204 A1 602116 RE140760 RE705967 RE705966 RE70596	R AW848723 AV	/3/6638 WA3/9811 WA3/9931 RC000031 BL131112
			BE696084 AW	48371 AW376782 AW848789 AW84907 C.W361413 BF92	7725 BF094211 A	W997139 BE8654/4 BE18518/ BE156621 BE/15089
			8E713297 BE7	13298 BE 179915 AW799309 BF872345 BF088676 BE70593	39 AW752599 BC	005197 BF350086 BE715196 BE715133 BF732396
70			BF093817 BF8	31190 BF752409 BE006561 BG959922 BF094833 BF09474 4403 Al392926 AU158477 B1467252 AU159919 Al760816 B	8 BF034583 AVV	5//699 AW60/236 BE082519 AW51/700 BF 34507
70			Al190590 Al55	4403 A1392926 AU158477 B1467252 AU159919 A1760816 B1 89975 AA946936 AA644381 BM314884 AA702424 A1417612	FU82316 AI43311	nera alanarra alarnase kisasara Ansasara Ansasara
			AJ142882 AAU	46078 W95070 AA149191 AA026864 AI830049 AW780435	ANT 1500505 A122	R4 AIR5R2R2 RI46R5RR AIR605R4 AI025932 AA026047
			4 4 702222 4 4 5	CO1EA A R1ECON AIR/1020RS A AQ182R1 T77R61 AIQ27207 A	11205263 RF0824	91 AWD21347 AL568096 BE939862 AAU88860 U12002
			A A OCCESS A A S	reston witoses waster awtenase a ansstal Y87181 HAA	ANS AID INA 3A RE	1137513 A1494Ub9 A127UU27 A1633676 AA126330
75			DOCCULATE DES	INCATO DOMANA DECEMBED DECTEGAT RETRAKING AANTERSA	AV745530 RI762	1796 R(328/391 AW/98/80 BE/00043 DE9204/4
15			414/2001110 DE	noznae DENA9973 AWB70451 AIS71A75 REAS77RS AV7313	プロ ムバクフスポラ バブタ	754 CD33/8 N84/6/ AA1310// N30140 DE7 14230
			AICOCOCO AICE	0000 AIG16606 AIW10661A AIRR7368 AI53R577 PF996A7A P	tE067737 RG319	4R6 AA247685 AW/98883 AW1U3521 BF9091/3
			AIMPEDOTO OF	nantat DE 10676A DE 714A64 DE 713BA3 DE 713R6R DE 7137	63 RG950164 RF	/1.910 AW365151 BG935469 BC007212 BF 313331
			AIMPCELAR AIC	MCM37 DEMO370N AWBE3813 DEBEAAA3 B177N853 RE679AI	<b>YA RG740837 RG</b>	KR1087 RG698430 AA455100 187267 BE696209 BE6962 10
80			D1000403 DE0	へんりょう ひこうさつううき みほごりいりいう ひとりつをもりを ひごをフプロリラ ひごうんりひ	70 AAN KARN RE	705999 KC6/715/ BEUU9U9U BUOD 13/0 BE7 1443
			BG961498 BG	678984 BI040941 AA337270 AW384371 AW847442 BI0586 714441 AW996245 BE711801 AI284090 BE064323 BE7193	DO DEGADA 49 DO	001212 RE375714 RE349522 RC006267 T48703 RD13702
			BG949393 BE	714441 AW996245 BE711801 AI284090 BE064323 BE7193 365156 AW365154 AW606653 BF763109 BE931637 BE167	70 DE 340 140 BU	F354008 RF678726 H90899 AW365145 W38382 A4498487
			BE001925 AW		101 001 1001 70	
				570		

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_	409010	10331_1	AA059411 A1799 A1373224 AA919 BG928396 BE89	1714 BM014781 BG542863 BG77123 1263 A494075 A1572127 AA420992 B 1169 A1758175 AA976350 BG701414 16883 BF435859 AA196423 AW23747	1F436083 A1648675 AA878 DE057794 AW135598 AA6	8813 BI488614 BG N62583 BI549631	6700886 AA 128609 A AI 185077 AA 933879	AW024454 AA 193289 AA045194			
5	400700	DCE4CE 4	BF027898 BG77	9448 16 T92950 AU184997 AA077551							
10	409760 410099	865166_1 16732_1	AK055674 AW9 BG714279 AW8 AA283724 BF10 BE327043 AA7 AA211402 AW8	NKO55674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BC813935 BC911971 BC820167 A1174254 AA348720 AA364303 SC714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BC029709 W52882 A1439658 BES51237 AA283724 BF109530 A1457096 A1805992 BE457736 AA693467 A1697593 A1887863 A1167419 AW901980 AW901768 BE702179 AAA084549 T22811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 A1418634 T31586 AA435630 A366472 AA706191 A1422304 A1204899 A1041169 BA327043 AA716027 AA917004 AA167714 BF339675 AA084618 A1418634 T31586 AA435630 A3366472 AA706191 A1422304 A1204899 A1041169 BA327043 AA716027 AA917004 AA167714 BF339675 AA084618 A1418634 T31586 AA435630 A3366472 AA706191 A1422304 A1204899 A1041169 BA327043 AA716027 AA917004 AA167714 BF339675 AA084618 A1418634 T31586 AA435630 A3366472 AA706191 A1422304 A1204899 A1041169							
	455047	0440007 4		5 D52685 T07735 BE702069 BE7021	72 1086/1 BE/6/121 BE/	16/11/ BE/0/113					
15	456247 412477	2142387_1 8669_2	AI220117 AI857 BF594181 BF11 AI281153 N518 AI383720 BE04	210170 R09746 1220117 A1857837 A1218371 BM091400 A304984 A1198508 A1400738 AW571549 AW950042 A1089943 AA437280 A1150878 BF 197070 A1267984 12790117 A1857837 A1218371 BM091400 A304984 A1198508 A1400738 AW571549 AW950042 A1089943 AA437280 A1150878 BF 197070 A1267984 12790118 BF 196688 A1433152 A1338921 A1620364 A1280197 AA652531 A1674938 A1342447 A1620350 A1281295 A1148621 N54787 A1338121 12790118 A1087072 AA954788 AW065054 A1346309 BG5259629 A1340135 BF083036 A1167365 AW8195657 AA955468 A1467868 AW148701 12790118 BF091708 AND A12854 AND A128548 AW706506 A148720 N99966 A1568933 A1915737 A1080691 A1185388 N48996 N68575 H26264 H50037 A12877247 T95664 BF993863 A1749637 AW088541 AA991294 AA887452 A1073726 AA633132 AA629674 AA629649 AA629656 AA578595 A116878							
20			AA804572 A108 AI382839 AA19	5786 AA994396 AA991209 AA94866 14837 AA406284 A1250750 R37035 A1	3 AA929054 AA927952 TE	37001 AA928210 A	A629296 AW802267	AW384129 BF744400 AA194110			
	444105	649788_1	A A COG704 DO7	23917 Al123926 304							
25	406851 444726	0_0 3503_2	8G285809 BES AW188320 AIS AW664668 AW AW849405 AW	40673 BG432524 BE157554 BG6769 98246 BE673290 AW297653 AA1565 274339 AA582788 AI345741 AW3014 874339 AW84773 BE673179 AI611	32 A1017342 A1916754 A1 433 A1873468 AW137388   327 AA705753 BE715478 BE715564 A1877577 AA0	190544 AI184302 BF718731 BF7184 AW849414 AW84 29457 C00338 AM	AA857671 BE657016 113 AA877495 BF001 9399 A1085759 A1140 169558 BE715577 AA	575 A1824693 AW849604 0849 T67412 A1889885 AW104647 0845413 BF843813			
	454194	171445_1	BE141599 AW	845896 AW178095 BE140914 BE140	909 AW178107 AW17809	4 AW845883 BF3	19267 AW845898 AW	/845811 AW845814 BF767720			
30	406799	0_0	AA908548								
	413659 454478	1526081_1 4273_16	BE155647 BE AW796921 AV	155627 1798102 AW805749 AW805872 BF98	5060 AW794380 BF38044	19 AW794466 AW	794538				
35	TABLE 59 Pkey:	I Inio	ue number corre	ponding to an Eos probeset							
33	Ref:	Sea	uence source. Ti	e 7 digit numbers in this column are C	Senbank Identifier (GI) nurr	nbers. "Dunham, e	et at." refers to the put	blication entitled "The DNA			
		seq	uence of human o	hromosome 22" Dunham, et al. (1999)	Nature 402:489-495.						
	Strand: Nupositio	n indi	cates UNA strand cates nucleotide (	from which exons were predicted. ositions of predicted exons.							
40	ПОО	71.									
	Pkey	Ref		Nt_position 28397-28617,28920-29045,29135-291	206 20/1						
	401780 402075	7249190 8117407	Plus	121907-122035,122804-122921,1240	19-12416						
	401785	7249190	Minus	165776-165996,166189-166314,1664	08-16656						
45	401781	7249190		83215-83435,83531-83656,83740-83 50004-50555	901,8423						
	406433 401760	.9256507 9929699	Plus Plus	58094-58565 83126-83250,85320-85540,94719-95	287						
	403903	7710671	Minus	101165-102597							
50	404467	8077630	Minus	24951-25853							
50											
	TABLE 6	OA: ABOUT 53	GENES UPREG	ULATED IN BENIGN NEVI RELATIVE	TO NORMAL TISSUES	stantad from EDC9	A contracte on the Ea	ne/Affumetrix Huft3 Genechin array			
	Table 60	A lists about 53 receion data fo	genes upregulati coch ombosel (	d in benign nevi relative to normal tiss blained from this analysis was expres	sues. I nese genes were s sed as average intensity (/	Al), a normalized v	alue reflecting the rel	ative level of mRNA expression.			
55	Pkey:	Uni	ique Eos probese	l identifier number		•	•				
	ExAccn:			number, Genbank accession number							
	Unigenel Unigene		igene number igene gene title								
	R1;	-	woma of basiss a	evi Als divided by the 90th percentile o	of normal tissue Als	450	l a a-maril Garage Ata wa	w cubtracted from both the			
60	R2:		erage of benign n merator and deno	evi Als divided by 90th percentile of no	xmal bssue Als, where the	15th percentile of	HORMAN USSUE ALS WE	2 2000 SC (20 11 OH) 100 1 110			
		1144	motor and con-	er in region							
	Pkey	ExAccn	UnigenelD	Unigene Title	noshroma dalla	R1 8.69	R2 5.62	•			
65	430377 409601	NM_00192 AF237621	2 Hs.301865 Hs.80828	dopachrome tautomerase (do keratin 1 (epidermolytic hyper		8.37	13.47				
05	430686	NM_00194		desmoglein 1		7.26	4.78				
	406964	M21305		FGENES predicted novel sec		6.50 6.40	3.73 7.35				
	426555 429852	NM_00037 AB010445	2 Hs.2053 Hs.225948	tyrosinase (oculocutaneous a small inducible cytokine subfi		6.23	8.85				
70	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate		5.49	4.32				
	420208		Hs.95972	silver (mouse homolog) like		5.45 3.88	9.84 3.00				
	431360 421773		7 Hs.251680 Hs.112457	loricrin ESTs		3.80	9.04				
	438380		Hs.6194	chondroitin sulfate proteoglyo		3.74	4.23				
75	431089	BE041395		ESTs, Weakly similar to unkr	nown protein	3.21	2.34				
	420798		Hs.99936	keratin 10 (epidermolytic hyp p53-responsive gene 5	erkeratosis	3.08 2.88	3.20 5.01				
	442503 405451		Hs.150853	pss-responsive gene s dihydropyrimidinase-like 3		2.88	2.85				
	452240	AI591147	Hs.61232	ESTs		2.86	1.90				
80	402525		Un 75040	NM_002699":Homo sapiens	POU domain, clas	2.78 2.65	2.72 5.58				
	413171 439496			tyrosinase-related protein 1 Homo sapiens, Similar to Ril	ŒN cDNA 1110	2.55	3.18				
	422656		Hs.1569	LIM homeobox protein 2		2.45	2.38				
					500						

	453317	NM_002277	Hs.41696	boardin bate autors a		
	420783	AI659838	Hs.99923	keratin, hair, acidic, 1 lectin, galactoside-binding, soluble, 7	2.34 2.33	3.76
	422511	AU076442	Hs.117938	collagen, type XVII, abha 1	2.33 2.28	2.43 2.00
5	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.28	2.50
J	459702 451668	AJ204995	II- 200444	gb:an03c03.x1 Stratagene schizo brain S1	2.25	1.85
	431703	Z43948 AA514264	Hs.326444 Hs.4437	cartilage acidic protein 1 triosephosphate isomerase 1	2.23	2.42
	453511	AL031224	Hs.33102	AP-2 beta transcription factor	2.15 2.13	2.20 2.20
••	401780			NM_005557*:Homo sapiens keratin 16 (foca	213	2.02
10	416640	BE262478	Hs.79404	neuron-specific protein	2.11	2.02
	444105 428748	AW189097	11-00705	ESTs	211	1.46
	418067	AW593206 Al127958	Hs.98785 Hs.83393	Ksp37 protein cystatin E/M	2.09	1.52
	417017	AA976064	Hs.180842	ribosomal protein L13	2.09 2.08	2.32 2.52
15	401781			Target Exon	2.02	2.03
	407178 452308	AA195651		AP-2 beta transcription factor	1.88	2.17
	452308 429348	AI167560 AJ242859	Hs.61297	ESTs	1.84	2.38
	402880	-ME42003	Hs.199731	Langerhans cell specific c-type tectin Target Exon	1.83	3.26
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	1.69 1.69	2.10 2.20
	401953			NM_006311:Homo sapiens nuclear receptor	1.66	2.02
	424010	AL080168	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	1.65	2.05
	432800 400328	BE391046 X87344	Hs.278962	AIM-1 protein	1.61	2.83
25	412580	AA113262	Hs.17901	transporter 2, ATP-binding cassette, sub	1.57	2.27
	435292	N20514	Hs.172965	Homo sapiens, clone (MAGE:3937015, mRNA, ESTs	1.55 1.53	2.42 2.21
	408561	AI308037	Hs.84120	hypothetical protein MGC13016	1.52	· 2.01
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.47	2.71
30	447763 454478	BE619911 AW805749	Hs.115803	hypothetical protein	1.40	2.10 .
	427289	AI097346		superoxide dismintase 2, mitochondrial phosphoserine aminotransferase	1.30	2.36
	430513	AJ012008	Hs.241586	G6C protein	1.24 1.20	2.02 2.18
	411388	X72925	Hs.69752	desmocollin 1	1.00	2.43
35	TABLE 6	NO:				
	Pkey:		ua Eos probeset	identifier number		
	CAT num	iber: Gen	e cluster number	actions individes		•
	Accessio	n: Gen	bank accession n	umbers .		
40	Pkey	CAT Number	Accomolog			
	431089	125941_2		/063489 AA715980 BF001091 BF880066 AA666102 AA6219	MC 4 4 404 00C	
	459702	539529_1	8G207209 BE	166299 Al204995 BG 199355 AW969908 AA528756 AW4407	MO AA491826 176 91044354	
	444105	649788_1	AW189097 AI	123917 Al123926		
45	407178 454478	683007_1	AW235123 AA			
• •	427289	4273_16 1820_2	ROM735921 AV	/798102 AW805749 AW805872 BF985060 AW794380 BF38 766159 BG769338 BG761999 BG744385 BG770572 AW370	0449 AW794466 A	W794538
			AW612968 AA	630644 AI751211 N26980 AI394506 AA747849 BF 154926 E	1010 AW3/0561 AV 1F4771RS &&&AGA	49/8353 AW32/9/
			AW012240 AA	5U5495 AA515380 BG760793 AW370651 BG766029 AW378	1595 RF229885 RC	2762422 RG26400
50			AV/U3420 H6	x047 AA485582 R56186 H90385 R55913 BI261497 BI01840.	3 BF376945 T7557	M RF933325 RF93
-0			BIU10121 N41	953 BF933343 BF932871 H08334 R14012 BF897622 T5081	6 BG698803 BF34	0083 Z20199
	TABLE 6					
	Pkey:	Uniq	ue number corres	sponding to an Eos probeset		
55	Ref:	Sequ	ience source. Th	e 7 digil numbers in this column are Genhank Identifier (GI) a	tumbers. "Ounhan	n, et al." refers to th
,,	Strand:	sequ	ieuce or umusu c	nromosome 22" Dunham, et al. (1999) Nature 402:489-495.		
	Nt_positio	m: Indic	ates onva strato ates nucleotide o	from which exons were predicted. ositions of predicted exons.		
	_			over a production excitation.		
50	Pkey	Ref		Vt_position		
JU	405451 402525	7622517		145949-146227		
	402323	9800048 7249190		19748-20683 19307-28617 28030 20045 20125 20205 2044		
	401781	7249190		28397-28617,28920-29045,29135-29296,2941 33215-83435,83531-83656,83740-83901,8423		
•	402880	9926561		11555-41865		
55	401963	3126783	Plus !	51382-51521		
	TABLE 6	IA: ABOUT 72	SENES UPREGU	LATED IN BENIGN NEVI RELATIVE TO PRIMARY MELANI	OMAC	
70	l abse o i /	N MSIS 200UT /2 0	enes upregulated	In benian agri relative to primary metanomae. Genes word	enlantad from CDCG	O nenhesets on the
70	GBHG CA	COSTON COM ICE	eaux proveset or	Named from this analysis was expressed as average intensity	(Al), a normalized	value reflecting the
	Pkey: ExAccn:	Outq	ue cos proceser	Denuner number		
	Unigenell	D: Utnin	eue unuper idiai viccezzion i	rumber, Genbank accession number		
	Unigene 1	Title: Unig	ene gene tide			
75	R1	aver	age of benian nev	ri Als divided by the 90th percentile of primary melanoma Als		
	R2	aven	aga of benign nev	i Als divided by the 90th percentile of primary melanoma Als.	where the 15th pe	I termon to etimeore
		num	erator and denom	in accor	•	
٠.	Pkey	ExAcon	UnigenetD	Unigene Title	R1	R2
80	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.60	2.50
	424897 429852	D63216 AB010445	Hs.153684 Hs.225948	Inizzled-related protein	3.40	2.69
	431089	BE041395	175.223390	small inducible cytokine subfamily A (Cy ESTs, Wealthy similar to unknown protein	2.90	3.25
				record owner to disknown brotein	2.82	1.56

: Eos probeset identifier number duster number nk accession numbers

BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA6211 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492 BG207209 BE166299 A/204995 BG199355 AW969908 AA528756 AW440

NM_024638:Homo sapiens hypothetical prot C1002500:gi[6754254]ref]NP_034610.1] hea C4000447-gi[7705570]ref]NP_038851.1] kI baculoviral IAP repeal-containing 7 (fiv

cytochrome c-1.
Homo sapiens cDNA: FLJ22105 fis, clone H
KIAAN55 gène product
NM_005311:Homo sapiens nuclear receptor
NM_0074631:Homo sapiens myxovirus (influ

hypothetical protein DKFZp434F1819 NM_021158*:Nomo sapiens protein kinase d morophage myristoylated alanine-rich C

ENSP00000174317":KIAA0303 (FRAGMENT).

ENSF00000174317-740AA0303 (FRAGMENT) Target Exon proteotipid protein 1 (Petizaeus Merzbac C4001432*:gi6009515(bi)[BAA94941.1] (AB gb/Human F-variabbe segment 5 to antith hypothetical protein FLU13074 beta sits APP-deaving enzyma 2 hypothetical protein PF3501 eutarpote translation initiation factor C12001707*:gi73052(15)reft/P_C08599.1] k hypothetical protein PF3501 eutarpote translation initiation factor C12001707*:gi73052(15)reft/P_C08599.1] k hypothetical protein PF3501 extrapote translation initiation factor C12001707*:gi73052(15)reft/P_C08599.1] k hypothetical sci 1 Stratagemen gray (937217)

ch.y65g12.s1 Stratagene ovary (937217) polassum voltage-gated channel, shaker-trinucleoide repeat containing 3 phosphosenine aminotransferase

matrix metalloproteinase 17 (membrane-in

hypothetical protein
ESTs, Weatry similar to C29149 proline-r
amyloid beta (A4) precursor protein-bind

zona pellucida glycoprotein 3A (sperm re

F-box only protein 7 microphthalmia-associated transcription

Target Exon gb:Human mRNA for pre-mRNA splicing fact Target Exon

hagea cturi NM_022355:Homo sapiens putative dipeptid hypothetical protein PP3501 gb:601275386F1 NIH_MGC_20 Homo sapiens c gb:TC8AP1E1967 Pediatric pre-8 cell acut

Target Exon
ESTs, Weakly similar to BING1 [H.sapiens
ceroid-lipotuscinosis, neuronal 2, late

small nuclear ribonucleoprotein 70kD pol leukocyte immunoglobulin-like receptor, gb;yd60d06.r1 Soares fetal liver spleen

ENSP0000034663:Zinc finger protein 131

ES18
hypothetical protein FLJ11006
NM_022490:Homo sapiens hypothetical prot
preferentially expressed antigen in mela
Homo sapiens mRNA full length insert cON

KIAA0468 gene product coronin, actin-binding protein, 28

cofiin 1 (non-muscle) **ESTs** 

leukocyte tyrosine kinase

ESTs

**ESTs** 

G protein-coupled receptor 27

C7002129*:gi]3638957[gb]AAC36301.1] (AC0 Target Exon natural killer-turnor recognition sequence

AIM-1 protein

Eos Control Target Exon

Target Exon

**ESTs** 

calpain 3, (p94)

Target Exon

ESTs cytochrome c-1

.256126 .40300

.129501

:13245

i.112095 i.75061 i.192352

£1787

s.10043 s.271411 s.301406 s.93379

s.298184 s.21858 s.159581

k 278962

is.115803 ls 187461 Is.279175

**b.241493** 

6.5912 ts.166017

ts.161757

ts.158287 ts.24907 ts.161851

±.301406 Hs.123164

Hs.25734 Hs.20478

Hs.174051 Hs.67846 Hs.210

Hs.278283

Hs.40527

Hs 47448

Hs.49344 Hs.30743 Hs.20034



•	459702	539529_1	BG207209 BI	E 166299 AIZ04995 BG 199355 AW969908 AA528756 AW440776 BI044354
	414221	685588_1	AA136653 AA	A136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE 168945
	455657 419200	1490185_1 9531_1	RENSENAS AV	C065364 BE065110 BE065111 N190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345
5	413200	3001_1	AAG37302 A	NR18444 RE9297RD RC49RE78 RE155010 RI59R271 BI59S811 BE161728 AW578737 AW753711 AW379707 AW381918 BG500608
			AW028637 A	W994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI576131 836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BID43239 AW474342 BG708553 AW362423 BF090028
			RFR27256 R	1655) R39478 R39479 R94358 RG540916 RM314745 AA251087 D54231 D55774 BF085805 D31589 AW966405 AW994425 D81879
10			RENGREAS AT	WQN1107 AA383529 RID21552 R56420 N39976 AA573281 HB2595 AA234955 BED93539 AW367006 BF358697 BF366318 AA663856
10			AV724531 D	F035969 A1267384 A1267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798
			BM128728 A	A193411 AW444709 AW952455 A1887612 BF431948 B1496876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595
			AA625761 A	A872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 A1184164 AA164411 BI495332 BE858113 10660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373329 AW373302
15	430540	713_2	RC017171 R	CD12195 NM 007126 AF100752 AL137377 Z70768 BM474855 BG754806 AU124376 BG75/203 BG/64420 BG/75028 BG824418
			BM045810 A	U120387 BC770238 BC686740 BC913323 BI759980 BC395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 - 196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399
			A1365196 AV	M337984 AWD2615D RE466591 BE674599 AIB18438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
20			RF732715 R	M043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 IE560537 BE903782 BE732947 B1227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 B1459099 BE391391 BE259420
20			BE209100 A	WYA CA 22 A 1423RA7 A 1914G 1R HROS 24 RF 301004 AL 5 31791 A 143S 581 BF 793112 A 1577303 AA 373265 BE 745965 BF 743630 BE 879296
			VISCOVOS BI	lintrerr aigropen awn77450 f.20201 aw151405 aw517572 aa773488 BG259694 BE391163 BG621529 A4421720 BG/6/231 BM402953
			W/58732 W/8	NSZS48 AA113434 BE785431 BID41981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BID91658 N72512 1669D BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
25			F13645 R41	394 AK025758 BG180977 BE349455 AA812018 AA740241 Al027722 Al150356 AA886395 AW977627 BE220225 AA884082 AW518114
			AJ243844 A	AB09493 AA481029 AA825718 AI347866 A431670 AA814436 A1251109 R07704 AA765606 AA724593 A1918399 AI537550 AA491103 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 B1860809
			BE002760 B	3G746251 BE962912 BM454584 AL134894 BF104082 HB0591
30	434596 427289	14701_1 1820_2	RC007350 I	199538 159589 159598 159542 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 AI889380 AA868504
30	421203	1020_2	AW612968	AAR30644 A1751211 N26980 A1394506 AA747849 BF154926 BF477185 AA649647 R39135 A1750216 T35363 W36278 AW0/9375
			AW612240	AAS0SA95 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 H55047 AA485582 R56186 H90385 R55913 B1261497 B1018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504
0.5			D1019121 N	M 1053 DE0333M3 DE033R71 M0R33A D 14012 DER97622 T50R16 DC69RR03 DE340083 Z20199
35	400263	18977_1	RM016525	1466 NM, 001961 M19997 B1224253 BCB30478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 AL560409 AL562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486
			B1517580 B	G876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF8057 I
	•		DMACAAAS	AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 AI937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385
40			RF772007	01100487 RE761700 RI261519 RE944452 RE898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BR015047 BF886479
			BF761350	BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG774174 BI015084
	414580	623093_1		BE385437 BE408833 BE387650
45	437026 419045	1240260_1 348516_2		AA742335 AA830000 BG723297 T85693 T81681 T81909
73	419043	340310_2	Br301324	00/2227/1000001/000007
	TABLE 6: Pkey:	l In	ioue number co	prresponding to an Eos probeset
50	Ref:	Se	quence source.	. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
50	Strand:			an chromosome 22' Dunham, et al. (1999) <u>Nature</u> 402:489-495. and from which exons were predicted.
	Nt_position			de positions al predicted exons.
	Pkey	Ref	Strand	Nt_position
55	404356	7630858	Minus	126433-126623
	401116 404977	9966559 3738341	Plus Minus	123579-1244 <i>4</i> 7 43081-43229
	402181	8575912	Plus	449746-450040
60	405451 402217	7622517 9795981	Minus Minus	145949-146227 21521-21757
	406040	6758938	Minus	23063-23599
	403532 402829	8076842 8918414	Minus Ptus	81750-81901 101532-101852,102006-102263
25				31755-32148
65	403828	9838214	Plus	
	405776	7159748	Minus	105911-107251
	405776 401963 402994	7159748 3126783 2996643	Minus Plus Minus	105911-107251 51382-51521 4727-4969
	405776 401963 402994 406016	7159748 3126783 2996643 8272661	Minus Plus Minus Plus	105911-107251 51382-51521 4727-4969 41341-41940
70	405776 401963 402994 406016 402911 403960	7159748 3126783 2996643 8272661 7263904 8224409	Minus Plus Minus Plus Plus Minus	105911-107251 51382-51521 4727-4969 41341-41940 142689-142979 90999-94843
70	405776 401963 402994 406016 402911 403960 406266	7159748 3126783 2996643 8272661 7263904 8224409 7528342	Minus Plus Minus Plus Plus Minus Minus	105911-107251 51382-51521 4727-4969 41341-41940 147689-142979 90999-94843 2365-2518
70	405776 401963 402994 406016 402911 403960 406266 403803 404790	7159748 3126783 2996643 8272661 7263904 8224409 7528342 8112965 7230958	Minus Plus Minus Plus Plus Minus Minus Plus	105911-107251 51382-51521 4727-4969 41341-41940 142689-142979 90999-94843 2365-2518 55513-55778 38611-38761
	405776 401963 402994 406016 402911 403960 406266 403803 404790 405318	7159748 3126783 2996643 8272661 7263904 8224409 7528342 8112965 7230958 3638954	Minus Plus Minus Plus Plus Plus Minus Minus Plus Plus Plus Plus Plus	105911-107251 51382-51521 4727-4969 41341-41940 142683-142979 90999-94843 2365-2518 55513-55778 33611-33761 79689-79967
70 75	405776 401963 402994 406016 402911 403960 406266 403803 404790 405318 402343 403986	7159748 3126783 299663 8272661 7263904 8224409 7528342 8112965 7230958 3638954 8099256 8576059	Minus Plus Minus Plus Plus Plus Minus Minus Plus Plus Plus Plus Plus	105911-107251 51382-51521 4727-4969 41341-41940 142689-142979 90999-94643 2365-2518 55513-55778 33611-38761 79689-79967 4577-6084
	405776 401963 402994 406016 403911 403960 406266 403803 404790 405318 402343 403986 401914	7159748 3126783 2996643 8272661 7263904 8224409 7528342 8112965 7230958 3638954 8099256 8576059 9369520	Minus Plus Minus Plus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus	105911-107251 51382-51521 4727-4969 41341-41940 147689-142979 90999-94843 2365-2518 55513-55776 33611-38761 79689-79967 4577-6084 90692-91238 62537-62945,63155-63308
75	405776 401963 402994 405016 402911 403960 406266 403803 404790 405318 402343 403986 401914 402450 404067	7159748 3126783 299661 7263904 8224409 7528342 8112965 7230958 3638954 8099256 8576059 9369520 9796674 3282162	Minus Plus Minus Plus Plus Plus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	105911-107251 51382-51521 4727-4969 41341-41940 142689-142979 90999-94643 2365-2518 55513-55778 33611-33761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071
	405776 401963 402994 406016 402911 403960 406266 403803 404790 405318 402343 403986 401914 402450 404667	7159748 3126783 2996643 8272661 7263904 8224409 7528342 8112965 7230958 3638954 8099256 8576059 9369520 9796674 3282162 9256126	Minus Plus Minus Plus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	105911-107251 51382-51521 4727-4969 41341-41940 142683-142979 90999-94843 2365-2518 55513-55778 33611-33761 79689-79967 4577-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071
75	405776 401963 402994 405016 402911 403960 406266 403803 404790 405318 402343 403986 401914 402450 404067	7159748 3126783 2996643 8272661 7263904 8224402 8112965 720958 86399256 8576059 9369520 9796674 3282162 9256126 9838275 9909420	Minus Plus Minus Plus Plus Plus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	105911-107251 51382-51521 4727-4969 41341-41940 142689-142979 90999-94643 2365-2518 55513-55778 33611-33761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071



404632 9796668 Plus 45096-45229

TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES

Table 63A lists about 181 genes upregulated in benign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pitary: Unique Eos probeset identifier number

ExAcor: Exemplar Accession number, Genbank accession number

UniquenelD: Uniquene unumber

Uniquene gene title

R1 average of benign nervi Als divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. 5

10

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene title
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als
average of benign nevi Als divided by the 90th percentile of melanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both
the numerator and denominator

		the nu	merator and deno	minator		
15				41 *	R1	R2
	Pkey	ExAcon	UnigenelD	Unigene Tide	19.33	19.21
	401781	A1 0070 AA9	N= 117079	Target Exon coflagen, type XVII, alpha 1	13.54	14.18
	422511 401780	AU076442	Hs.117938	NM_005557*:Homo sapiens keratin 16 (foca	12.97	13.63
20	401760	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	12.61	31.19 ;
20	412636	NM_004415	1-3,50020	desmoptakin (DPI, DPII)	11.73	6.91
	420783	Al659838	Hs.99923	tectin, galactoside-binding, soluble, 7	10.18	14.08
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	8.48	6.79
0.5	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	8.28	9.62
25	430685	NM_001942	Hs.2633	desmoglein 1	7.26 7.12	5.64 10.88
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy ESTs	7.12	6.59
	442577 406964	AA292998 M21305	Hs.163900	FGENES predicted novel secreted protein	6.50	8.82
	400304	M21303		NM_002275*:Homo sapiens keratin 15 (KRT1	6.40	9.77
30	410001	AB041036	Hs.57771	kallikrein 11	6.18	6.16
- •	417515	L24203	Hs.82237	ataxia-tetangiectasia group D-associated	5.73	16.57
	418686	Z36830	Hs.87268	annexin A8	5.32	5.27
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.89	9.81
26	452240	A1591147	Hs.61232	ESTs	4.89 4.74	6.67 4.80
35	402525	NIA 000437	Hs.251680	NM_002699*:Homo sapiens POU domain, clas toricrin	4.66	3.98
	431360 431103	NM_000427 M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63	5.69
	418067	Al127958	Hs.83393	cystatin E/M	4.56	6.78
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	4.56	5.73
40	418663	AK001100	Hs.41690	desmocollin 3	4.44	5.23
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	4.24	6.49
	439706	AW872527	Hs.59761	ESTs, Wealthy similar to DAP1_HUMAN DEATH	3.95 3.88	3.37 9.60
	421773	W69233	Hs.112457	ESTS	3.82	10.18
45	408536 418394	AW381532 AF132818	Hs.135188 Hs.84728	ESTs Kruppel-like factor 5 (intestinal)	3.78	6.33
73	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.77	4.92
	432374	W68815	Hs.301885	Homo saciens cDNA FLJ11346 fis, clone PL	3.70	5.30
	424049	AB014524	Hs.138380	KIAA0624 protein	3.68	4.41
	421948	L42583	Hs.334309	keratin 6A	3.62	3.13
50	427666	AI791495	Hs.180142	catmodutin-like skin protein (CLSP)	3.59	4.40
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.48 3.42	6.09 3.28
	436895	AF037335	Hs.5338	carbonic anhydrase XII serine protease inhibitor, Kazal type, 5	3.42	3.89
	437191 401760	NM_006846	Hs.331555	Target Exon	3.21	7.11
55	431089	BE041395		ESTs, Wealdy similar to unknown protein	3.21	5.78
	434293	NM_004445	Hs.3796	EphB6	3.14	3.11
	412432	AA126311	Hs.9879	ESTs	3.14	4.85
	442503	AF147078	Hs.150853	p53-responsive gene 5	3.11	5.92 4.89
60	41,4987	AA524394	Hs.294022	hypothe6cal protein FLJ14950	3.07 2.99	3.09
OU	420798 433339	W93774 AF019226	Hs.99936 Hs.8036	keratin 10 (epidermotytic hyperkeratosis glioblastoma overexpressed	2.96	2.75
	414876	AW950925	Hs.924	crystallin, mu	2.94	3.82
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA.	2.87	3.42
	424897	D63216	Hs.153684	frizzled-related protein	2.87	1.96
65	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.73	2.54
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.72 2.71	2.92 2.21
	427318	AF186081	Hs.175783	zinc transporter	2.67	6.47
	452887 452308	AI702223 AI167560	Hs.107253 Hs.61297	hypothetical protein DKFZp761F24	2.67	4.61
70	492300	BE514982	Hs.38991	S100 calcium-binding protein A2	2.64	2.68
, 0	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.57	3.91
	451541	BE279383	Hs.26557	plakophilin 3	2.49	5.47
	453317	NM_002277		keratin, hair, acidic,1	2.45	4,17
76	412633	AF001691	Hs.74304	periptakin 3 0 0	2.42	4.90
75	417233	W25005	Hs.24395	small inducible cytokine subfamily 8 (Cy	2.41 2.39	2.68 2.67
	424797	AA622394	Hs.153177	ribosomal protein S28	2.39	4.07
	424010 453241	AL080188 H58995	Hs.137556 Hs.37648	Homo sapiens mRNA; cDNA DKFZp434A132 (fr ESTs	2.39	2.34
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	2.36	1.88
80	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	2.32	2.24
	432222		===,	gb:an03c03.x1 Stratagene schizo brain \$1	2.31	1.99
	430168	AW968343	Hs.145582	DKFZP43411735 protein	2.30	2.60
	457121	AJ743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	2.28	1.91
				586		

	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.27	8.50
	446989	AK001898	Hs.16740	hypothetical protein FU11036	2.27 2.25	2.21 2.54
	429365	AA451798	Hs.99249	ESTs qb:an03c03.x1 Stratagene schizo brain S1	2.25	2.35
5	459702	AI204995	LL- 0049E	gap junction protein, beta 3, 31kD (conn	2.23	2.17
,	420511 444946	AF052692 AW139205	Hs.98485 Hs.156457	hypothetical protein FLJ22408	2.23	3.23
	417017	AA976064	Hs.180842	ribosomal protein L13	2.21	2.74
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.21	1.68
	430152	AB001325	Hs.234642	aguaporin 3	2.20	3.32
10	444726	NM_006147		interferon regulatory factor 6	2.15	5.20
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.15	2.82
	425483	AF231022	Hs.158159	FAT turnor suppressor (Drosophila) homolo	2.14	2.96
	419912	AF249745	Hs.6066	Rho guanine mudeotide exchange factor (	2.14	2.25
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 atpha	2.12	2.99
15	444105	AW189097		ESTs	2.11	2.98
	428748	AW593206	Hs.98785	Ksp37 protein	2.09 2.09	1.51 3.25
	456826	AIB71742	Hs.302428	wingless-type MMTV integration sile fami	2.09	4.97
	413163	Y00815	Hs.75216 Hs.65424	protein tyrosine phosphatase, receptor t tetranectin (plasminogen-binding protein	2.05	5.68
20	410677	NM_003278 AI917602	Hs.106440	ESTs	2.06	2.04
20	430285 444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.05	5.92
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.04	2.19
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	2.04	3.08
	433428	T29975	Hs.33104	Huntingtin Interacting protein C	2.04	1.63
25	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	2.03	3.92
	446727	AB011095	Hs.16032	KIAA0523 protein	2.01	2.60
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.01	2.05
	452554	AW452434	Hs.58006	ESTs, Wealdy similar to ALU5_HUMAN ALU S	1.99	4.04
20	439625	AF086453	Hs.58611	ESTs	1.99	231
30	402880			Target Exon	1.99	2.75 2.10
	428471	X57348	Hs.184510	stratifin	1.98 1.97	3.16
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.95	3.89
	452547	AA335295	Hs.74120	adipose specific 2 inositol(myo)-1(or 4)-monophosphatase 2	1.94	2.06
35	437679	NM_014214 AA420450	Hs.5753 Hs.292911	Plakophilin	1.93	2.96
33	429259 406387	AV4420430	115.232311	Target Exon	1.92	2.97
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.91	3.46
	437202	AA326110		nuclear transcription factor Y, gamma	1.89	2.00
	426150	NM_003658	Hs.167218	Bart-like homeobox 2	1.86	2.60
40	434574	AI424458	Hs.33470	ESTs	1.85	4.61
	446051	BE048061	Hs.37054	ephrin-A3	1.85	3.48
	424471	AA341329	Hs.311524	ESTs	1.84	2.62
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.83	4.69
	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocytic 2	1.82	2.00
45	451849	AI199261	Hs.27191	hypothetical protein from clone 24796	1.81	2.31
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.79	3.07
	423523	AW299828	Hs.193580	ESTs	1.77	3.37 2.46
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.76 1.73	2.06
50	403828	**300015		C4000447*:gi 7705570 re  NP_038851.1  KI	1.68	3.16
20	412446	A1768015	Hs.94581	ESTs suffotransferase family, cytosofic, 28,	1.67	2.22
	420039 411274	NM_004605 NM_002776		kallikrein 10	1.66	2.26
	401963	14141_002770	113,03423	NM_006311:Homo sapiens nuclear receptor	1.66	2.52
	435016	AI284219	Hs.130749	ESTs, Weakly similar to (38022 hypotheti	1.65	2.20
55	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	1.64	3.21
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	1.63	2.94
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.62	2.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62	3.92
<b>C</b> 0	456898	NM_001928		D component of complement (adipsin)	1.60	3.43 2.18
60	423526	AB011086	Hs.129739	KIAA0514 gene product	1.60	
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	1.60 1.59	2.47 2.99
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm Homo sapiens cDNA: FLJ23165 fis, clone L	1.59	2.82
	414217	A1309298 A1620463	Hs.279898 Hs.347408	hypothetical protein MGC13102	1.57	2.64
65	429299 432647		Hs.278581	fibroblast growth factor receptor 2 (bac	1.56	2.74
05	*****	41404040400		junction plakoglobin	1.56	2.97
	429002 430171		Hs.234766	skin-specific protein	1.54	2.18
	422717		Hs.119475	cold inducible RNA-binding protein	1.51	2.19
	414323			KIAA0273 gene product	1.51	3.73
70	423184			ephrin-A1	1.50	2.18
	433101			Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.50	2.00
	424362	AL137646		Homo sapiens mRNA; cDNA DKFZp586F0824 (f	1.48	2.04
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.46	2.83
	445431		Hs.12701	plasmolipin	1.46	2.00
75	456906		Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	1.44	2.04
	442599		Hs.324051	RelA-associated inhibitor	1.42	3.50
	445656		Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.42	2.53 2.36
	444672		Hs.11669	taminin, alpha 5	1.40 1.40	2.29
80	447990			small inducible cytokine subfamily A (Cy Integrin, bela 4	1.40	2.86
00	418462			serine protease inhibitor, Kunitz type,	1.38	2.28
	453023 416340		Hs.79226	fasciculation and elongation protein zet	1.38	2.24
	433417			Homo sapiens, Similar to RIKEN cDNA 5830	1.38	2.14
	400411			507		

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	407015	AM/272000	U= 40306A	hunothetical matrix EL 120277	1.36	2.34	
	407815 432894	AW373860 AW167668	Hs.183860 Hs.279772	hypothetical protein FLJ20277 brain specific protein	1.36	5.09	
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.36	2.00	
	454478	AW805749	ns. 10/203	superoxide dismutase 2, mitochondrial	1.35	2.85	
5	423515	AA327017	Hs.176594	ESTs	1.35	2.45	
,	436663	AW410458	Hs.5258	chromosome 11 open reading frame2	1.35	2.07	
	404246	A14410430	NS.3230	Target Exon	1.34	2.96	
	41 1939	AI365585	Hs. 146246	ESTs	1.33	2.31	
	409178	BE393948	Hs.50915	kallikrein 5	1.33	2.03	
10	427795	BE268268	Hs.180842	ribosomal protein L13	1.33	2.29	
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.32	2.78	
	447330	BE279949	Hs.18141	ladinin 1	1.32	3.37	
	433399	N46406	Hs.84700	similar to phosphatidytcholine transfer	1.31	2.71	
	403986			Target Exon	1.31	2.09	
15	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	1.30	2.28	
	450796	NM_001988	Hs.25482	envoplakin	1.30	3.45	
	415550	L13720	Hs.78501	growth arrest-specific 6	1.29	2.76	
	415512	Y16270	Hs.78482	paralemmin	1.26	2.49	
•	430513	AJ012008	Hs.241586	G6C protein	1.26	3.07	
20	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor	1.23	2.04	
	420048	AW206824	Hs.25766	ESTs	1.23	2.01	
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.23	2.22	
	430560	228942	Hs.243960	N-myc downstream-regulated gene 2	1.23	2.42	
25	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.23	2.20	
25	402218			NM_022165*:Homo sapiens Lin-7b protein (	1.23	2.01	
	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	1.18	2.24	
	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	1.16	2.16	
	426068	AF029778	Hs.166154	jagged 2	1.15	2.07 2.33	
20	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.14	2.61	
30	411388	X72925	Hs.69752	desmocollin 1	1.00 1.00	263	
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.00	2.03	
	TABLE 63	RR-					
	Pkey:		que Eos probeset idea	ntifier number			
35	CAT numl		e cluster number				
	Accession	n: Gen	bank accession numb	bers			
	Pkey	CAT Number	r Accession				77.05 111/770077 111/770017
40	412636	1438_1	M77830 NM_0044	415 AF 139065 BG681115 BG740377 BI712964 BG000	1056 AA1284/C	) 81438324 H27408 BE33 1630 BE II	1/105 AW3/002/ AW3/0013
40			J05211 BG69886	5 BG740734 BG680618 BG739778 BI765807 BM3534	UJ BMJ3J240 i	MAN I I I 104 WASTOS WAS SOLD I 9 I	499040332 DE 102104
						OFFICER A DECORAGE DECOMPANA A A	
			BF149266 BE940	1187 B1060445 B1060444 BF350983 BE720095 BE720	269 BE715154	BE082584 BE082576 BE004047 A	VB57316 B1039774 BE713818
			BE713548 AW170	0253 BE160433 BI039775 AW886475 BM462504 BE9	369 BE715154 31734 BF1492	64 AA340777 BF381183 BG621737	AU127260 AW364859
			BE713548 AW170 BF993352 BG223	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AA8522	069 BE715154 31734 BF1492 112 AW366566	64 AA340777 BF381183 BG621737 BI090358 BF087707 BE819046 BE	AU127260 AW364859 819005 AA377127 BE073467
45			BE713548 AW170 BF993352 BG223 BE819069 BE819	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AA8522 1048 BI036306 BG990973 BI040954 BF919911 AU140	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766	64 AA340777 BF381183 BG621737 BK090358 BF087707 BE819046 BE AI434518 AW804674 BF752969 BE	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265
45			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF331184 BE715956 R58704 AAB522 0048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98	369 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192	64 AA340777 BF381183 BG621737 Bi090358 BF087707 BE819046 BE AI434518 AW804674 BF752969 BE I3 BF933510 AW265328 BG436319	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE182166 AW365175
45			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW847688 BE818	0253 BE160433 B1039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AA8522 0048 B1036306 BG990973 B1040954 BF919911 AU140 4264 B1039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF	369 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF0869	64 AA340777 BF381183 BG621737 B1090358 BF087707 BEB19046 BE A1434518 AW804674 BF752969 BE 23 BF933510 AW265328 BG436319 994 BF592276 BE082507 BE08251	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE182166 AW365175 4 BE082505 BF873693
45			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW847688 BE814 AW068840 AW84	0253 BE 160433 BI039775 AW886475 BIM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AA8522 1048 BI036036 BC990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 E880 AW177933 BF873679 AW178000 BE08256 BF- 17678 BF804153 AW385157 BE813930 BE002303 AW	369 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF0869 7365153 BE184	64 AA340777 BF381183 BG621737 B0990358 BF687707 BE819046 BE A1434518 AW804674 BF752969 BE 23 BF933510 AW265328 BG436319 994 BF592276 BE082507 BE08251 1941 BF749421 BE184920 BF83956	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE182166 AW365175 4 BE082505 BF873693 12 BE184933 BF842254
45			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE810 AW847688 BE810 AW068840 AW84 BE698470 BE931	0253 BE 160433 BI039775 AW886475 BIM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AAB522 0048 BI03506 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE002526 BF- 1678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF993889 BF368816 BE184924 BE159646 BE71	069 BE715154 31734 BF14921 12 AW366566 1155 AI951766 15642 BE00192 476866 BF0869 1365153 BE184	64 AA340777 BF381183 BG621737 BI090358 BF087707 BE819046 BE A434518 AW804674 BF752969 BE 33 BF933510 AW265328 BG436319 994 BF592276 BE082507 BE08251 J941 BF749421 BE184920 BF83956 J8 BG986845 AA131128 AA099831	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE182166 AW365175 4 BE082505 BF873693 22 BE184933 BF842254 W39488 C04715 BF096124
			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW068840 AW84 BE698470 BE931 BE865341 AW79	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE713956 R58704 AA8522 0408 Bi036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE703863 BF98 B280 AW177933 BF873679 AW178000 BE082526 BF- 17678 BF804153 AW365157 BE813930 BE002330 AW 1048 BF999889 BF368816 BE184924 BE15966 BE71 9304 AL603116 GE149760 BE705967 BE705966 BE7	069 BE715154 31734 BF14921 12 AW366566 1155 AI951766 15642 BE00192 476866 BF0869 1365153 BE184 14632 BE18494 05968 AW8487	64 AA340777 BF381183 BG621737 BI090358 BF087707 BE819046 BE A434518 AW804674 BF752969 BE 33 BF933510 AW265328 BG436319 994 BF592276 BE082507 BE08251 BB BF38542 AA131128 AA099831 123 AW376699 AW376817 AW3766	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE 182166 AW365175 4 BE082505 BF873693 12 BE184933 BF842254 W39488 CO4715 BF096124 97 BG005097 BF751115
45			BE713548 AW170 BF993352 BG223 BE81965615 BE814 AW945685 BE814 AW068840 AW84 BE698470 BE931 BE6956084 AW64 BE713297 BE713	0253 BE 160433 BI039775 AW886475 BIM462504 BE9 489 BEB19009 BF381184 BE715956 R58704 AA8522 4048 BI03506 BC990973 BI040954 BF919911 AU140 4264 BI033782 AU140407 BE144243 BE709863 BF98 6280 AW177933 BF873679 AW178000 BE082556 BF- 167678 BF804153 AW365157 BEB13930 BE002303 AW 1048 BF993899 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7 3371 AW376782 AW848789 AW849074 AW361413 B 3298 BE179915 AW799309 BF872345 BF088676 BE7	069 BE715154 31734 BF14921 112 AW366566 1155 AI951766 15642 BE00192 476666 BF0669 47665153 BE184 44632 BE18494 05968 AW8487 F927725 BF09	64 AA340777 BF381183 BG621737 BI090358 BF087707 BE819046 BE AI434518 AW804674 BF752969 BE 23 BF933510 AW265328 BG436319 994 BF592276 BE02507 BE08251 1941 BF749421 BE184920 BF83956 18 BG986845 AA131128 AA099891 123 AW376699 AW376817 AW3766 24211 AW997139 BE865474 BE1851 1999 BG005197 BF350088 BE71519	AU127260 AW364859 819005 AA377127 BE073467 837009 BE925826 BF149265 BE182166 AW365175 4 BE082505 BF873693 22 BE184933 BF0842254 W39488 C04715 BF096124 97 BG005097 BF751115 B87 BE156621 BE715089 5 BE715155 BF752396
			BE713548 AW176 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW847688 BE814 AW66840 AW84 BE696341 AW79 BE696084 AW64 BE713297 BE713 BF7933817 BE733	0253 BE 160423 BI039775 AW886475 BIM462504 BE9 4849 BEB19009 BF3811B4 BE715956 R58704 AA8522 4048 BI035006 BC990973 BI040954 BF919911 AU140 4264 BI035006 BC990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 2880 AW177933 BF873673 AW178000 BE092556 BF 17678 BF804153 AW365157 BEB13930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE7 3074 AL603116 BE149760 BF705967 BE705966 BE7 8371 AW376782 AW848789 AW849074 AW361413 B 1289 BE179915 AW799309 BF872345 BF08667 BE7 100 BF752409 BE006561 BC959922 BF09483 BF0	069 BE715154 31734 BF1492 112 AW366566 1155 AI951766 15642 BE00192 476866 BF086 1365153 BE184 4632 BE18494 05968 AW8487 F9277725 BF09 05939 AW7525 4748 BF09458	64 AA340777 BF381183 BG621737 BB1809058 BF087707 BB19046 BE AI434518 AW804674 BF752969 BE 33 BF933510 AW265328 BG436319 B948 F552276 BE08251 BE08251 BF49421 BE184920 BF83956 BB0986845 AA131128 AA099831 AW376817 AW3766 4211 AW37673 BF885474 BE1851 BF93 B0005197 BF350086 BE715198 33 AW377699 AW607238 BE082519 BB02519 BF035086 BE715198 BF035086 BF03508	AU127260 AW364859 B19005 AA377127 BE073467 B37009 BE925826 BF149265 BE 182166 AW355175 4 BE082505 BF973693 i2 BE184933 BF842254 W39488 C04715 BF096124 97 BG000509 BF751115 BI7 BE156621 BE715089 5 BE715155 BF752396 J AW377700 BF349467
			BE713548 AW176 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW648840 AW84 BE698470 BE931 BE865341 AW79 BE696084 AW84 BE713297 BE713 BF993817 BE733 A1190590 A15544	0253 BE 160433 BI039775 AW886475 BIM462504 BE9 4849 BE819009 BF381184 BE715956 R58704 AA8522 k048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 4268 BI039782 AU140407 BE144243 BE709863 BF98 4268 BW177933 BF873679 AW178000 BE008256 BF 17678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE7 3371 AW376782 AW848789 AW849078 AW361413 B 3289 BE179915 AW799309 BF872345 BF098676 BE7 1100 BF752409 BE006561 BC959922 BF094833 BF08 03 A1392926 AU158477 BI467252 AU159919 AI76081	069 BE715154 31734 BF1492 112 AW365666 1155 A1951766 15642 BE00192 476866 BF0856 1365153 BE184 44632 BE18494 05968 AW8487 F927725 BF09 05939 AW7525 47448 BF09458 6 BF082516 A	64 AA340777 BF381183 BG621737 BI090358 BF087707 BE819046 BE AI434518 AW804674 BF752369 BE 3 BF933510 AW265328 BG436319 994 BF592276 BE082507 BE08251- 1941 BF749421 BE184920 BF83956 18 BG986845 AA131128 AA099891 273 AW376699 AW376817 AW3766 4211 AW997139 BE865474 BE1851 939 BG005197 BF350088 BE71519 31 AW377699 AW607238 BE082519 1439101 AA451923 AJ340326 AJ590	AU127260 AW364859 819005 AA377127 BE073467 837005 BE925826 BF149265 BE182166 AW355175 4 BE082505 BF8735693 12 BE184933 BF942254 W39488 CO4715 BF096124 97 BG005097 BF751115 187 BE156621 BE715089 5 BE715155 BF752396 1 AW377700 BF349467 1975 BI791553 AI700963
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5	412446	63467_1	BE090279 BC021735 BF960659 BF090026	R42918 H10757 R10703 C01061 R27637 AI827230 AW151953 AA651675 AA228006 AA233950 BE858910 R30801 W32704 H39784 BB6697660 AW877265 BI818938 BF528291 AW953624 R57461 BF969694 AI669212 AL 120184 AI769949 BE721002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 AA987807 Z41449 BF960059 BF908053 BF908049 BE699424 BF968060 BF962832 BF952020 BF963134 BI033558 BF908052 BF908057 BF943183 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 A768015 F09778 F04816 F02721 AA102645 AI633838 BF947001 BI035448 BE338376 AW890837 AW898804 BF957405 BF963433 BG704815
	424362	2318_7	AF284421 A1 534639	AL 137646 BG542551 A1278088 A1423919 A1274095 BE838965 BE839174 BE839102 BF924520 BI913343 AW230803 AL 134300 AW793289 T97116 AWR55182 C02210 A17R3480 AW024874
10	454478	4273_16	AW796921	AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
10	TABLE 63 Pkey: Ref:	Unic	uence source	orresponding to an Eos probeset . The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Ounham, et al." refers to the publication entitled "The DNA an chromosome 27 Dunham, et al. (1999) <u>Nature</u> 402:483-495.
15	5 Strand: India		icates DNA str	and from which exons were predicted.  de positions of predicted exons.
20	Pkey 401781 401780 401785 402525	Ref 7249190 7249190 7249190 9800048	Strand Minus Minus Minus Minus	Nt_position 83215-83435,83531-83656,83740-83901,8423 28397-28617,28920-29045,29135-29295,2941 165776-165996,166189-166314,166408-16656 19748-20683
25	401760 402880 406387 403828 401963 404246 403986	9929699 9926561 9256180 9838214 3126783 7406725 8576059	Plus Minus Plus Plus Plus Plus Plus	83126-83250.85320-85540,94719-95287 41555-41865 116229-116371,117512-117651 31755-32148 51382-51521 82477-82628,82721-82817,82910-83071,8314 90692-91238
30	402218	7689783	Ptus	127677-127886

TABLE 64A: ABOUT 929 GENES DOWNREGULATED IN PRIMARY MELANOMAS AND/OR MELANOMA METASTASES RELATIVE TO NORMAL SKIN
Table 64A lists about 929 genes downregulated in primary melanomas and/or melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the
Cos/Affymetrix Hud3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the
relative level of mRNA expression.
Pitey:
Unique Eos probeset identifier number
ExAccn:
Exemplar Accession number, Genbank accession number
Unigene Tide:
Unique Tide:
Unique gene title
90th percentile of normal skin Als divided by the 90th percentile of primary melanoma and melanoma metastasis Als
90th percentile of normal skin Als divided by the 90th percentile of primary melanoma and melanoma metastasis Als, where the 15th percentile of normal tissue
Als was subtracted from both the numerator and denominator 35

40

45	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	420813	X51501	Hs.99949	protactin-induced protein	27.72	20.12
	408591	AF015224	Hs.46452	mammaglobin 1	26.40	24.26
	431360	NM_000427	Hs.251680	toricrin	26,16	20.45
	401781			Target Exon	19.68	19.56
50	412636	NM 004415		desmoplakin (DPI, DPII)	18.12	10.36
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	16.61	18.06
	418067	Al127958	Hs.83393	cystatin E/M	16.00	25.32
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	15.64	11.81
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	15.03	37.51
55	401780			NM_005557*:Homo sapiens keratin 16 (foca	14.20	14.86
-	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	13.95	28.08
	420783	AI659838	Hs.99923	tectin, galactoside-binding, soluble, 7	13.52	18.85
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	13.14	13.81
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.78	6.35
60	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	12.78	15.22
••	428824	W23624	Hs.173059	ESTs	12.67	13.24
	453309	A1791809	Hs.32949	defensin, beta 1	12.02	12.42
	446227	AI281459	Hs.270114	ESTs	11.79	12.32
	421948	L42583	Hs.334309	keratin 6A	11.58	9.02
65	432877	AW974111	Hs.292477	ESTs	11.18	11.30
•••	412047	AA934589	Hs.49696	ESTs	11.04	11.07
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	421296	NM_002666	Hs.103253	perilipin	10.73	7.94
	410001	AB041036	Hs.57771	kattikrein 11	10.72	10.70
70	418026	8E379727	Hs.83213	fatty acid binding protein 4, adipocyte	10.33	7.16
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Hornolog of rat Z	10.09	9.67
	401203			Target Exon	9.95	7.37
	452308	AI167560	Hs.61297	ESTs	9.71	20.05
	425580	£11144	Hs.1907	galanin	9.66	8.41
75	433124	U51712	Hs.13775	hypothetical protein SMAP31	9.50	4.96
• -	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	6.34
	443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58
	427656	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	9.19	11.73
	431369	BE184455	Hs.251754	secretory teukocyte protease inhibitor (	8.85	17.76
80	408536	AW381532	Hs.135188	ESTs	8.82	26.43
•	430686	NM_001942	Hs.2633	desmoglein 1	8.73	6.58
	436895	AF037335	Hs.5338	carbonic anhydrase XII	8.69	6.81
	418663	AK001100	Hs.41690	desmocollin 3	8.61	9.15
				600		

	420053	40040445	U= 225049	ermell inducible audation multi-peride A / Cu	8.51	13.13
	429852 424012	AB010445 AW368377	Hs.225948 Hs.137569	small inducible cytokine subfamily A (Cy tumor protein 63 kDa with strong homotog	8.44	9.61
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	8.39	5.13
_	442577	AA292998	Hs.163900	ESTs	8.34	7.92
5	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	8.16	10.08
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran Homo sapiens pyruvate dehydrogenase kina	8.04 7.68	7.55 7.81
	413859 452240	AW992356 AI591147	Hs.8364 Hs.61232	ESTs	7.63	9.39
	442757	A1739528	Hs.28345	ESTs	7.62	7.31
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	6.17
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	7.12
	407328	AA508857	Us 270000	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35 7.16	7.20 8.39
	414217 417240	A1309298 N57568	Hs.279898 Hs.48028	Homo sapiens cDNA: FLJ23165 fis, clone L EST	7.13	15.05
15	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.13	7.28
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.85
	439394	AA149250	Hs.56105	ESTs	7.00 6.99	4.53 5.30
20	422963 417515	M79141 L24203	Hs.13234 Hs.82237	ESTs ataxia-telangiectasia group D-associated	6.97	20.68
20	410530	M25809	Hs.64173	ATPasa, H transporting, lysosomal (vacuo	6.96	7.04
	446989	AK001898	Hs.16740	hypothetical protein FLJ 11036	6.96	6.68
	427890	AA435761		ESTs	6.94	6.68
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL ESTs, Wealdy similar to 1313184B alpha1	6.84 6.83	8.44 6.37
25	429624 451029	AA458648 AA852097	Hs.99476 Hs.25829	ras-related protein	6.81	8.96
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	6.80	7.68
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	6.77	14.06
20	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.11
30	451253	H48299	Hs.26126 Hs.294022	claudin 10     hypothetical protein FLJ14950	6.71 6.67	7.17 11.68
	414987 400304	AA524394 AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	7.90
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	6.58	6.78
35	421773	W69233	Hs.112457	ESTs	6.55	17.59 6.79
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol desmocollin 1	6.55 6.55	8.97
	411388 401785	X72925	Hs.69752	NM_002275°:Homo sapiens keratin 15 (KRT1	6.51	9.94
	406867	AA157857	Hs.182265	keratin 19	6.50	6.23
40	429504	X99133	Hs.204238	tipocatin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	426106	A1678765	Hs.21812	ESTs	6.41 6.39	7.69 7.09
	413172 407395	M38180 AF005082	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3 gb:Homo sapiens skin-specific protein (x	6.39	7.71
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.36	9.23
45	437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.30	5.45
	440383	AA884208	Hs.30484	ESTs	6.26	6.25
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	6.22 6.19	10.13 6.14
	418686 440116	Z36830 A1798851	Hs.87268	annexin A8 hemoglobin, gamma G	6.18	4.28
50	424049	AB014524	Hs.138380	KIAA0624 protein	6.18	6.91
• •	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	6.17	7.42
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	6.16	6.86 3.93
	414449	AA557660	Hs.76152 Hs.255609	decorin ESTs	6.15 6.12	6.68
55	441188 424008	AW292830 R02740	Hs.137555	gulative chemokine receptor; GTP-binding	6.12	5.33
-	431319	AA873350	Hs.302232	ESTs	6.11	6.84
	444105	AW189097		ESTs	5.97	6.20
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94 5.71	5.15 5.83
60	407788 439706	BE514982 AW872527	Hs.38991 Hs.59761	S100 catcium-binding protein A2 ESTs, Weakly simitar to DAP1_HUMAN DEATH	5.69	4.49
00	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	410541	AA065003	Hs.64179	syntenin-2 protein	5.62	5.84
	431926			gb:EST384815 MAGE resequences, MAGL Homo	5.61	5.75 e 70
65	430332		Hs.239483	Human clone 23933 mRNA sequence hypothetical protein FLJ22408	5.60 5.53	5.76 9.25
05	444946 430714		Hs.156457 Hs.287601	Homo saciens cDNA FLJ13830 fis, clone TH	5.48	5.38
	435538		Hs.4930	low density tipoprotein receptor-related	5.46	3.19
	414407		Hs.76704	ESTs	5.43	5.29
70	417035		Hs.22968	Homo sapiens done IMAGE:451939, mRNA se	5.40	5.40 3.87
70	442315 416931		Hs.7956 Hs.80485	ESTs, Moderately similar to ZN91_HUMAN Z adipose most abundant gene transcript 1	5.40 5.39	9.12
	431048		Hs.249129	cell death-inducing DFFA-like effector a	5.39	6.06
	436090		Hs.332879	EST	5.37	5.33
~ ~	411274	NM_00277		katlikrein 10	5.37	5.97
75	418394		Hs.84728	Kruppel-like factor 5 (intestinal)	5.36 5.34	9.35 4.08
	406706		Hs.231581	myosin, heavy polypeptide 1, skeletal mu skin-specific protein	5.34 5.32	4.08 10.40
	430171 452747		Hs.234766 Hs.61460	ka superfamily receptor LNIR	5.31	6.01
	426451		Hs.169946	GATA-binding protein 3 (T-cell receptor	5.31	3.81
80	414602			Homo sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	5.92
	424399		11. 00000-	Al905687:IL-BT095-190199-019 BT095 Homo	5.25 5.20	16.94 5.01
	430071 431416			transcription factor 8 (represses interl ESTs	5.18	5.38
	43 14 10	, 17402110	113,170004	500	****	

	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.17	5.72
	446082	Al274139	Hs.156452	ESTs	5.16	5.14
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	5.14	4.97
5	434525 426101	W01370 AL049987	Hs.46824	ESTs Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.12 5.11	6.18 3.79
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	5.08	13.64
	438962	BE046594		gb:hn41c11x1 NCI_CGAP_RDF2 Homo sapiens	5.08	4.09
	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (	5.08	4.77
10	420583	H77859	Hs.65450	reticulan 4	5.06	5.56
10	432125 445263	AW972667 H57646	Hs.183006 Hs.42586	Horno sapiens cDNA FLJ12300 fis, clone MA KIAA1560 protein	5.05 5.03	6.32 5.22
	407839	AA045144	Hs.161566	ESTs	5.03	5.27
	434293	NM_004445	Hs.3796	Eph86	5.03	4.91
	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	4.99	16.04
15	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	4.94	8.14
	445493 429365	AI915771 AA451798	Hs.99249	metallothionein 1E (functional) ESTs	4.93	4.33 5.19
	412633	AF001691	Hs.74304	periptakin	4.90 4.90	11 71
	448490	AI523897	Hs.271692	ESTs, Weakly similar to 138022 hypotheti	4.85	4.88
20	408491	A1088063	Hs.7882	ESTs	4.80	4.39
	430168	AW968343	Hs.145582	OKFZP434I1735 protein	4.80	6.05
	407102 421998	AA007629 R74441		glycerol-3-phosphate dehydrogenase 1 (so	4.78	7.23 4.78
	422633	X56832	Hs.118804	poly(A)-binding protein, nuclear 1 enolase 3, (beta, muscle)	4.77 4.72	6.24
25	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	3.72
	439652	W67826	Hs.55412	ESTs, Wealtly similar to K1CJ_HUMAN KERAT	4.70	3.60
	450626	AW190989	Hs.1508	insufin-degrading enzyme	4.68	5.14
	456898	NM_001928 AA053401	Hs.155597	D component of complement (adipsin)	4.68	15.83
30	408239 415192	D17793	Hs.78183	ESTs, Moderately similar to ALU7_HUMAN A aldo-keto reductase family 1, member C3	4.67 4.64	6.17 4.48
-0	443827	AID87867	Hs.134667	ESTs	4.63	5.06
	431441	U81961	Hs.2794	sodium channel, nonvollage-gated 1 alpha	4.63	8.48
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	4.63	3.19
35	427318 453767	AF186081	Hs.175783	zinc transporter	4.62	3.57
33	424046	AB011792 AF027866	Hs.35094 Hs.138202	extracellular matrix protein 2, fernale o serine (or cysteine) proteinase inhibito	4.62 4.61	5.14 6.80
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	4.60	6.19
	446525	AW967069	Hs.211556	hypothetical prutein MGC5487	4.59	2.45
40	402294			Target Exon	4.57	5.47
40	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57	5.12
	420798 418021	W93774 M15881	Hs.99936 Hs.1137	keratin 10 (epidermolytic hyperkeratosis uromodulin (uromucoid, Tamm-Horsfall gly	4.57 4.54	4.76 4.49
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	4.54	4.32
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	4.53	3.04
45	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	4.53	2.91
	400109	******		Eos Control	4.52	3.94
	407242 431901	M18728 AW295050	Hs.272023	gb:Human nonspecific crossreacting antig transforming, acidic coiled-coil contain	4,51 4.50	4.07 4.16
	435992	AI033259	Hs.118317	Homo sapiens cONA FLJ12088 fis, clone HE	4.50	4.77
50	447365	BE383676	Hs.334	Rho guarrine nucleotide exchange factor (	4.50	3.99
	449785	A1225235	Hs.288300	hypothetical protein FLJ23231	4.49	4.02
	424620	AA101043	Hs.151254	kathkrein 7 (chymotryptic, stratum com	4.47	5.43
	432559 459290	AW452948 NM_001546	Hs.257631 Hs.34853	ESTs inhibitor of DNA binding 4, dominant neg	4.47 4.45	3.10 3.17
55	422313	AF045941	Hs.115166	sciellin	4.45	5.07
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	4.44	5.25
	432314	AA533447	Hs.312989	ESTs	4.44	3.52
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	4.43	2.64
60	424670 414489	W61215 AI620677	Hs.116651 Hs.73105	epithelial V-like antigen 1 ESTs	4.42 4.41	4.27 3.77
•••	413040	AA193338	Hs.12321	sodium calcium exchanger	4.36	4.58
	426974	AB002298	Hs.173035	KIAA0300 protein	4.35	4.97
	448249	AW855331	Hs.337124	ESTs	4.35	4.49
65	451743	AW074266 AA173942	Hs.23071 Hs.326416	ESTS	4.34	4.52
UJ	427919 422305	A1928242	Hs.293438	Home sapiens mRNA; cDNA DKFZp564H1916 (f	4.33 4.32	3.94 7.20
	408104	AW972927	Hs.293968	ESTs, Highly similar to AF198488 1 crans ESTs	4.31	3.53
	447945	AI922838	Hs.9670	ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.30	3.72
70	439349	A1660898	Hs.6834	ESTs	4.29	4.16
70	433339	AF019226	Hs.8036 Hs.178589	glioblastoma overexpressed	4.29	3.94
	427074 453574	AA527435 A1767947	Hs.50841	hepatoçellular carcinoma antigen gene 52 ESTs	4.28 4.25	4,97 3.66
	410677	NM_003278		tetranectin (plasminogen-binding protein	4.25	17.64
26	424833	NM_003894	Hs.153405	period (Drosophila) homolog 2	4.22	3.13
75	426248	T18988	Hs.293668	ESTs	4.21	4.09
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	4.19	276
	406805 438533	A1686003 A1440266	Hs.296031 Hs.170673	ESTs ESTs, Wealdy similar to T24832 hypotheti	4.19 4.18	3.87 5.93
	451831	NM_001674		activating transcription factor 3	4.18	4.74
80	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.17	2.83
	434936	AJ285970	Hs.183817	ESTs	4.17	4.39
	430361 448429	Al033965 D17408	Hs.239926 Hs 21223	sterol-C4-methyl oxidase-like calponin 1, basic, smooth muscle	4.17 4.16	2.38 5.15
	410453	51,400	Hs.21223	Aspendi 1, pasic, sinoul) Muscle	4,10	J. 13

	421978	AJ243662	Hs.110196	NICE-1 protein	4.15	8.07
	437135	AL038624	Hs.208752	ESTs, Wealtly similar to ALUS_HUMAN ALU S	4.14	4.92
	442554	AW467376	Hs.129640	ESTs	4.12	4.00
•	451814	AA847992	Hs.137003	ESTs .	4,11	4.58
5	410023	AB017169	Hs.57929	slit (Orosophila) hornolog 3	4,10	3.92
	457121	AI743770	Hs. 180513	ESTs, Weakly similar to KIAA0822 protein	4.09	3.19
	426539 430191	AB011155 Al149880	Hs.170290 Hs.188809	discs, targe (Drosophila) homotog 5 ESTs	4.09 4.07	3.69 4.49
	430433	AA478883	Hs.273766	ESTs	4.07	3.74
10	425992	AA367069	Hs.100636	ESTs	4.06	4.37
-	428931	AA994979	Hs.98967	ATPase, H()-transporting, lysosomal, non	4.05	4.15
	452392	L20815	Hs.507	comeodesmosin	4.04	11.00
	402845			ENSP00000246267:KIAA0444 PROTEIN (FRAGME	4.03	4.18
15	439873	BE159253	Hs.300638	ESTs	4.03	3.86
1.5	432305 420789	M62402 A1670057	Hs.274313 Hs.199882	insufin-fike growth factor binding prote ESTs	4.02 4.02	8.79 4.34
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	4.02	5.13
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	4,01	4.29
~~	429556	AW139399	Hs.98988	ESTs	4.01	4.59
20	448585	AB020676	Hs.21543	KIAA0869 protein	4.01	4.52
	403710			C4000160:gi]12735793[ref]XP_011928.1[ pr	4.00	3.31
	423634 421485	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.98 3.98	6.61
	437611	AA243499 AA897108	Hs.104800	hypothetical protein FLJ 10134 gb:am08a06.s1 Soares_NFL_T_GBC_S1 Horno s	3.96 3.97	3.79 4.24
25	426500	NM_014638	Hs.170156	KIAA0450 gene product	3.96	4.93
	448710	T62926	Hs.304184	ESTs	3.96	4.54
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	3.95	5.57
	428340	AF261088	Hs.154721	aconitase 1, soluble	3.94	3.24
30	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.94	9.16
30	456972	AI054347	Hs.2017	ribosomal protein L38	3.93	4.37
	418381 444781	AA682393 NM_014400	Hs.119237 Hs.11950	ESTs GPI-anchored metastasis-associated prote	3.93 3.92	3.45 15.00
	456332	AA228357	143.11550	gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	3.91	4.88
	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	3.91	3.19
35	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	3.90	4.50
	446733	AA863360	Hs.26040	ESTs, Wealdy similar to fatty acid omega	3.90	3.89
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.89	5.11
	452894	AI598065	Hs.61558	ESTs	3.88	3.73
40	430570 439625	AJ417881 AF086453	Hs.292464 Hs.58611	ESTs ESTs	3.87 3.86	4.47 4.81
70	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.85	3.01
	431247	AL021578	Hs.278489	mainin 4	3.85	3.35
	426350	NM_003245		transglutarninase 3 (E polypeptide, prote	3.85	5.15
4.5	441319	Al354869	Hs.133081	ESTs, Wealty similar to T08700 hypotheti	3.84	5.03
45	452877	AI250789	Hs.32478	ESTs	3.84	3.26
	444252	R21135	Hs.54985	ESTs	3.83	5.58
	416265	AA177088	Hs.190065	ESTs	3.82	3.87
	418875 440509	W19971 BE410132	Hs.233459 Hs.134202	ESTs ESTs, Wealdy similar to T17279 hypotheti	3.80 3.80	2.92 4.36
50	442503	AF147078	Hs.150853	p53-responsive gene 5	3.80	7.53
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !	3.77	4.81
	458222	AW139592		hypothetical protein DKFZp434K1421	3.77	3.56
	445107	Al208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	3.77	3.20
55	436283	AJ480319	Hs.120058	ESTs	3.76	3.76
"	436557 448988	W15573 Y09763	Hs.5027 Hs.22785	ESTs, Wealdy simitar to A47582 B-cell gr gamma-aminobutyric acid (GABA) A recepto	3.76 3.75	2.65 7.59
	434206	AW136973	113.22103	ESTs, Weakly similar to S69890 mitogen i	3.72	3.96
	424824	AJ217440	Hs.143873	ESTs	3.72	3.52
<b>~</b>	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.71	3.05
60	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	3.70	4.84
	421845	AW021631	Hs.16515	ESTs	3.69	3.59
	413922 422746	AI535895 NM_004484	Hs.221024 Hs.119651	ESTs	3.68 3.68	4.22 4.29
	433934	AW273261	Hs.216292	glypican 3 ESTs	3.68	4.39
65	452547	AA335295	Hs.74120	adipose specific 2	3.66	12.23
	400295	W72838		AI905687:IL-BT095-190199-019 BT095 Homo	3.66	9.25
	419098	AA234041	Hs.87271	ESTs	3.66	4.94
	417054	AF017060		aldehyde oxidase 1	3.65	4.51
70	423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: harny2)	3.65	4.32
70	431362 420506	A1874223	Hs.293560 Hs.194613	ESTs ESTs	3.65	3.73
	448065	AW977779 AI459177	Hs.172759	ESTs, Moderately similar to ALU7_HUMAN A	3.65 3.64	3.25 4.62
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 atpha-1C-	3.64	4.54
~~	451951	AW082B70	Hs.210954	ESTs	3.64	3.69
75	435579	Al127483	Hs. 120451	ESTs, Wealtly similar to unnamed protein	3.64	3.39
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.62	3.62
	412668	AA456195		hypothetical protein FLJ14621	3.62	4.22
	413899	AF083892	Hs,75608	tight junction protein 2 (zona occludens	3.62 3.59	3.06
80	444726 428722	NM_006147 U76456	Hs.190787	interferon regulatory factor 6 tissue inhibitor of metalloproteinase 4	3.59 3.59	10.65 3.31
-0	429973		Hs. 164680	ESTs	3.59	3.71
	452413		Hs.215030	ESTs	3.58	4.66
	416157	NM_003243		transforming growth factor, beta recepto	3.58	4.44

					3.57	3.74
	430397	AI924533	Hs.105607	bicarbonate transporter related protein	3.57 3.57	12.42
	411939 450353	A1365585 A1244661	Hs.146246 Hs.103296	ESTs ESTs, Wealdy similar to \$65657 atpha-1C-	3.57	4.11
	432406	AI340571	Hs.343666	KIAA0969 protein	3.57	2.84
5	439609	AW971945	Hs.293236	ESTs	3.56	3.14
-	435381	AW136397	Hs.175382	ESTs	3.56	3.48
	410173	AA706017	Hs.119944	ESTs	3.56	3.37
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	3.56 3.55	9.93 4.24
10	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L ESTs	3.55	4.77
10	434360 423973	AW015415 AF038461	Hs.127780 Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.53	5.65
	425681	AB018297	Hs.159183	KIAA0754 protein	3.52	4.79
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.46
	451184	T87943		transcription factor 7-like 2 (T-cell sp	3.51	363
15	448496	BE379077	Hs.130849	ESTs, Weakly similar to 138022 hypotheti	3.51 3.48	3.30 8.66
	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member monoamine oxidase A	3.48	9.54
	428232 425483	BE272452 AF231022	Hs.183109 Hs.158159	FAT tumor suppressor (Drosophila) homolo	3.48	6.05
	401760	AF231022	rs.130133	Target Exon	3.48	7.86
20	427899	AA829286	Hs.332053	serum amyloid A1	3,47	3.67
	451767	AI625014	Hs.187328	ESTs	3.46	3.85
	452849	AF044924	Hs.30792	hook2 protein	3.45	5.66
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	3.45 3.45	5.02 3.61
25	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.45 3.45	7.71
25	422083	NM_001141 AA918425	Hs.111256 Hs.177744	arachidonate 15-lipoxygenase, second typ ESTs	3.44	8.46
	420876 421114	AW975051	Hs.293156	ESTs, Weakly similar to 178885 serine/th	3.44	4.47
	426233	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC0	3.44	3.96
	428221	U96781	Hs.183075	ATPase, Ce transporting, cardiac muscle,	3.42	4.32
30	403593			Target Exon	3.42	6.35
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	3.42	3.34
	447731	AA373527	Hs.19385	CGI-58 protein	3.41 3.40	2.44 3.46
	456327	H68741	Hs.38774	ESTs	3.37	3.61
35	413880 429501	A1660842 A1700588	Hs.110915 Hs.293388	interleukin 22 receptor ESTs, Weakly similar to A34612 zinc fing	3.37	3.44
33	437575	AW954355	Hs.36529	hypothetical protein MGC11242	3.36	4.87
	420231	R06866	Hs.19813	ESTs	3.36	8.60
	424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	3.36	6.20
	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.34	3.40
40	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.34	3.35
	420693	NM_001972		elastase 2, neutrophil	3.34 3.33	4.06 4.36
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3 protein tyrosine phosphatase, receptor t	3.32	9.47
	413163 428496	Y00815 AA769986	Hs.75216 Hs.185802	ESTs	3.32	3.88
45	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.31	4.01
	409095	AW337272	Hs.293656	ESTs, Moderately similar to \$72481 proba	3.31	3.31
	443072	AI937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	3.31	4.40
	437596	AA761490		ESTs, Moderately similar to S65657 alpha	3.30	5.31 3.47
50	444094	A1695764	Hs.202394	ESTs	3.29 3.29	3.75
30	437150 407334	R51407 AA494411	Hs.77910 Hs.296031	3-hydroxy-3-methylghitaryl-Coenzyme A sy ESTs	3.28	4.30
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	3.28	3.78
	447875	R22029	Hs.13905	ESTs	3.28	3.44
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.27	3.71
55	411962			gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.27	4.28
	424395	AA165082	Hs.146388	microtubule-associated protein 7	3.27 3.27	3.82 2.60
	400494	00000	Hs.36029	ENSP00000238970*:CIG30 (Fragment). heart and neural crest derivatives expre	3.26	6.19
	430418 409231		Hs.692	GA733-2 antigen; epithelial glycoprotein	3.26	4.24
60	434952		Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	3.26	5.17
•	445234		Hs.146059	ESTs	3.25	5.59
	426150	NM_003659	B Hs.167218	Bartl-like homeobox 2	3.25	5.21
	400076			Eos Control	3.25 3.25	3.60 3.93
65	421462		Hs.104624	aquaporin 9 ESTs	3.25	3.53
03	420677 424125		Hs.246096 Hs.1735	inhibin, bela B (activin AB bela polypep	3.24	3.68
	443672		Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.24	5.64
	420682		Hs.88802	ESTs	3.24	4.13
	423725		Hs.132127	hypothetical protein LOC57822	3.23	4.90
70	431157		Hs.132678	ESTs	3.23	3.97 3.39
	440469			gb:ny40e07.s1 NCI_CGAP_Pr12 Homo sapiens	3.23 3.21	5.36
	44996			ESTs ICEBERG caspase-1 inhibitor	3.21	4.61
	407941 40083		Hs.56279	chromosome 2 open reading frame 2	3.21	3.62
75	41332		Hs.133539	ESTs	3.21	3.43
	41482		Hs.77432	epidermal growth factor receptor (avian	3.21	3.72
	45086			integrin, beta 8	3.20	5.89
	44481		Hs.283742	H.sapiens mRNA for retrotransposon	3.19	6.84
0.0	45385			ESTs, Weakly similar to ALUB_HUMAN !!!!	3.19 3.19	3.59 3.51
80	43227			hypothetical protein FLJ23563	3.18	5.50
	42007 41848		Hs.190074	ESTs CO34 antigen	3.18	3.65
	40852		Hs.46320	Small proline-rich protein SPRK (human,	3.18	7.43

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	435337	AI078307	Hs.134317	ESTs, Wealtly similar to PC4259 ferritin	3.17	3.51
	445502	AW379160	Hs.12813	DKFZP434J214 protein	3.17	3.62
	412477	AA150864		microsomal glutathione S-transferase 1	3.17 3.16	5.39 3.60
5	421757	Z20897	Hs.296259	paraoxonase 3	3.16	5.56
,	413835 420309	A1272727 AW043637	Hs.249163 Hs.21766	fatty acid hydroxylase ESTs, Wealdy similar to ALU5_HUMAN ALU S	3.15	1.99
	444895	A1674383	Hs.22891	solute carrier family 7 (cationic amino	3.15	4.45
	414869	AA157291	Hs.21479	ubinuclein 1	3.13	4.40
10	412947	AA122277		gb:zl97e09.s1 Soares_pregnant_uterus_NbH	3.13	3.30 4.62
10	443265	Al916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.12 3.11	11.54
	421335 401905	X99977	Hs.103505	ARS component B ENSP00000252232":Sterol regulatory eleme	3.10	2.85
	443514	BE464288	Hs.141937	ESTs	3.09	3.66
	418817	AA913229	Hs.19339	ESTs	3.08	3.88
15	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	3.08	4.18
	435858	AF254260	Hs.283009	tuftelin 1	3.08 3.07	3.96 3.30
	430285 448106	A1917602 A1800470	Hs. 106440 Hs. 171941	ESTs ESTs	3.07	5.19
	432908	AI861896	113.17 1341	ESTs	3.07	3.85
20	450086	AW016343	Hs.233301	ESTs	3.07	3.38
	451529	AI917901	Hs.208641	ESTs	3.07	3.29
	418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 o	3.06 3.05	4.12 4.34
	426848 429506	H72531 D49835	Hs.36190 Hs.171942	ESTs ras responsive element binding protein 1	3.05	3.97
25	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	3.05	3.29
	413822	R08950	Hs.272044	ESTs, Wealthy similar to ALU1_HUMAN ALU S	3.05	3.89
	434230	AA551569		hypothetical protein PRO2822	3.04 3.04	3.63 8.09
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto ESTs	3.03	3.43
30	415696 449618	A1821552 A1076459	Hs.188682 Hs.15978	KIAA1272 protein	3.01	3.29
50	414665	AA160873	113.10370	serum amyloid A1	3.01	9.22
	446682	AW205632	Hs.211198	ESTs	3.00	3.30
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	2.99 2.99	3.74 4.47
35	412446	A1768015	Na 7000	ESTs Homo sapiens cDNA FLJ11946 fis, clone HE	2.99	4.35
33	449271 435702	AW338067 AI033647	Hs.7869 Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.98	3.49
	403180	7.10000	10.12.001	Target Exon	2.98	3.92
	434442	AA737415		ESTs	2.98	3.61
40	439593	BE073597	Hs.124863	ESTs	2.98	3.86 3.49
40	410453 414766	AW749036 AW293452	Hs.16228	gb:RC2-BT0318-241199-011-110 BT0318 Homo ESTs	2.98 2.97	3.63
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	2.97	3.99
	451541	BE279383	Hs.26557	plakophilin 3	2.97	6.90
4.5	452195	AA994712	Hs.116878	ESTs	2.97	3.30
45	401747			Homo sapiens keratin 17 (KRT17)	2.97 2.96	4.10 3.05
	431316 445437	AA502663 AJ224165	Hs.145037 Hs.148725	ESTs ESTs	2.95	7.12
	421690	AW162667	Hs.106857	calbindin 2, (29kD, catretinin)	2.95	5.68
	456371	S76825	Hs.89695	insulin receptor	2.94	4.59
50	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	2.94	4.12
	436664	AW197887	Hs.253353	ESTs	2.93 2.93	3.57 2.66
	406962 422158	M13485 L10343	Hs.112341	gb:Human metallothionein I-B gene, exon protease inhibitor 3, skin-derived (SKAL	2.92	7.48
	428769	AW207175	Hs.106771	ESTs	2.92	3.28
55	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.92	3.48
	444204	Al129194	Hs.143040	ESTs	2.92 2.91	3.92 6.55
	421407 453180	T82331 N46243	Hs.182278 Hs.110373	ESTs, Weakly similar to CGHU6C collagen ESTs, Highly similar to T42626 secreted	2.90	3.92
	429538	BE182592	Hs.139322	small proline-rich protein 2A	2.88	4.75
60	452554	AW452434	Hs.58006	ESTs, Wealthy similar to ALU5_HUMAN ALU S	2.88	6.74
	417184	N52510	Hs.268597	Homo sapiens cDNA: FLJ21498 fis, clone C	2.87	3.97
	412093	BE242691	Hs.14947	ESTs Homo saciens mRNA; cDNA DKFZp762H106 (fr	2.86 2.86	3.48 3.32
	424135 437167	AW994455 AL050184	Hs.140978 Hs.21610	DKFZP434B203 protein	2.86	3.87
65	454065	BE394588	113.21010	gb:601311808F1 NIH_MGC_44 Homo sapiens c	2.86	3.43
	420230	AL034344	Hs.284186	forkhead box C1	2.85	3.67
	403108			ENSP00000241415":Hypothetical 67.7 kDa p	2.85 2.84	2.62 3.35
	434433	AW629759 AA677577	Hs.98732	gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens Homo sapiens Chromosome 16 BAC done CIT	2.83	2.66
70	420544 429429		Hs.334437	hypothetical protein MGC4248	2.83	3.59
	451721			spectrin, beta, non-erythrocytic 2	2.83	3.36
	424982			phosphorytase, glycogen; muscle (McArdle	2.83	4.50
	429259		Hs.292911	Plakophilin	2.81 2.80	4.81 7.08
75	423523 433637			ESTs ESTs	2.80	3.39
,,	452089		Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	2.80	3.62
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	2.80	3.52
	421965			gb:EST14128 Testis tumor Homo sapiens cD ·	2.79 2.79	3.49 2.31
80	432098 429128		Hs.91546 Hs.119316	cytochrome P450 retinoid metabolizing pr ESTs	2.78	4.17
30	438913		Hs.172445	ESTs	2.77	3.65
	445029	AF196481		midline 2	2.76	3.79
	419923	AW081455	5 Hs.120219	ESTs	2.76	3.00

	416508	R39769	Hs.56406	ESTs, Moderately similar to ALU8_HUMAN A	2.76	3.59
	412507	L36645	Hs.73964	EphA4	2.76	3.90
	446339	AL046962	Hs.14845	forkhead box O3A	2.75	3.50
5	433710	AI341867	Hs.188920	ESTs	2.75	3.33
J	432375 409213	BE536069 U61412	Hs.2962 Hs.51133	S100 calcium-binding protein P	2.74	5.77 3.76
	426653	AA530892	Hs.171695	PTK6 protein tyrosine kinase 6 dual specificity phosphatase 1	2.74 2.74	8.19
	408839	AW277084	113.171030	gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.73	3.93
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.73	11.46
10	444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.73	6.17
	433713	AW976511	Hs.112592	ESTs	2.72	3.42
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.72	4.76
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.72	3.74
1.5	432947	AA570710	Hs.270998	ESTs, Wealdy similar to 138022 hypotheti	2.72	3.44
15	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	2.72	4.95
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.72	4.29
	435016 449667	AI284219 AB023227	Hs.130749 Hs.23860	ESTs, Weakly similar to I38022 hypotheti	2.71	4.45
	407112	AA070801	Hs.51615	KIAA1010 protein ESTs, Weakly similar to ALU7_HUMAN ALU S	2.71 2.70	3.72 3.82
20	433848	AF095719	Hs.93764	carboxypeptidase A4	2.70	2.76
	430152	AB001325	Hs.234642	aquaporin 3	2.69	4.26
	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	2.69	6.72
	424471	AA341329	Hs.311524	ESTs	2.68	4.57
0.5	453201	AI432195	Hs.135098	ESTs	2.68	3.69
25	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	2.68	4.25
	404996			Target Exon	2.67	4.28
	409453	AI885516	Hs.95612	ESTs .	265	6.51
	430937 452887	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.65	3.78
30	444169	A1702223 AV648170	Hs.107253 Hs.58756	hypothetical protein DKFZp761F241 ESTs	2.64 2.64	6.38 3.40
50	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.64	3.47
	408395	BE072425	Hs.44579	hypothetical protein FLJ20199	2.64	4.01
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	2.63	4.08
	451621	AJ879148	Hs.26770	falty acid binding protein 7, brain	2.62	2.51
35	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	2.61	3.62
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.61	3.68
	431166	AW971186	Hs.293839	ESTs	2.61	3.33
	440659	AF134160	Hs.7327	claudin 1	2.61	3.53
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	2.61	4.48
40	413956 407299	AI821351 AA460205	Hs.193133 Hs.289770	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.60	3.51
	449539	W80363	Hs.58446	ESTs, Weakly similar to I38022 hypotheti ESTs	2.59 2.58	3.82 4.05
	413884	AI668892	Hs.239758	hypothetical protein FLJ12389 similar to	2.58	4.19
	445620	AI245225	Hs.17441	ESTs	2.57	3.44
45	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	2.56	3.57
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.56	3.47
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	3.61
	406790	AA293303		ribosomal protein L27a	2.54	4.36
50	450472	Al190071	Hs.55278	ESTs	2.54	4.30
30	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.54	3.82
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.54	3.44
	430821 402575	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.54	4.55
	429554	NM_012275	Hs.207224	Rho GTPase activating protein 1 interleukin 1, delta	2.53 2.53	5.47 2.40
55	431631	AA548906	Hs.122244	ESTs	2.53 2.52	3.79
	408806	AW847814	Hs.75608	Homo sapiens cDNA: FLJ21532 fis, clone C	2.52	4.51
	420235	AA256756	Hs.31178	ESTs	2.51	4.21
	436314	A1983409		ESTs	2.51	3.11
-	432906	BE 265489	Hs.3123	lethal giant larvae (Drosophila) homotog	2.50	5.62
60	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.49	2.60
	410532	T53088	Hs.155376	hemoglobin, beta	2.49	4.73
	413475	AW021488 AW088739	Hs.26981	ESTs	2.49	3.90
	429325 424604	AW865388	Hs.243770 Hs.151076	ESTs	2.48	3.71
65	414320	U13515	Hs.75893	KIAA1243 protein ankyrin 3, node of Ranvier (ankyrin G)	2.48 2.48	4.16 3,80
-	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.47
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.47	2.09
	444935	AA262449	Hs.223569	ESTs	2.47	5.96
	445389	NM_016831		period (Drosophila) homolog 3	2.47	3.41
70	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.47	6.80
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.46	7.37
	409178	BE393948	Hs.50915	kallikrein 5	2.46	5.59
	452865	A1924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	2.46	6.03
75	447179 414459	AW015633 Y11525	Hs.157299	ESTS CCAAThebase histing matein (CERR)	2.46	3.23
,,	428188	M98447	Hs.76171 Hs.22	CCAAT/enhancer binding protein (C/EBP),	2.46	3.95
	428593	AW207440	Hs.185973	transglutaminase 1 (K potypeptide epider degenerative spermatocyte (homotog Droso	2.45 2.44	3.94 2.17
	436009	H57130	Hs.120925	ESTs (normolog Droso	244	2.94
-	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.43	3.61
80	416749		comp Hs.79732	fibulin 1	243	4.46
	444672	295636	Hs.11669	laminin, alpha 5	2.42	6.39
	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.42	3.45
	406997	U07807		metallothionein IV	2.42	3.92

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	423184 421321	NM_004428 NM_005309	Hs.1624	ephrin-A1	2.41	4.34 5.08
	456826	AI871742	Hs.103502 Hs.302428	glutamic-pyruvate transaminase (alanine wingless-type MMTV integration site fami	2.41 2.41	3.92
_	428897	AJ245719	Hs.194385	hypothetical protein FL120234	2.41	5.18
5	400232			NM_001895".Homo sapiens casein kinase 2.	2.41	3.82
	421481	AW391972	Hs. 104696	KIAA1324 protein	2.40	4.03
	442083 422287	R50192 F16365	Hs.165062 Hs.114346	ESTs cytochrome c oxidase subunit VIIa polype	2.39 2.39	4.21 8.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.39	2.57
10	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown (H.sapie	2.39	3.85
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, atp	2.38	3.84
	431179 432563	AI338644 NM_013261	Hs.195432 Hs.198468	aldehyde dehydrogenase 2 family (mitocho peroxisome proliferative activated recep	2.37 2.37	7.89 3.77
	402338	MM_013201	FIS.130400	Target Exon	2.37	3.46
15	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.37	4.57
	436723	AW975895	Hs.307486	ESTs	2.37	6.39
	452669 409212	AA216363 AI082423	Hs.262958 Hs.141892	hypothetical protein DKFZp434B044	2.37	3.92
	451323	A1903313	Hs.34579	ESTs ESTs, Moderately similar to ALUS_HUMAN A	2.36 2.35	3.79 3.29
20	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.35	9.96
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	2.35	5.16
	451092 445948	A1207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	2.34	5.24
	424425	BE409053 AB031480	Hs.299629 Hs.146824	peroxisomal long-chain acyl-coA thioeste SPR1 protein	2.34 2.34	3.77 4.43
25	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	2.34	5.64
	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.33	3.51
	422106 423503	D84239 M92843	Hs.111732	Fc fragment of IgG binding protein	2.33	6.95
	453999	BE328153	Hs.343586 Hs.240087	zinc finger protein homologous to Zfp-36 ESTs	2.33 2.32	5.57 3.40
30	419358	178763	Hs.90063	neurocalcin delta	2.32	6.72
	430468	NM_004673	Hs.241519	angiopoietin-fike 1	2.32	3.90
	456876 454947	AL044870 AW846590	Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.32	3.27
	429211	AF052693	Hs.198249	gb:QVO-CT0180-011099-025-d07 CT0180 Homo gap junction protein, beta 5 (connexin 3	2.32 2.31	4.43 7.22
35	438282	BE268288	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.31	3.34
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.31	8.47
	419245 444920	AJ732742 AW450967	Hs.87440 Hs.235240	ESTs ESTs	2.31	3.39 3.30
	417314	N68168	16.233240	gb:za11c01.s1 Soares fetal liver spleen	2.30 2.30	3.30 3.12
40	409586	AL050214	Hs.55044	DKFZP586H2123 protein	2.30	3.52
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	2.29	6.11
	451176 410531	AA046457 AW752953	Hs.60677	ESTs gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29 2.29	6.5 <del>9</del> 3.29
	425982	R05327	Hs.189726	ESTs	2.29	3.25
45	435684	NM_001290	Hs.4980	LIM domain binding 2	2.29	4.54
	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	2.28	3.70
	434411 407394	AA632649 AF005081	Hs.201372	ESTs gb:Homo sapiens skin-specific protein (x	2.28 2.28	4.40 10.57
50	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-tike protein LSm7	2.28	4.06
50	401205			Target Exon	2.27	2.71
	443102 422109	AI247472 S73265	Hs.132965 Hs.1473	ESTs	2.27 2.26	5.66 3.94
	434987	AW975114	15.1415	gastrin-releasing peptide ESTs	2.26	3.72
56	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	2.26	3.42
55	423515	AA327017	Hs.176594	ESTs	2.25	6.21
	434903 443049	AF161369 AI028613	Hs.187763 Hs.132343	Homo sapiens HSPC106 mRNA, partial cds ESTs	2.25 2.25	3.62 3.13
	444637	T19101	Hs.11494	fibulin 5	2.24	6.43
60	41,0026	AI912061	Hs.55016	hypothetical protein FLJ21935	2.23	3.31
VV	418629 429587	BE247550 AA283969	Hs.86859 Hs.334706	growth factor receptor-bound protein 7 Homo sapiens cDNA FLJ11801 fis, ctone HE	2.23 2.23	4.17 3.79
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	2.22	3.54
	409571	AA504249	Hs.187585	ESTs	2.22	3.87
65	446051	8E048061	Hs.37054	ephrin-A3	2.22	4.57
05	422418 453023	AK001383 AW028733	Hs.116385 He 31439	hypothetical protein FLJ10521 serine protease inhibitor, Kunitz type,	2.21	4.25 5.07
	435748	AA699756	Hs.117335	ESTs C	2.21 2.20	5.07 3.35
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.19	6.55
70	444922	A1921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	2.19	3.51
70	433052 430310	AW971983 U60115	Hs.293003 Hs.239069	ESTs, Weakly similar to PC4259 ferritin four and a half LIM domains 1	2.19 2.19	3.32 3.83
	447205	BE617015	Hs. 11006	ESTs, Moderately similar to T17372 plasm	2.19	15.65
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.18	3.54
75	452689	F33868	Hs.284176	transferrin	2.18	3.30
, ,	417061 432647	A1675944 A1807481	Hs.188691 Hs.278581	Homo sapiens cDNA FLJ12033 fis, clone HE fibroblast growth factor receptor 2 (bac	2.18 2.18	3.77 5.64
	401192			Target Exon	2.17	3.33
	421752	AK001521	Hs.107882	hypothetical protein FLJ10659	2.16	3.44
80	456646 421263	AJ243662 AB020638	Hs.110196 Hs.103000	NICE-1 protein KIAA0831 protein	2.16	2.39
-00	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	2.16 2.16	3.37 5.17
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	2.15	3.87
	429350	A1754634	Hs.131987	ESTs	2.15	3.90

	448144	AW169230		ESTs, Moderately similar to PC4259 terri	2.14	3.28
	429002	AW248439	Hs.2340	junction plakoglobin	2.14	5.05
	429297	XB2494	Hs.198862	fibriin 2	2.14	4.32
5	452093 428848	AA447453 NM_000230	Hs.27860 Hs.194236	Homo sapiens mRNA; cDNA DKFZp585M0723 (I	214	3.99
-	407584	W25945	Hs.8173	leptin (murine obesity homolog) hypothetical protein FLJ10803	2.14 2.14	3.39 3.38
	453155	AF052126	Hs.552	steroid-5-alpha-reductase, alpha polypep	2.14	2.51
	453283	AA694386	Hs.290914	ESTs	2.13	3.28
10	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	213	3.76
10	414815 417155	AW292140 175125	Hs.130286 Hs.299148	ESTs hypothetical protein FLJ21801	2.13 2.13	4.16
	416673	177052	Hs.14039	ESTs	213	3.57 3.43
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	2.12	5.67
1.5	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	2.12	4.76
15	430967	H16791	Hs.100895	ESTs	2.12	2.64
	429015 439518	BE 168484 W76326	Hs.194737	KIAA0453 protein gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	212 211	3.30 2.59
	426468	AA379306	Hs.117558	ESTs	210	3.56
	407555	248511		gb:H.sapiens XG mRNA (clone PEP11).	2.10	3.66
20	418226	AA424202	Hs.83834	cytochrome b-5	2.10	5.14
	423441 436961	R68649 AW375974	Hs.278359	absent in melanoma 1 like	2.10	3.64
	432633	A1796390	Hs.156704 Hs.210667	ESTs ESTs	2.10 2.10	3.21 2.58
~~	426102	AF200496	Hs.166371	interleutin 1, zeta	2.09	3.77
25	445467	AI239832	Hs.15617	ESTs, Wealty similar to ALU4_HUMAN ALU S	2.09	3.85
	437124	AAS54458		KIAA0666 protein	2.09	3.35
	407757 407815	BE048414 AW373860	Hs.165215 Hs.183860	hypothetical protein MGC5395	2.08 2.08	4.41 5.01
	443906	AA348031	Hs.7913	hypothetical protein FLJ20277 ESTs	2.08	3.40
30	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.92
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	2.08	4.19
	437704 412533	AA766142 AA679863	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A	2.07	3.30
	426310	NM_000909	Hs.69606 Hs.169266	ESTs neuropeptide Y receptor Y1	2.07 2.06	3.39 3.55
35	411821	BE299339	Hs.72249	three-PDZ containing protein similar to	2.06	4.98
	442599	AF078037	Hs.324051	RelA-associated inhibitor	2.06	7.23
	432212	AW137742	11- 20040	ESTs	2.04	3.52
	453469 443652	AB014533 AI080692	Hs.33010 Hs.134229	KIAA0633 protein 2 ESTs, Weakly similar to 154401 hypertens	2.04 2.04	4.01
40	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.03	3.36 3.64
	424464	R68537	Hs.17962	ESTs	2.03	4.36
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	2.03	3.31
	439908 412825	AI168031 AW167439	Hs.155507 Hs.190651	ESTS	2.03	3.83
45	406784	AI144297	Hs.169401	Homo sapiens cDNA FLJ13625 fis, clone PL apolipoprotein E	2.02 2.02	5.56 3.40
	427309	NM_005714	Hs.175218	potassium channel, subfamily K, member 7	2.02	4.58
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	2.02	3.57
	404246 443679	AK001810	LI- 0070	Target Exon	2.01	7.30
50	410669	AW805749	Hs.9670	hypothetical protein FLJ10948 superoxide dismutase 2, mitochondrial	201 201	5.81 3.05
	446193	A1279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	2.01	2.32
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.00	5.10
	434346 456098	AA630445	H- 65046	ESTs	2.00	3.51
55	452467	AW747800 AW500815	Hs.55016	hypothetical protein FLJ21935 ESTs	2.00 2.00	4.96 4.66
	442866	AI743317	Hs.283622	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.98	3.72
	434699	AA643687	Hs.149425	Homo sapiens cONA FLJ11980 fis, clone HE	1.98	3.11
	417553 449142	L09190	14- 104007	trichohyalin	1.98	2.09
60	407597	R15913 AA043925	Hs.194987 Hs.339352	ESTs Homo sapiens brother of CDO (BOC) mRNA.	1.98 1.98	3.50 6.25
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.97	3.77
	423031	AI278995		ESTs	1.97	3.62
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.96	4.57
65	430420 420139	AW140027 NM_005357	Hs.26373 Hs.95351	Homo sapiens cDNA: FLJ23449 fis, clone H lipase, hormone-sensitive	1.96 1.95	6.09 5.77
	418462	BE001596	Hs.85266	integrin, beta 4	1.95	6.09
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.95	3.33
	437220	AL117542	Hs.334305	GS 1999tull	1.94	3.45
70	407601 443595	AC002300 AF169312	Hs.37129 Hs.9613	sodium channel, nonvoltage-gated 1, beta PPAR(gamma) angiopoletin related protein	1.94	5.46
	409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (f	1.94 1.94	4.67 3.59
	408717	AF045458	Hs.47061	unc-51 (C. elegans)-like kinase 1	1.94	4.29
	420055	NM_001487	Hs.94672	GCN5 (general control of amino-acid synt	1.94	3.38
75	430392 425078	NM_000627 NM_002599	Hs.241257	latent transforming growth factor beta b	1.93	3.75
	423527	AI206965	Hs.154437 Hs.105861	phosphodiesterase 2A, cGMP-stimulated hypothetical protein FLJ13824	1.93 1.93	4.06 4.70
	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.91	3.77
	422101	AW404176	Hs.111611	nbosomal protein L27	1.91	3.18
80	456653	A1807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.41
50	443444 420924	AW952619 R01026	Hs.17235 Hs.245321	Homo sapiens clone TCCCIA00176 mRNA sequ ESTs	1.91 1.91	3.52 3.22
	426048	A1768853	Hs.134478	ESTs	1.90	3.56
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	1.90	4.15

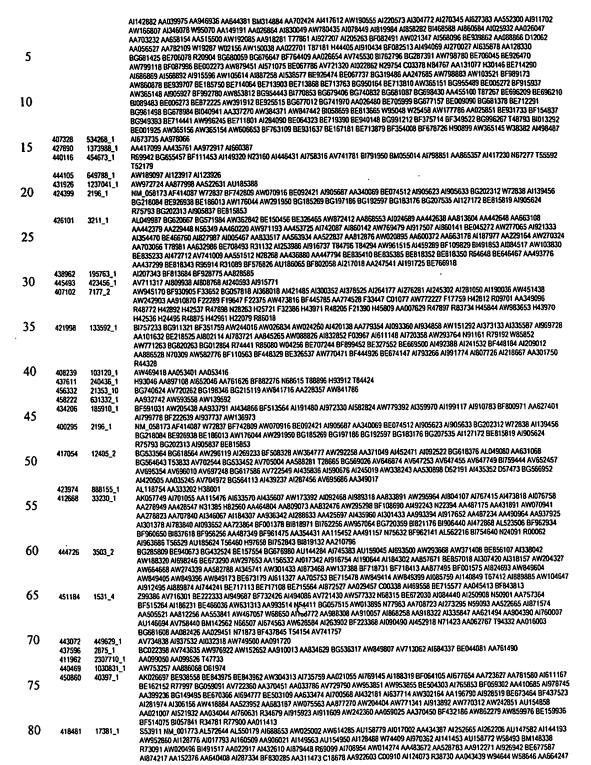
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.90	5.88
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	2.28
	418418	R61527	Hs.237517	ESTs	1.90	3.56
5	449372	AA001266	Hs.133521	ESTs	1.89	3.90
,	438752	AW238673	Hs.146038	ESTs	1.89	5.24
	428193 433251	NM_004235	Hs.322735	Kruppel-like factor 4 (gut)	1.89	5.21 5.00
	430560	AB040955 Z28942	Hs.322733 Hs.243960	KIAA1522 protein	1.89 1.89	7.09
	427795	BE268268	Hs.180842	N-myc downstream-regulated gene 2 ribosomal protein L13	1.69	4.51
10	410209	AI583661	Hs.60548	hypothetical protein PRO1635	1.89	3.35
	449243	AW295031	Hs.198671	ESTs	1.89	4.26
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	1.88	6.20
	443932	AW888222	Hs.9973	tensin	1.88	9.28
	427929	BE613835	. Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.87	4.25
15	400078			Eos Control	1.07	6.73
	422639	AI929377	Hs.173724	creatine kinase, brain	1.87	5.51
	447374	AF263462	Hs.18376	KIAA1319 protein	1.87	3.42
	430346	AK000331	Hs.297641	KIAA0462 protein	1.87	4.15
20	428223	AA424313	Hs.98402	ESTs	1.87	3.70
20	408792	L29433	Hs.47913	coagulation factor X	1.87	4.08
	433855 451583	AA834082 A1653797	Hs.307559	ESTs	1.87	4.16
	426377	AK001921	Hs.24133 Hs.169575	ESTs hypothetical protein MGC2550	1.87 1.86	3.81 5.55
	431647	AL138578	Hs.266738	hypothetical protein dJ796117.1	1.86	3.74
25	422055	NM_014320	Hs.111029	putative heme-binding protein	1.86	4.68
	425750	AL050276	Hs.42400	zinc finger protein 288	1.86	4.04
	422491	AA338548	Hs.117546	neuronatin	1.86	4.37
	438942	AW875398	Hs.6451	PRO0659 protein	1.85	5.06
20	400198			Eos Control	1.85	5.22
30	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	1.85	3.41
	427605	NM_000997	Hs.337445	ribosomal protein L37	1.85	4.73
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.84	5.94
	441912	AA971484	Hs.159938	ESTS	1.84	3.73
35	421632	AA825426	Hs.334689	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.83	3.62
33	440602 431882	AI743491 NM_001426	Hs.292692 Hs.271977	ESTs engraited homolog 1	1.83 1.83	2.39
	420772	AW752656	Hs.222707	KIAA1718 protein	1.83	3.30 3.73
	429197	H24471	Hs.26930	ESTs, Weakly similar to T20272 hypotheti	1.82	3.41
	450796	NM_001988	Hs.25482	envoplakin	1.82	7.73
40	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-ci	1.82	3.38
	415409	AW993701		NS1-associated protein 1	1.82	3.60
	401131			NM_001651":Homo sapiens aquaponn 5 (AOP	1.82	5.53
	421324	BE257515	Hs.103503	deoxyribonuclease 1-like 2	1.61	5.53
A.E	400079			Eos Control	1.81	6.79
45	430513	AJ012008	Hs.241586	G6C protein	1.81	7.49
	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.81	3.55
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.80	5.43
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.79	5.90
50	432417 406467	AL040350	Hs.162203	ESTs, Weakly similar to alternatively sp	1.79 1.79	3.63 4.16
50	444135	AK000374	Hs.10346	Target Exon hypothetical protein FLJ20154	1.79	3.32
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.78	3.51
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.78	3.72
	425880	X01630	Hs.160786	argininosuccinate synthetase	1.78	3.29
55	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	1.78	3.44
	451304	M92642	Hs.26208	collagen, type XVI, alpha 1	1.78	3.57
	400082			Eos Control	1.78	3.82
	446603	NM_014835		oxysterol-binding protein-related protei	1.77	3.48
60	425415	M13903	Hs.157091	involucrin	1.77	4.64
00	400083	anazar		Eos Control	1.77	6.31
	427620	NM_003705 AI652143		solute carrier family 25 (mitochondrial	1.76	3.47
	446971 429807	AK002138	Hs.288382 Hs.306227	hypothetical protein FLJ13111	1.76	4.21
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ11276 fis, clone PL Homo sapiens cDNA FLJ10705 fis, clone NT	1.76 1.76	2.63 3.82
65	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.76	4.31
• •	439927	AA854650	Hs.124597	ESTs	1.75	3.63
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	1.75	3.79
	414500	W24087	Hs.76285	DKFZP564B167 protein	1.75	3.55
70	448182	AF244137	Hs.20597	host cell factor homolog	1.75	3.40
70	439651	AF085480	Hs.56255	ESTs	1.75	2.55
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	1.75	3.54
	424389	AA339786		lymphocyte-specific protein 1	1.75	4.48
	450837	D58463	Hs.85969	hypothetical protein FLJ 12270	1.74	3.40
75	425920	AL049977	Hs.162209	claudin 8	1.74	3.33
13	435680	H50946	Hs.284183	Homo sapiens galectin-related inhibitor	1.74	3.47
	439639 416950	AA370045	Hs.6607	AXIN1 up-regulated	1.73	5.22
	416950	AL049798	Hs.80552	dermatopontin Eos Control	1.73 1.73	4.99 6.25
	409737	AB011539	Hs.56186	EGF-like-domain, multiple 3	1.73	4.28
80	424420	BE614743	Hs.146688	prostaglandin E synthase	1.72	3.42
	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	1.72	2.12
	414323	NM_014759		KIAA0273 gene product	1.71	4.82
	407228	M25079	Hs.155376	hemoglobin, beta	1.70	7.02
				-		

	406643	N77976	Hs.347939	homostatic state 9	170	200
	447299	AF043897	Hs. 18075	hemoglobin, alpha 2 chromosome 9 open reading frame 3	1.70 1.70	3.60 5.10
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.69	2.92
-	415512	Y16270	Hs.78482	paratemmin	1.69	4.92
5	407100	R29657	II- 450000	gb:F1-1179D 22 week old human fetal five	1.69	3.96
	425503 433738	W92517 Al684802	Hs. 158203	actin binding LIM protein 1 ESTs	1.68 1.68	5.97 2.88
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.68	3.44
10	428975	NM_004672	Hs. 194694	mitogen-activated protein kinase kinase	1.68	2.74
10	435661	AF220263	Hs.193920	MOST2 protein	1.67	3.56
	459317 426923	BRCA1b AF112977	Hs.172887	Eos Control	1.67 1.67	3.34 4.53
	426682	AV660038	Hs.2056	phytanoyl-CoA hydroxylase (Refsum diseas UDP glycosyltransferase 1 family, polype	1.67	4.33 3.36
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.67	5.22
15	437201	F29279	Hs.171625	hypothetical protein MGC14697	1.67	5.75
	454478 406710	AW805749 A1708347	Hs.184014	superoxide dismutase 2, mitochondrial	1.67 1.66	4.55
	431593	NM_002108	Hs.276590	ribosomal protein L31 ESTs	1.66	3.80 2.45
••	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	1.66	2.44
20	441899	A1372588	Hs.6022	TUSA protein	1.66	4.06
	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	1.65	6.52
	418116 403105	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot Target Exon	1.65 1.64	3.44 4.12
	450014	N41322	Hs.18441	ESTs	1.64	2.90
25	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp434M245 (fr	1.64	4.49
	401429 420983	WEDE 200		C14001067:gi 4126465 db  BAA36581.1  (AB	1.64	3.82
	433126	W95228 AB021262	Hs.100764 Hs.99816	cathepsin G beta-catenin-interacting protein ICAT	1.64 1.63	3.64 3.29
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polype	1.63	7.05
30	412295	AW088826		poly(A)-binding protein, nuclear 1	1.63	4.01
	430831	AA703239	Hs.269804	ESTs, Wealthy similar to ALU1_HUMAN ALU S	1.63	3.60
	429348 407082	AJ242859 Z47055	Hs.199731	Langerhans cell specific c-type lectin gb:Human partial cDNA sequence, famesyl	1.62 1.62	2.64 2.13
	452556	H78517	Hs.33905	ESTs	1.62	4.64
35	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	1.62	3.33
	446515	AL048875	11. 00.000	hypothetical protein DKFZp566I133	1.62	3.66
	445919 447330	T53519 8E279949	Hs.334692 Hs.18141	hypothetical protein MGC14141 ladinin 1	1.62 1.61	5.65 5.61
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61	5.18
40	400229			NM_021724*:Homo sapiens nuclear receptor	1.61	3.57
	414814	D14697	Hs.77393	farnesyl diphosphate synthase (farnesyl	1.61	2.08
	424397 451335	AI950320 AB023192	Hs.26285	gb:wp08d10.x1 NCI_CGAP_Kid12 Horno sapien imidazofine receptor candidate	1.60 1.60	3.59 5.54
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	1.60	4.79
45	456267	Al127958	Hs.83393	cystatin E/M	1.60	2.50
	436950 421397	L05779 \$67368	Hs.113	epoxide hydrolase 2, cytoplasmic	1.60	3.98
	419092	J05581	Hs.103998 Hs.89603	gamma-aminobutyric acid (GABA) A recepto mucin 1, transmembrane	1.60 1.60	3.28 3.69
	440160	BE560269	Hs.7010	NPD002 protein	1.59	2.49
50	417481	AA203281	Hs.6191	ESTs	1.59	3.60
	406778 402991	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.58 1.58	3.98
	425169	AW292500	Hs.128514	Target Exon ESTs	1.58	3.36 4.00
	446429	AI681807	Hs.201391	ESTs	1.58	3.20
55	426445	AA378739	Hs.187711	ESTs	1.57	3.63
	425196 422581	AL037915 NM_016339	Hs.155097 Hs.118562	carbonic anhydrase II Link guanine nucleotide exchange factor	1.57 1.57	3.44 3.55
	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.56	3.39
<b>~</b>	415988	BE407713	Hs.78943	bleomycin hydrolase	1.56	2.43
60	441860	AW451330	Hs.348198	hypothetical protein FLJ 20262	1.55	3.38
	428462 449518	AI571486 BE395253	Hs.30258 Hs.30861	ESTs ESTs	1.55 1.55	3.65 3.80
	420075	AF142482	Hs.203846	TEA domain family member 3	1.55	3.81
	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	1.54	3.87
65	450787	AB006190	Hs.25475	aquaporin 7	1.54	4.06
	419659 408543	N78098	Hs.92186 Hs.44289	Leman coiled-coil protein ESTs	1.54	3.82
	410169	Al373741	Hs.59384	hypothetical protein MGC3047	1.54 1.54	3.10 4.73
70	426068	AF029778	Hs.166154	jagged 2	1.54	4.82
70	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	1.54	5.83
	415166 410048	NM_003652 W76467	Hs.78068 Hs.343874	carboxypeptidase Z proline oxidase homolog	1.54 1.54	4.58 4.66
	430502	A1123657	Hs.127264	ESTs, Wealdy similar to JC5314 CDC28/cdc	1.53	3.41
70	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.53	4.57
75	413353	AW293542	Hs.75309	eukaryotic translation elongation factor	1.53	3.59
	431021 431243	A1869664 U46455	Hs.252189	thiosulfate sulfurtransferase (modanese	1.53	3.73
	433019	AI208513	Hs.279915	syndecan 4 (amphiglycan, ryudocan) translocase of inner mitochondrial membr	1.52 1.52	6.09 4.49
00	406801	AW242054	Hs.190813	ribosomal protein L9	1.51	5.56
80	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.51	3.77
	432894 415550	AW167668 L13720	Hs.279772 Hs.78501	brain specific protein growth arrest-specific 6	1.51 1.50	6.72 4.02
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis, clone MA	1.49	4.02
	•					

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		*****	70000				
	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-I		.48	3.61
	445071 440763	A1280246 A8028988	Hs.149504 Hs.7407	ESTs KIAA1065 protein		1.48	3.39
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1		1.48	4.03
5	427841	AW883367	1021410	hypothetical protein MGC5306		1.47 1.47	3.58
_	426335	AI054347	Hs.2017	ribosomal protein L38		1.47	3.61 3.76
	454098	W27953	Hs.292911	Plakophilin		1.46	2.95
	456766	R87310	Hs.7740	oxysterol binding protein-like 1		1.46	3.40
	440526	AJ832243		ESTs		1.46	3.38
10	452586	AW958479	Hs.289043	spindlin		1.45	3.48
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer		1.45	3.44
	430238	N72519	Hs.236545	hydroxyacid oxidase 2 (long chain)		1.45	4.00
	425456	T70445	Hs.157850	ribosomal protein L9		1.45	4.79
1.5	411085	AF022991	Hs.68398	period (Drosophila) homotog 1		1.45	4.43
15	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc		1.44	3.89
	445156	N89367	Hs.12373	adenylate cyclase 6		1.44	3.60
	446576	AI659477		dystroglycan 1 (dystrophin-associated gl		1.44	3.07
	440433	AA252452	Hs.7187	hypothetical protein FLJ 10707		1.43	3.67
20	434536	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho		1.42	3.35
20	423513	AF035960	Hs.129719	transglutaminase 5		1.42	3.18
	418681	AA287786	Hs.23449	insufin receptor tyrosine kinase substra		1.42	3.38
	421935	AA131632	Hs.109672	CMP-NeuAC:(beta)-N-acetylgatactosaminide		1.41	4.04
	406712	M31212	Hs.77385	myosin, light polypeptide 6, atkati, smo		1.41	4.27
25	413944 435879	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,		1.41	3.80
23	417967	AW084463 BE244373	Hs.30002	SH3-containing protein SH3GLB2, KIAA1848		1.41	3.55
	412669	AW880841	Hs.1119 Hs.96908	nuclear receptor subfamily 4, group A, m		1.40	4.07
	415523	ALD42003	Hs.296847	p53-induced protein		1.40	3.59
	406713	U02629	Hs.77385	cell matrix adhesion regulator		1.40	4.38
30	439606	W79123	Hs.58561	myosin, light polypeptide 6, afkati, smo G protein-coupled receptor 87		1.39	4.03
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate		1.39	3.65
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti		1.37	3.99
	408198	AA131111	110.01010	gb:zo16b06.r1 Stratagene colon (937204)		1.36 1.36	3.30 3.33
	419600	AA448958	Hs.91481	NEU1 protein		1.35	3.49
35	437141	BE304917	Hs.31097	hypothetical protein FLJ21478		1.34	3.47
	408250	R92918	Hs.19597	KIAA1694 protein		1.34	3.89
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2		1.32	4.24
	425183	W76098	Hs.19223	HCCA2 protein		1.32	3.52
	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU S		1.32	3.50
40	438303	AB028998	Hs.6147	KIAA1075 protein		1.32	3.71
	406800	AA505535		gb:nh84h10,s1 NCI_CGAP_Br1.1 Homo sapien		1.32	3.65
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD)		1.32	4.14
	428475	AF172940	Hs.184542	CGI-127 protein		1.31	3.43
45	406742	AJ468091	Hs.279860	turnor protein, translationally-controlle		1.30	3.34
45	432295	BE091049	Hs.343665	ribosomal protein \$15a		1.30	3.29
	422959	AV647015		paired immunoglobulin-like receptor beta		1.28	3.53
	402956			ENSP00000244002":KIAA1335 protein (Fragm		1.24	3.38
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle		1.24	3.70
50	437142	AI791617	Hs.145068	ESTs, Moderately similar to A46010 X-lin		1.23	3.48
50	424372	AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fis, clone HE		1.18	2.44
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2		1.18	3.43
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)		1,15	2.49
	406587 409574	AW419080	U- 250616	C15000544*:gi[5454148 ref NP_006368.1  U		1.06	2.25
55	417435	NM_005181	Hs.250645	ESTs		1.00	3.60
	402075	11111_003101	Hs.82129	carbonic anhydrase III, muscle specific		1.00	3.44
	422330	D30783	Hs.115263	ENSP00000251056":Plasma membrane calcium epiregulin		1.00	3.37
	418986	AI123555	Hs.81796	ESTs .		1.00	3.35
	404175	7 120000	10.01100	Target Exon		1.00 1.00	3.28 3.08
60	452640	AA027115	Hs.100206	ESTs, Weakly similar to A53856 aryl-acyl		1.00	2.82
	443564	A1921685	Hs.199713	ESTs		1.00	2.51
							2.01
	TABLE 64	4B:					
	Pkey:	Uniq	ue Eos probeset iden	tifier number			
65	CAT num	ber: Gene	cluster number	•			
	Accession	n: Gent	oank accession numb	ers			
	Pkey	CAT Number					
70	412636	1438_1	M77830 NM_0044	15 AF 139065 BG681115 BG740377 BI712964 BG000	656 AA 128470 BI4	38324 H274	08 BE931630 BE167165 AW370827 AW370813
70			J05211 BG698865	BG740734 BG680618 BG739778 BI765807 BM35340	)3 BM353248 AW1	77784 AW20	5789 AW951576 AW848592 BE182164
			BF 149266 BE9401	87 BI060445 BI060444 BF350983 BE720095 BE7200	69 BE715154 BE0	82584 BE08:	2576 BE004047 AA857316 BI039774 BE713818
			BE/13548 AW1/0	253 BE160433 BI039775 AW886475 BM462504 BE93	11734 BF149264 A	A340777 BF:	381183 BG621737 AU127260 AW364859
			BESSON DESCRIPTION	489 BE819009 BF381184 BE715956 R58704 AA85221	Z AW366566 BI09	U358 BF087	7U7 BEB19046 BEB19005 AA377127 BE073467
75			RE019009 BE8190	048 BI036306 BG990973 BI040954 BF919911 AU1401	55 AI951766 AI43	4518 AW804	674 BF752969 BE837009 BE925826 BF149265
, ,			AVV550010 BEB14	264 BI039782 AU140407 BE144243 BE709853 BF985	642 BE001923 BF	933510 AW	705328 BG436319 BE182166 AW365175
			WAXD41099 RF819	280 AW177933 BF873679 AW178000 BE082526 BF4	/6856 BF 086994 B	s-592276 BE	UBZ5U/ BE082514 BE082505 BF873693
			AVVUOCISSU AW84	7678 BF804153 AW365157 BE813930 BE002030 AW3	8515J BE184941	BF749421 B	E 18492V BF839562 BE 184933 BF842254
			DESCENT NAMED OF THE STATE OF T	304 AL 603116 RE148760 DE 705867 RE205866 RE714	1032 BE 164948 BC	386845 AA1	31120 AAU33891 W39488 C04715 BF096124
80			BERDEDAY WANA	304 AL603116 BE149760 BE705967 BE705966 BE70 371 AW376782 AW848780 AW849074 AW361442 BE	3308 AVV848/23 A	ANDOS 4 2011	9379017 AW370097 BG005097 BF751115
~0			RE713207 RE713	371 AW376782 AW848789 AW849074 AW361413 BF: 298 BE 179915 AW799309 BF872345 BF088676 BE70	521123 BFV34211 5030 AW763600 D	ו פכן ובכיואת יים דמו בחתם	35000714 DE 103107 BE 136621 BE /15089
			BE093817 RE8311	90 BF752409 BE006561 BG959922 BF094833 BF094	748 85004682 41	1377600 AM	
				13 Al392926 AU158477 B1467252 AU159919 Al760816			
				600			





			BE061934 H01096 R69613 AJ383162 ALJ133723 AA311526 R67942 H01097 H72113 R72430 R39494 AV744074 AA535925 BJ759288 BJ052385
			DEDE 4607 AWENG 786 AANA 7479 D77478 ALG 17811 DGQ 714 AA 188475 AAN 54965
	412477	occo a	A1200117 A1257027 A1212771 DM001400 A1204064 A1108508 AM00738 AW571549 AW950042 A1089943 AA437280 AU150878 BF197070 A1267984
_	*****		DEEDA181 DE106688 AIA33150 AI338001 AI60036A AIORN107 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 NO4767 AIJ36121
5			A1281153 N51899 A1087072 AA954788 AW059054 A1346309 BC529629 A1340135 BF083036 A1167365 AW819657 AA935468 A467868 AW148701 A1383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 A1553922 A1560688 AW950043 A1961682
			AN CONCERN DOLOGY ANAMORIA NICOSES ALCOCOM ALCOCOM ALCOCOM ALARTON MODOCA ALSERVAN ALIGNOSTICA ALCOCOM
			APAZZAZ TOCCCA DECORDES ALZAGESZ ALMOSSEA1 A AGOLSOA AARRZASZ AIRZSZZÓ AARZSILIZ AARZSILIZ AARZSILIZ AARZSILIZ
			AAB04572 AID85786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110
10			AI382839 AA194837 AA406284 AI250750 R37035 AI525586 W01244
	412947	1568055_1	AA122277 BE183957 BE183956
	432908 434230	452541_1 41110_1	AF150424 AIB61896 AA570057 AV738855 AF119900 NM_018539 AA702388 N53043 BF351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252
	414665	23751_3	BGS67713 AW665841 AI814924 AW978339 AW264036 AI373950 AW183157 AW082249 AI201658 AI364196 AA150743 AA160873 AA463757
15		_	OCO24646 DEG2464 AASEC244 AAGROS44 D40152 AARR7154 T77900 AV751591
	412446	63467_1	BC021725 AIG69212 AI 120184 AI769949 BE701002 BE184363 BE819031 BC702228 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057
			BF090026 BF943158 A632924 BF512340 BF952021 BF950776 BF943437 BF942847 A/T68015 F09778 F04816 F02721 AA102645 Al633838
			AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
20	434442	111738_1	AA662701 AA633929 AA737415
	410453	1027545_1	BE065904 AW749036 BE175746 BE175746 BE175745 BE175745 T64217
	454065	517162_1	BE394588 AW024754 BE183167 BE183166 BE378353 AA633408 AW749955 AW629759 AI651005
	434433 424982	111338_1 25362_1	AKOS7547 BIG181248 AAR83756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967
25	721302	25002	EDGODD ED1078 ED4666 E01176 ED6373 E01076 ED7406 ED7130 ED8742 ED4176 EZ9891 AA195965 AAU86351 W69291 E26800 E32791 EJ 1311
			F32380 F35216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F3399 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783
			A A 100210 E204/2 E17762 E17/49 E006/2 A A 107170 A A 197017
	445029	82093_1	DOSCESTON A ANALOSSE MICHOSOR DE 027022 DE 641CEN AMBROCRY A1651246 A1339033 A1078183 A1686504 AAR13616 RF056955 R43664 BF509917
30			AW663717 W95054 Al382907 Al399929 F10511 AA427819 AW269408 BEB25398 BG654856 AA037082 Al203007 AW593522 H55211 AA010218
	408839	234669_1	Al355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662
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TABLE 55A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN
Table 65A lists about 838 genes downregulated in benign nevi relative to normal skin. Genes were selected from 59880 probesets on the Eos/Affymetrix Huti3 Genechip array. Gene
expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

#### WO 03/025138

Pkey: ExAcon: UnigeneID: Unigene Title: R1: R2:

5

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene title
Unigene gene title
Soth percentille of normal skin Als divided by the average of benign nevi Als
90th percentille of normal skin Als divided by the average of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both the
numerator and denominator

		1,00.0	100 0~ 00 00 min	•		
• •	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
10	420813	X51501	Hs.99949	prolactin-induced protein	27.72	28.59
	408591	AF015224	Hs.46452	mammaglobin 1	26.40	28.34
	422166 418026	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	21.33	21.57
	429441	BE379727 AJ224172	Hs.83213 Hs.204096	fatty acid binding protein 4, adipocyte lipophilin B (uteroglobin family member)	18.06 16.61	18.96 18.06
15	428087	AA100573	Hs.182421	troponin C2, fast	14.70	14.60
	407245	X90568	Hs.172004	tiin	13.08	13.84
	428824	W23624	Hs.173059	ESTs	12.89	13.36
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.78	13.98
20	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.26	9.86
20	453309	A1791809	Hs.32949	defensin, beta 1	12.02	10.62
	423024 446227	AA593731 AI281459	Hs.325823 Hs.270114	ESTs, Moderately similar to ALU5_HUMAN A ESTs	11.90	10.86 12.32
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	11.79 11.19	10.82
	432877	AW974111	Hs.292477	ESTs	11.18	11.30
25	426752	X69490	Hs.172004	titin	10.97	12.63
	427899	AA829286	Hs.332053	serum amyloid A1	10.85	13.85
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	451029	AA852097	Hs.25829	ras-related protein	10.78	10.35
30	421296 431211	NM_002666 M86849	Hs.103253 Hs.323733	perlipin	10.73	11.25
50	422633	X56832	Hs.118804	gap junction protein, beta 2, 26kD (conn enclase 3, (beta, muscle)	10.66 10.57	7.24 9.92
	405121	70001	15.710004	mitogen-activated protein kinase 8 inter	10.41	10.54
	450912	AW939251	Hs.25647	v-los FBJ murine osteosarcoma viral onco	10.26	23.20
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	10.25	9.45
35	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	10.15	9.88
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	10.13	11.58
	447966	AA340605	Hs.105887	ESTs, Wealdy similar to Homolog of rat Z	10.09	5.51
	401203 425545	N98529	Hs.158295	Target Exon	9.95 9.94	10.74
40	425580	L11144	Hs.1907	Homo sapiens, clone MGC:12401, mRNA, com galanin	9.94 9.66	11.47 6.60
. •	414092	214244	Hs.75752	cytochrome c oxidase subunit VIIb	9.45	6.44
	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	10.49
	443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58
45	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.91	10.27
45	452322	BE566343	Hs.28988	glutaredoxin (thioftransferase)	8.90	7.26
	430071 417240	AA355986 N57568	Hs.232068 Hs.48028	transcription factor 8 (represses interl EST	8.86	8.94
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	8.81 8.72	18.90 6.86
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	8.39	10.26
50	408491	AI088063	Hs.7882	ESTs	8.00	8.20
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	7.99	8.14
	409738	8E222975	Hs.56205	insulin induced gene 1	7.95	7.75
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.89	8.86
55	451831 410867	NM_001674 X63556	Hs.460 Hs.750	activating transcription factor 3 fibrillin 1 (Marfan syndrome)	7.79	7.51
33	444984	H15474	Hs.132898	fatty acid desaturase 1	7.76 7.75	7.55 5.64
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	7.68	5.65
	410532	T53088	Hs.155376	hemoglobin, beta	7.64	4.73
	442757	AI739528	Hs.28345	ESTs	7.62	7.66
60	412047	AA934589	Hs.49696	ESTs .	7.61	7.48
	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.52	7.28
	439394 442941	AA149250 AU076728	Hs.56105 Hs.8867	ESTs	7.52	6.72
	450680	AF131784	Hs.25318	cysteine-rich, angiogenic inducer, 61 Homo sapiens clone 25194 mRNA sequence	7.51 7.51	6.27 4.10
65	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (catgran	7.49	8.08
	407334	AA494411	Hs.296031	ESTs	7.48	6.78
	414449	AA557660	Hs.76152	decorin	7.39	8.30
	432305	M62402	Hs.274313	insufin-like growth factor binding prote	7.38	8.79
70	407328	AA508857		ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
70	431842	NM_005764 X03350	Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488 445502	AW379160	Hs.4 Hs.12813	alcohol dehydrogenase 18 (class i), beta	7.03	7.85
	419285	D31887	Hs.89868	DKFZP434J214 protein KIAA0062 protein	7.01 7.01	6.63 5.82
	409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.99	4.58
75	422963	M79141	Hs.13234	ESTs	6.99	4.08
	447918	Al129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	6.98	6.49
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	444381 417993	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	6.95	8.08
80	417993 443060	AW963705 D78874	Hs.301183 Hs.8944	molecule possessing ankyrin repeats indu	6.94 6.94	7.12
55	427890	AA435761	P#E0.611	procollagen C-endopeptidase enhancer 2 ESTs	6.94 6.94	6.79 6.68
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.93	4.66
	442083	R50192	Hs.165062	ESTs	6.92	6.92
				<b>604</b>		

	****	4141000000				
	441633 407722	AW958544 BE252241	Hs.112242 Hs.38041	normal mucosa of esophagus specific 1 pyridoxal (pyridoxine, vitamin 86) kinas	6.87 6.87	5.07 4.99
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	6.84	5.33
_	414841	H55601	Hs.77490	glutathione S-transferase theta 1	6.84	3.47
5	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	6.79	7.14
	427704	AW971063	Hs.292882	ESTs .	6.72	7.30
	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.10
	451253 453187	H48299 Al161383	Hs.26126 Hs.34549	claudin 10 ESTs, Highly similar to \$94541 1 clone 4	6.71 6.68	7.20 3.02
10	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	6.08
	434525	W01370	Hs.46824	ESTs	6.61	6.92
	408063	8E086548	Hs.42346	catcineurin-binding protein catsarcin-1	6.60	7.29
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	6.55	6.79
15	411388 413731	X72925 BE243845	Hs.69752 Hs.75511	desmocollin 1 connective tissue growth factor	6.55 6.52	3.44 4.86
1.5	455863	AA907305	Hs.36475	ESTs	6.50	4.24
	412247	AF022375	Hs.73793	vascular endothelial growth factor	6.49	4.56
	407102	AA007629		glyceroi-3-phosphale dehydrogenase 1 (so	6.47	7.23
20	421407	T82331	Hs.182278	ESTs, Wealthy similar to CGHU6C collagen	6.47	6.55
20	406867 429504	AA157857 X99133	Hs.182265 Hs.204238	keratin 19	6.44 6.43	6.23
	446945	A1193115	Hs.16611	lipocelin 2 (oncogene 24p3) (NGAL) tumor protein D52-like 1	6.43	6.79 5.66
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
25	407395	AF005082		gb:Homo sapiens skin-specific protein (x	6.39	4.76
25	450626	AW190989	Hs.1508	insulin-degrading enzyme	6.37	6.22
	450713 437596	AL133611	Hs.25362	Homo sapiens mRNA; cDNA DKFZp43401317 (f	6.37	4.91
	430191	AA761490 AI149880	Hs.188809	ESTs, Moderately similar to S65657 alpha ESTs	6.35 6.34	5.31 6.15
	433713	AW976511	Hs.112592	ESTs	6.34	5.67
30	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	6.33	6.39
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	6.33	5.77
	437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.30	5.45
	433412 447335	AV653729 BE617695	Hs.8185 Hs.286192	CGI-44 protein; suffide dehydrogenase fi hypothetical protein FLJ20940	6.29 6.28	6.68 10.35
35	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.21	5.98
	440116	A1798851		hemoglobin, gamma G	6.18	6.86
	454229	AW957744	Hs.278469	lacrimal proline rich protein	6.17	6.54
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
40	451144 431319	AW956103 AA873350	Hs.61712 Hs.302232	pyruvate dehydrogenase kinase, isoenzyme ESTs	6.12 6.11	5.79 7.91
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	6.10	5.63
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	6.08	6.96
	418321	D63477	Hs.84087	KJAA0143 protein	6.08	4.71
45	443072	AI937532	11-04000	gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	6.07	5.48
7)	423712 442679	W46802 R53718	Hs.81988	disabled (Drosophila) homolog 2 (mitogen hypothetical protein FLJ 10659	6.04 6.03	5.81 5.67
	424824	AI217440	Hs.143873	ESTs	6.02	5.45
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.01	7.05
50	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	7.17
20	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	5.92	5.79
	424670 424673	W61215 AA345051	Hs.116651 Hs.294092	epithelial V-like antigen 1 ESTs, Wealdy similar to 138022 hypotheti	5.92 5.91	5.63 6.81
	418205	L21715	Hs.83760	troponin I, skeletal, fast	5.91	6.95
	400440	X83957	Hs.83870	nebulin	5.89	7.01
55	444239	R57988	Hs.10706	epithelial protein lost in neoptasm beta	5.89	5.49
	419517 432626	AF052107 AA471098	Hs.90797	Homo sapiens clone 23520 mRNA sequence	5.86 6.00	5.88
	407584	W25945	Hs.278544 Hs.8173	acetyl-Coenzyme A acetyltransferase 2 (a hypothetical protein FLJ10803	5.86 5.81	5.58 5.09
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	5.79	6.33
60	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	5.78	5.91
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	5.78	3.74
	412630 408819	AA738437 AW163483	Hs.26226 Hs.48320	Homo sapiens cDNA: FLJ21286 fis, clone C	5.76 5.74	4.21 4.59
	433027	AF191018	Hs.279923	double ring-finger protein, Dorfin putative nucleotide binding protein, est	5.71 5.70	4.71
65	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	5.68	6.12
	408515	A1289507	Hs.299883	hypothetical protein FLJ23399	5.67	4.81
	443827	AI087867	Hs.134667	ESTs	5.67	5.54
	429693	8E254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	5.67	4.12
70	427373 428666	AB007972 AL080190	Hs.130760 Hs.189242	myosin phosphatase, target subunit 2 Horno sapiens mRNA; cDNA DKFZp434A202 (fr	5.66 5.65	4.27 5.16
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	5.65	4.52
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN!	5.65	4.81
	419731	S47242	Hs.92909	SON DNA binding protein	5.64	3.77
75	420787	AA564248 AJ380552	Me goens	ESTs, Weakly similar to 138022 hypotheti	5.64	3.27
,,	420682 410541	AJJ80552 AA065003	Hs.88602 Hs.64179	ESTs syntenin-2 protein	5.63 5.62	4.13 5.84
	431360	NM_000427		loricia	5.62 5.61	5.14
	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	5.61	4.28
0Λ	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
80	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	5.51	16.04
	429679 422082		Hs.211600 Hs.111244	tumor necrosis factor, alpha-induced pro hypothetical protein	5.49 5.49	5.28 5.23
	419461	AJ452601	Hs.288869	nuclear receptor subtamily 2, group F, m	5.49	4.40
				* · • · · · · · · · · · · · · · · · · ·		-

	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH	5.48	5.38
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	5.46 5.45	5.11 3.63
	400494		11- 40753	ENSP00000238970":CIG30 (Fragment).	5.43	4.25
5	415062	H45100	Hs.49753 Hs.23440	uveal autoantigen with colled coll domai KIAA1105 protein	5.41	3.82
	449291 435538	BE176893 AB011540	Hs.4930	low density lipoprotein receptor-related	5.41	2.62
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
	434535	AI611729	Hs.167619	ESTs, Moderately similar to ALUC_HUMAN!	5.40	5.20
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	5.39	4.59
10	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	5.37	14.96
	436090	AI640635	Hs.332879	EST	5.37	5.33
	406805	A1686003	Hs.296031	ESTs	5.35	5.49
	426510	AW861225	Hs.251928	BANP homolog, SMAR1 homolog	5.35	6.83
16	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34	7.50 4.88
15	456332	AA228357	440000	gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	5.34 5.34	4.75
	421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006 mannosidase, alpha, class 1A, member 2	5.34	3.59
	418479 417059	AA829976 AL037672	Hs.81071	extracellular matrix protein 1	5.34	4.71
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	5.34	4.5
20	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	5.34	8.69
20	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	5.31	5.81
	449271	AW338067	Hs.7869	Horno sapiens cDNA FLJ11946 fis, clone HE	5.30	4.35
	437135	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.29	4.92
	419925	AA159850	Hs.93765	liporna HMGIC fusion partner	5.29	5.02
25	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	5.28	5.33
	453999	BE328153	Hs.240087	ESTS	5.28	3.40
	408958	T99607	Hs.49346	signal recognition particle 54kD	5.28	2.84
	452496	AA114926	Hs.169531	ESTs	5.28 5.27	5.48 3.72
30	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	5.27 5.26	4.62
30	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr gb:Human nebulin mRNA, partial cds	5.26	6.21
	407013 414602	U35637 AW630088	Hs.83870 Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	4.21
	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	5.26	4.43
	445107	AJ208121	Hs.147313	ESTs, Weakly similar to 138022 hypotheti	5.25	5.61
35	446267	AW450103	Hs.151124	ESTs	5.24	4.44
	422278	AF072873	Hs.114218	frizzied (Drosophila) homolog 6	5.23	3.14
	448585	AB020676	Hs.21543	KIAA0869 protein	5.23	6.21
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	5.22	6.84
40	414407	AA147026	Hs.76704	ESTs	5.22	5.29
40	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	5.22	5.85
	415997	NM_003590	Hs.78946	cuttin 3	5.21	3.66
	411531	AB014511	Hs.70604	ATPase, Class II, type 9A	5.21 5.20	3.95 4.38
	441619	NM_014056		DKFZP564K247 protein	5.20 5.19	4.52
45	435232	NM_001262		cyclin-dependent kinase inhibitor 2C (p1	5.19	3.13
4)	415167	AA160784	Hs.26410 Hs.178604	ESTs ESTs	5.18	5.38
	431416 439995	AA532718 AL137480	Hs.6834	KIAA1014 protein	5.17	3.14
	416784	AA334592	Hs.79914	turnican	5.17	6.18
	446082	AI274139	Hs.156452	ESTs	5.16	5.14
50	400196	7-21 1100		Eos Control	5.16	5.05
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	5.16	4.31
	414242	AA74923D	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	5.15	4.89
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	5.14	5.22
	440383	AA884208	Hs.30484	ESTs	5.13	5.09
55	431628	AF146277		CD2-associated protein	5.13 5.13	5.03 4.31
	407047	X65965	N- 440030	gb:H.sapiens SOD-2 gene for manganese su	5.12	3.57
	433688	AA628467	Hs.112572 Hs.131810	Homo sapiens cDNA FLJ14130 fis, clone MA ESTs, Moderately similar to ALU1_HUMAN A	5.12	3.30
	437704 426101	AA766142 AL049987	NS.131010	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.11	6.08
60	428297	AA235291	Hs.183583	serine (or cysteine) proteinase inhibito	5.10	4.31
00	416382	D86985	Hs.79276	KIAA0232 gene product	5.10	3.79
	437150	RS1407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.10	6.58
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	5.09	4.82
	434647	W74158	Hs.103189	lipopolysaccharide specific response-68	5.09	4.90
65	418730	AA091027	Hs.325625	Homo sapiens clone 23938 mRNA sequence	5.09	3.46
	449338		Hs.394	adrenomedullin	5.09	6.26
	438962			gb:hn41c11.x1 NCI_CGAP_RDF2mo sapiens	5.08	5.60
	431693			serine (or cysteine) proteinase inhibito	5.07 5.06	2.83 6.71
70	420583		Hs.65450	reticulon 4	5.06	6.06
70	431048		Hs.249129 Hs.183006	cell death-inducing DFFA-like effector a Horno sapiens cDNA FLJ12300 fis, clone MA	5.05	6.32
	432125 447945		Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	3.72
	442547		Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	2.86
	414176		Hs.75794	EDG-2 (endothelial differentiation, lys	5.03	4.43
75	445263		Hs.42586	KIAA1560 protein	5.03	6.67
	448490		Hs.271692	ESTs, Weakly similar to 138022 hypotheti	5.03	4.88
	450515			biphenyl hydrolase-like (serinė hydrolas	5.03	4.36
	440624		Hs.7306	secreted frizzled-related protein 1	5.01	5.48
00	417165	R80137	Hs.302738	Homo sapiens cONA: FLJ21425 fis, clone C	5.01	5.61
80	417640		Hs.82353	protein C receptor, endothelial (EPCR)	5.01	5.32
	413475			ESTs	5.01 5.00	3.90 4.54
	414792			hypothetical protein FLJ23309	5.00 5.00	3.19
	424074	1 AJ902456	Hs.210761	ESTs, Weakly similar to 138022 hypotheti	3.00	3.13

	424620	AA101043	Hs.151254	kalītkrein 7 (chymotryptic, stratum com	4.99	6.25
	439039	AI656707	Hs.48713	ESTs	4.99	6.60
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.98	9.59
5	410579	AK001628	Hs.64691	KIAA0483 protein Homo sapiens clone IMAGE:119716, mRNA se	4.98 4.98	4.52 3.84
,	449710 434230	AA002207 AAS51569	Hs.17385	hypothetical protein PRO2822	4.98	3.63
	426468	AA379306	Hs.117558	ESTs	4.98	3.56
	421690	AW162667	Hs.106857	calbindin 2, (29kD, catretinin)	4.96	6.41
10	448144	AW169230	11- 33454	ESTs, Moderately similar to PC4259 ferri	4.96 4.96	3.28 5.75
10	412129 450071	M21984 AA018283	Hs.73454 Hs.24359	troponin T3, skeletal, fast Homo sapiens cDNA FLJ11174 fis, clone PL	4.96	3.21
	433934	AW273261	Hs.216292	ESTs	4.95	4.39
	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	4.95	4.01
16	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	4.94 4.94	4.54 4.49
15	453225 444476	BE258769 AF020038	Hs.11223	acetyl-Coenzyme A acyttransferase 2 (mit isocitrate dehydrogenase 1 (NADP), solub	4.94	4.19
	445493	AP020036 AI915771	115.11223	metallothionein 1E (functional)	4.93	5.68
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	4.93	5.47
20	417054	AF017060		aldehyde oxidase 1	4.93	4.51 3.34
20	425917	W28517	Hs.117167 Hs.281462	Homo sapiens cDNA: FLJ23067 fis, clone L ESTs, Wealdy similar to 138022 hypotheti	4.93 4.93	5.61
	408681 451267	AW953853 Al033894	Hs.117865	solute carrier family 17 (anion/sugar tr	4.92	3.27
	447137	AW970192	Hs.171942	ras responsive element binding protein 1	4.91	4.26
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	4.90	6.00
25	432314	AA533447	Hs.312989	ESTs	4.90 4.89	3.79 3.71
	440692 428594	AL031591 BE387236	Hs.7370 Hs.75415	phosphotidylinositol transfer protein, b beta-2-microglobulin	4.89	3.27
	437802	AI475995	Hs.122910	ESTs	4.87	4.06
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.86	6.54
30	427156	BE621719	Hs.173802	KIAA0603 gene product	4.86	5.15 5.50
	433179	AW362945	Hs.162459 Hs.194679	ESTs WNT1 inducible signaling pathway protein	4.86 4.85	5.29
	428957 453855	NM_003881 AA039576	Hs.37858	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.85	3.59
_	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALUS_HUMAN ALU S	4.85	3.45
35	429279	AB018271	Hs.198689	KIAA0728 protein	4.83	3.80
	445773	H73456	Hs.13299	Homo sapiens mRNA, cDNA DKFZp761M0111 (f	4.82 4.82	4.20 4.01
	416349 408138	X69089 AA535740	Hs.79227	myomesin (M-protein) 2 (165kD) tumor protein p53-binding protein, 1	4.81	4.19
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	4.80	3.99
40.	444677	AL110212	Hs.301005	purine-rich element binding protein B	4.80	3.50
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	4.80 4.79	10.20 4.39
	431926 407839	AW972724 AA045144	Hs.161566	gb:EST384816 MAGE resequences, MAGL Horno ESTs	4.79	2.98
	421998	R74441	115.101300	poly(A)-binding protein, nuclear 1	4.77	4.78
45	416987	D86957	Hs.80712	KIAA0202 protein	4.76	3.99
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	4.76	7.59
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha ESTs, Highly similar to T42626 secreted	4.75 4.75	4.38 3.92
	453180 413276	N46243 Z24725	Hs.110373 Hs.75260	mitogen inducible 2	4.75	5.68
50	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	4.74	5.57
	414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	4.74	11.58
	429587	AA283969	Hs.334706	Homo sapiens cONA FLJ11801 fis, clone HE gb:Human nonspecific crossreacting antig	4.74 4.73	3.79 4.88
	407242 445229	M18728 BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	4.73	4.79
55	447429	AB007920	Hs.18586	KIAA0451 gene product	4.72	2.38
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	5.10
	414848	A1803447	Hs.77496	small nuclear ribonucleoprotein polypept ESTs, Wealdy similar to K1CJ_HUMAN KERAT	4,71 4,70	2.51 6.13
	439652 453145	W67826 R63438	Hs.55412 Hs.183454	Homo sapiens cDNA FLJ14883 fis, clone PL	4.70	3.06
60	421302	T34462	Hs.103291	neuritin	4.69	4.96
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.68	5.01
	448079	R76981	Hs.39168	thyroid hormone receptor-associated prot	4.68 4.67	3.97 3.42
	434558 408239	AW264102 AA053401	HS.39100	ESTs ESTs, Moderately similar to ALU7_HUMAN A	4.67	6.17
65	454416	AI912097	Hs.163208	ESTs	4.66	3.97
	427215		Hs.268371	hypothetical protein FLJ20274	4.66	3.37
	451583		Hs.24133	ESTs	4.65	3.81 6.14
	446525		Hs.211556 Hs.54900	hypothetical protein MGC5487 serologically defined colon cancer antig	4.65 4.65	3.65
70	436176 450528			PRO0461 protein	4.64	2.99
	417259			chondroitin sulfate proteoglycan 2 (vers	4.64	4.72
	408741		Hs.646	carboxypeptidase A3 (mast cell)	4.63	5.55
	417733		Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	4.63 4.63	5.04 3.55
75	436280 428744		Hs.192853	Homo sapiens cDNA: FLJ22562 fis, clone H ubiquitin-conjugating enzyme E2G 2 (homo	4.63	2.85
, ,	427007			transforming, acidic coiled-coil contain	4.63	3.00
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.62	5.14
	449971	AA807346		Homo sapiens cDNA FLJ14296 fis, clone PL	4.62 4.62	4.49 3.56
80	409598 413305			mitochondrial ribosomal protein S28 Homo sapiens cDNA: FLJ23176 fis, clone L	4.62 4.62	3.36 4.24
50	413303		Hs.74076	CD163 antigen	4.61	8.03
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.61	6.86
	452289		Hs.28827	mitogen-activated protein kinase kinase	4,61	4.33

	458971		Hs.101874	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.61	4.16
	433256	AW604447	Hs.339408	ESTs, Weakly similar to \$26689 hypotheti	4.61	3.58 3.22
	440596	H13032	Hs.103378	hypothetical protein MGC11034	4.61 4.60	4.74
5	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (I ESTs	4.60	4.11
J	424651 436701	AJ493206 AW959032	Hs.32425	ESTs, Moderately similar to 178885 serin	4.60	2.34
	413691	AB023173	Hs.75478	ATPase, Class VI, type 118	4.59	4.38
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.59	4.00
	436283	AI480319	Hs.120058	ESTs	4.59	3.76
10	451710	AW867467	Hs.278712	eukaryotic translation initiation factor	4.59	3.51
••	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	4.59	3.64
	434597	AL133033	Hs.4084	KIAA1025 protein	4.58	5.10
	402294			Target Exon	4.57	5.47
	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57	5.12
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.57	4.66
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	4.57	4.15
	441566	AA604110	Hs.151725	ESTs	4.57 4.56	3.21 4.76
	400109	4 0003035	N- 02004	Eos Control	4.56	3.63
20	419740	AB037835 AW391972	Hs.92991	KIAA1414 protein KIAA1324 protein	4.55	7.16
20	421481 440266	AA088809	Hs.104696 Hs.19525	hypothetical protein FLJ22794	4.55	4.44
	421979	AW062518	Hs.233150	hypothesical protein MGC5560	4.55	4.36
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	4.54	5.78
	418021	M15881	Hs.1137	uromodulin (uromucoid, Temm-Horsfall gly	4.54	4.61
25	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	4.54	4.32
	421986	AL137438	Hs. 110454	SEC15 (S. cerevisiae)-like	4.54	2.59
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	4.53	6.18
	410132	NM_003480	Hs.300945	Microfibril-associated plycoprotein-2	4.53	5.87
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	4.53	4.87
30	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	4.53	10.61
	452924	AW580939	Hs.97199	complement component C1q receptor	4.51	6.07
	454000	AA040620	Hs.5672	hypothetical protein AF140225	4.51	4.59
	404730			Target Exon	4,51	4.30 3.40
25	449943	AF104266	Hs.24212	latrophilin	4.51 4.50	2.97
35	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.50 4.50	4.77
	435992	AI033259	Hs.118317	Homo sapiens cDNA FLJ12088 fis, clone HE	4.50	3.30
	421311	N71848	Hs.283609 Hs.288300	hypothetical protein PRO2032 hypothetical protein FLJ23231	4.49	5.06
	449785	AI225235	H\$.200300	gb:am08a06.s1 Soares_MFL_T_GBC_S1 Homo s	4.49	4.24
40	437611 419612	AA897108 AI498267	Hs.110613	KIAA0421 protein	4.49	4.16
70	414496	W73853	115.110013	ESTs	4.49	3.15
	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.48	3.38
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	4.47	4.45
	432559	AW452948	Hs.257631	ESTs	4,47	5.39
45	442554	AW467376	Hs.129640	ESTs	4.47	4.00
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-fi	4.46	4.47
	422313	AF045941	Hs.115166	sciellin	4.45	5.07
	435748	AA699756	Hs.117335	ESTs	4.45	3.35
	453283	AA694386	Hs.290914	ESTs	4.45	3.28
50	441925	R83113		protein kinase C substrate BOK-H	4.45	3.28
	440030	AA932693		EST	4.45 4.44	3.20 3.66
	446515	AL048875	11- 021	hypothetical protein DKFZp5661133	4.44	5.90
	406707	S73840 AL137662	Hs.931 Hs.274401	myosin, heavy potypeptide 2, skeletal mu Homo sapiens mRNA; cDNA DKFZp434P086 (fr	4.44	3.99
55	432341 410453	AW749036	115.274401	gb:RC2-BT0318-241199-011-f10 BT0318 Homo	4.44	3.49
"	450196	AW956868	Hs.24608	DKFZP564D177 protein	4.43	4.13
	444147	AB002306	Hs.10351	KIAA0308 protein	4.43	3.95
	427809	M26380	Hs.180878	lipoprotein lipase	4.42	3.88
	428157	AI738719	Hs.198427	hexokinase 2	4.42	5.46
60	413299	AA857487	Hs.75275	ubiquitination factor E4A (homologous to	4.42	3.77
	440245		Hs.7100	hypothetical protein	4.42	3.51
	442379			transglutaminase 2 (C polypeptide, prote	4.42	1.79
	408569		Hs.86412	chromosome 9 open reading frame 5	4.42	3.35 5.78
45	430361		Hs.239926	sterol-C4-methyl oxidase-like	4.41 4.41	5.43
65	414489		Hs.73105	ESTs	4.41	5.28
	447/31		Hs.19385	CGI-58 protein Homo sapiens cDNA FLJ14201 fis, clone NT	4.41	4.41
	443195		Hs.193063 Hs.21332	BT8 (POZ) domain containing 1	4.41	3.68
	448503 432546		Hs.180638	hypothetical protein FLJ13081	4.41	3.55
70	445620		Hs.17441	ESTs	4.41	3.44
	454065		10.1741	gb:601311808F1 NIH_MGC_44 Homo sapiens c	4.41	3.43
	418802		Hs.88500	mitogen-activated protein kinase 8 inter	4.40	2.04
	431816		Hs.190738	ESTs	4.39	4.26
	429138		Hs.197298	NS1-binding protein	4.39	4.47
75	426643		Hs.171595	HIV TAT specific factor 1	4.39	3.09
	448943		Hs.193288	ESTs	4.39	2.63
	414002		2 Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.37	19.16
	403593			Target Exon	4.37	6.35
00	408104			ESTs	4.31	5.82 4.14
80	429624		Hs.99476	ESTs, Weakly similar to 13131848 alpha1	4,31 4,25	4.14 6.61
	42953		Hs.139322	small proline-rich protein 2A	4.25 4.18	5.28
	41450		Hs.23558	ESTs, Weakly similar to A48042 lysosomal ESTs, Weakly similar to T24832 hypotheti	4.18	5.81
	43853	3 AI440266	Hs.170673	CS1S, Weakly Sitted to 124652 hypotheti		

	426143	8E379836		proteasome (prosome, macropain) subunit,	4.15	5.12
	414527	BE241739	Hs.76359	catalase	4.14	5.13
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	4.13	8.60
5	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	4.12	5.94
,	412477 411558	AA150864 AA102670	Hs.70725	microsomal glutathione S-transferase 1 gamma-aminobutyric acid (GABA) A recepto	4.10 4.09	10.00 5.39
	444252	R21135	Hs.54985	ESTs	4.07	6.01
	400295	W72838		Al905687:IL-BT095-190199-019 BT095 Homo	4.06	13.32
10	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	4.06	7.57
10	429856 422168	AA971576 AA586894	Hs.225951 Hs.112408	topoisomerase-related function protein 4 \$100 calcium-binding protein A7 (psorias	4.05 4.01	6.24 4.61
	403710	AV-200024	TS.112400	C4000160:gij12735793(ref)XP_011928.11 pr	4.00	4.06
	406643	N77976	Hs.347939	hemoglobin, alpha 2	3.97	7.22
1.5	436372	AW972301	Hs.310286	ESTs	3.96	5.41
15	428340 424604	AF261088	Hs.154721	aconitase 1, sotuble	3.94	5.33
	426653	AW865388 AA530892	Hs.151076 Hs.171695	KIAA1243 protein dual specificity phosphatase 1	3.91 3.91	7.59 14.81
	410204	AJ243425	Hs.326035	early growth response 1	3.87	9.96
20	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.87	5.09
20	443021	AA368546	Hs.8904	lg superfamily protein	3.86	7.65
	430418 447796	R98852 AW953622	Hs.36029 Hs.223025	heart and neural crest derivatives expre RAB31, member RAS oncogene family	3.81 3.76	6.19 5.10
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	3.76	5.12
0.5	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.75	5.46
25	426281	AK000987	Hs.169111	oxidation resistance 1	3.74	5.14
	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.74	6.30
	445234 457411	AW137636 AW085961	Hs.146059 Hs.130093	ESTs iroquois-class homeobox protein IRX2	3.72 3.71	5.59 4.85
	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	3.71	6.72
30	413880	AI660842	Hs.110915	interleukin 22 receptor	3.71	4.01
	422640	M37984	Hs.118845	troponin C, slow,	3.71	9.10
	452241 453560	AL050204 AA348626	Hs.28540 Hs.5890	Homo sapiens mRNA; cDNA DKFZp586F1223 (f hypothetical protein FLJ23306	3.70 3.69	3.21 5.13
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.69	7.69
35	413922	A1535895	Hs.221024	ESTs	3.68	4.80
	428698	AA852773	Hs.334838	KIAA1866 protein	3.64	5,22
	451951	AW082870	Hs.210954	ESTs	3.64	3.69
	452308 441128	A1167560 AA570256	Hs.61297	ESTs ESTs, Weakly similar to 723273 hypotheti	3.64 3.63	4.35 2.91
40	421978	AJ243662	Hs.110196	NICE-1 protein	3.61	6.05
_	418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	3.61	6.22
	452413	AW082633	Hs.215030	ESTs	3.58	3.03
	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	3.55	6.39
45	408522 423503	AI541214 M92843	Hs.46320 Hs.343586	Small proline-rich protein SPRK (human, zinc finger protein homologous to Zfp-36	3.54 3.53	10.68 15.11
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.53	5.29
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.46
	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.51	3.67
50	418067 420202	Al127958 AL036557	Hs.83393 Hs.95910	cystatin E/M putative lymphocyte G0/G1 switch gene	3.51 3.50	3.74 14.64
-	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.50	2.79
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	3.48	7.91
	450860	AA021007		integrin, beta 8	3.47	5.89
55	414665 413663	AA160873 BE247585	Hs.75462	serum amyloid A1 BTG family, member 2	3.46 3.46	9.22 5.63
55	427408	AA583206	Hs.2156	RAR-related orphan receptor A	3.45	3.08
	430171	AF086289	Hs.234766	skin-specific protein	3.45	4.77
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3,42	8.09
60	450607 412596	AL050373 AA161219	Hs.25213 Hs.799	hypothetical protein diphtheria toxin receptor (heparin-bindi	3.41 3.41	6.43 6.10
00	427681	AB018263	Hs.180338	turnor necrosis factor receptor superfami	3.39	6.59
	440590	AIB63446	Hs.266308	mosaic senne protease	3.34	3.09
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3,31	10.06
65	422101 431986	AW404176 AA536130	Hs.111611 Hs.149018	ribosomal protein L27 Novel human gene mapping to chomosome 20	3.30 3.30	3.93 3.54
05	412649	NM_002206		integrin, alpha 7	3.28	5.89
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	3.28	5.44
	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain	3.28	5.93
70	412061	AA833763	Hs.330211	ESTs	3.27	5.75
70	437592 452849	NM_003851 AF044924	Hs.5710 Hs.30792	cellular repressor of E1A-stimulated gen hook2 protein	3.27 3.26	5.83 5.66
	421462	AF016495	Hs.104624	aquaporin 9	3.25	4.98
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.24	6.56
75	444935	AA262449	Hs.223569	ESTs	3.24	5.96
75	422057 410017	AI205785 AW952426	Hs.30348 Hs.109438	ESTs	3.22 3.21	5.72 5.26
	407948	AW085161	Hs.56279	Homo sapiens clone 24775 mRNA sequence ICEBERG caspase-1 inhibitor	3.21 3.21	5.26 4.61
	452089	T97294	Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	3.19	4.42
9Λ	448249	AW855331	Hs.337124	ESTs	3.18	2.97
80	430869 443623	D10511 AA345519	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	3.17	5.66
	452865	AI924046	Hs.9641 Hs.119567	complement component 1, q subcomponent, ESTs, Weakly similar to A47582 B-cell gr	3.16 3.16	12.00 6.03
	452392	L20815	Hs.507	comeodesmosin	3.15	5.70

	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	3.15	5.87
	420309		Hs.21766	ESTs. Weakly similar to ALU5_HUMAN ALU S	3.15	4.98
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	3.13	17.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.12	4.63
5	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.12	3.02
_	432375	BE536069	Hs.2962	S100 catcium-binding protein P	3.12	8.51
	417713	D42047	Hs.82432	KIAA0089 protein	3.12	5.82
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	3.11	6.51
	444195	AB002351	Hs.10587	KIAA0353 protein	3.11	5.44
10	415704	NM_001677	Hs.78629	ATPase, Na? transporting, beta 1 polypep	3.11	6.61
10	401905	14m_001017	110.10025	ENSP00000252232":Sterol regulatory eleme	3.10	3.52
		AL080021	Hs.8986	complement component 1, q subcomponent,	3.10	5.10
	443071			ubiquinol-cytochrome c reductase core pr	3.10	5.39
	427095	AA316080	Hs.173554		3.08	5.56
15	413835	A1272727	Hs.249163	fatty acid hydroxytase ESTs	3.07	5.19
15	448106	A1800470	Hs.171941		3.07	3.47
	432908	AI861896		ESTs	3.07	7.48
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL		3.97
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05 3.02	
20	424998	U58515	Hs.154138	chitinase 3-like 2		6.75
20	419358	T78763	Hs.90063	neurocalcin delta	3.00	7.68
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.99	5.44
	426402	BE387327	Hs.80475	polymerase (RNA) (I (DNA directed) polyp	2.99	6.84
	450472	AI190071	Hs.55278	ESTs	2.98	5.06
	421335	X99977	Hs.103505	ARS component 8	2.97	9.31
25	431316	AA502663	Hs.145037	ESTs	2.96	4.30
	420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.96	2.97
	451175	AA046457	Hs.60677	ESTs	295	6.59
	444204	Al129194	Hs.143040	ESTs	2.93	3.92
	436723	AW975895	Hs.307486	ESTs	2.93	6.64
30	436664	AW197887	Hs.253353	ESTs	2.93	3.82
50	406962	M13485	110.20000	gb:Human metallothionein I-B gene, exon	2.93	3.10
	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed in	2.93	5.35
		NM_001360	Hs.11806	7-dehydrocholesterol reductase	2.91	9.84
	444734			four and a half LIM domains 1	291	7.02
35	430310	U60115	Hs.239069		291	5.41
33	420876	AA918425	Hs.177744	ESTs	2.91	5.64
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	2.90	9.54
	428232	BE272452	Hs.183109	monoamine oxidase A	2.89	5.37
	413796	AW408094	Hs.75545	interleukin 4 receptor		5.34
40	413884	A1668892	Hs.239758	hypothetical protein FLJ 12389 similar to	2.88	
40	411372	Al147861	Hs.213289	low density lipoprotein receptor (famili	2.86	6.31
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.86	3.93
	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	2.86	6.05
	452689	F33868	Hs.284176	transferrin	2.85	6.11
	403108			ENSP00000241415*:Hypothetical 67.7 kDa p	2.85	3.17
45	434433	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.83	4.05
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	3.57
	406922	S70284	Hs.119597	ob:stearoyl-CoA desaturase (human, adipo	2.82	3.60
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.82	6.40
50	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	2.82	2.97
-	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.81	5.15
	415409	AW993701	14.100021	NS1-associated protein 1	2.80	6.16
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.80	2.88
	425750	AL050276	Hs.42400	zinc finger protein 288	2.79	5.99
55	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc	2.78	5.25
"	429128	AA446869	Hs.119316	ESTs	2.78	4.17
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.77	7.37
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.76	6.09
	419923	AW081455	Hs.120219	ESTs	2.76	4.31
60			113.120213	gb:H.sapiens XG mRNA (clone PEP11).	2.76	4.12
00	407555	Z48511	LIA 1900	phosphoglucomulase 1	2.74	5.92
	425240	AA306495	Hs.1869	Eas Control	2.74	19.85
	459317	BRCA16	14-02221	- 11 ·	2.74	5.72
	425819		Hs.93231	ESTS	2.73	3.93
CE	408839			gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.72	5.94
65	418253		Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	2.72	6.51
	409453		HS.95612	ESTs		3.80
	406625		Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.72	4.04
	420074		Hs.190074	ESTs	2.71	
70	429547	AW009166		FGENESH predicted novel secreted protein	2.71	2.84
70	444026		Hs.10119	hypothesical protein FLJ14957	2.71	6.17
	407112		Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.70	5.23
	429615		Hs.211562	ATP-binding cassette, sub-family A (ABC1	2.69	5.33
	419098	AA234041	Hs.87271	ESTs	2.69	3.22
	424206	NM_00373	4 Hs.198241	amine oxidase, copper containing 3 (vasc	2.69	6.64
75	443102		Hs.132965	ESTs	2.68	5.85
	411939		Hs.146246	ESTs .	2.68	5.38
	453201		Hs.135098	ESTs	2.68	3.69
	420231		Hs.19813	ESTs	2.67	4.70
	404996			Target Exon	2.67	4.97
80	452955		Hs.31130	transmembrane 7 superfamily member 2	2.66	6.36
	44720			ESTs, Moderately similar to T17372 plasm	2.65	15.65
	417365		Hs.82028	transforming growth factor, beta recepto	2.65	7.74
	444169			ESTs	2.64	3.40

	431247	AL021578	Hs.278489	matriin 4	2.64	3.35
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	2.63	5.12
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbH8st Homo	2.63	4.08
5	408669	Al493591	Hs.78146	platelet/endothetial cell adhesion molec	2.61	6.44
J	440924	AF151872	Hs.7527	small fragment nuclease	2.59	6.37
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.59	6.46
	425320	U29344	Hs.83190	fatty acid synthase	2.59	3.93
	402315			NM_003430:Homo sapiens zinc finger prote	2.58	6.09
10	449539	W80363	Hs.58446	ESTs	2.58	4.05
10	418271	NM_000919	Hs.83920	peptidylgtycine alpha-amidating monooxyg	2.58	5.61
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.58	3.54
	438752	AW238673	Hs.146038	ESTs	2.58	5.24
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.57	5.16
1.5	438763	AL583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.57	6.45
15	413630	AL036883	Hs.75450	delta steep inducing peptide, immunoreac	2.56	6.38
	424834	AK001432	Hs.153408	Homo sapiens cONA FLJ10570 fis, clone NT	2.56	2.90
	427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.56	2.67
	426403	NM_000361	Hs.2030	#srombomodulin	2.56	5.19
20	432906	BE 265489	Hs.3123	. lethal giant larvae (Drosophila) homolog	2.55	5.62
20	420924	R01026	Hs.245321	ESTs	2.55	3.22
	427527	A1809057	Hs.153261	immunoglobulin heavy constant mu	2.55	5.45
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	4.50
	445437	AJ224165	Hs.148725	ESTs	2.54	4.72
25	425097	NM_014247		PDZ domain containing guanine nucleotide	2.54	5.28
25	420105	AW015571	Hs.32244	ESTs, Wealdy similar to FMOD_HUMAN FIBRO	2.53	6.55
	429554	NM_012275	Hs.207224	interleukin 1, della	2.53	2.84
	408896	A1610447	Hs.48778	niban protein	2.53	7.08
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	2.52	B.68
20	420235	AA256756	Hs.31178	ESTs	2.51	4.21
30	436314	AI983409		ESTs	2.51	3.11
	440602	AJ743491	Hs.292692	ESTs	2.50	2.71
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.48	2.86
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	2.48	5.37
25	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.21
35	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	2.48	7.88
	421811	AA022550	Hs.108548	PABP-interacting protein 2	2.48	5.28
	414420	AA043424	Hs.76095	Immediate early response 3	2.47	8.33
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	2.47	2.78
40	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	2.46	10.12
40	447179	AW015633	Hs.157299	ESTs	2.46	3.45
	451687	AL041260	Hs.26837	Homo sapiens mRNA; cDNA DKFZp586K1123 (f	2.46	5.47
	420322	AB014555	Hs.96731	huntingtin interacting protein-1-related	2.45	6.18
	421064	A1245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.45	5.75
4.0	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	2.45	6.73
45	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.44	10.55
	439539	AA370045	Hs.6607	AXIN1 up-regulated	2.44	5.22
	436009	H57130	Hs.120925	ESTs	2.44	2.94
	414814	D14697	Hs.77393	famesyl diphosphate synthase (famesyl	2.43	5.17
	434060	AA744902	Hs.197922	hypothetical protein PRO1489	2.43	5.56
50	425335	BE394327	Hs.296267	follistatin-like 1	2.43	10.52
	406997	U07807		metaflothionein IV	2.42	4.35
	431545	AF095703	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase	2.42	6.72
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	2.41	5.22
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	2.41	5.56
55	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.41	5.24
	448954	AB014564	Hs.22616	KIAA0664 protein	2.40	5.31
	447218	BE617762	Hs.10748	hypothetical protein DKFZp434B195	2.40	5.24
	423810	AL132665	Hs.132955	BCL2/adenovirus E18 19kD-interacting pro	2.39	5.55
<b>~</b>	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.39	7.63
60	430356	N87990	Hs.239870	Homo sapiens mRNA; cDNA DKFZp564H0764 (f	2.38	5.99
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	2.38	3.84
	416273	AW575691	Hs.79123	KIAA0084 protein	2.38	5.22
	427272	NM_001096	Hs.174140	ATP citrate lyase	2.38	5.41
65	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	2.35	5.13
65	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	2.33	5.81
	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (rpincho	2.33	7.89
	418400	BE243026	Hs.301989	KIAA0246 protein	2.33	5.36
	456876	AL044870	Hs.208780	ESTs, Weakly similar to 129647 hypotheti	2.32	3.27
70	407082	Z47055		gb:Human partial cDNA sequence, famesyl	2.31	4.65
70	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	2.31	9.37
	408536	AW381532	Hs.135188	ESTs	2.31	2.60
	410552	X66945	Hs.748	fibroblast growth factor receptor 1 (fms	2.30	5.94
	437201	F29279	Hs.171625	hypothetical protein MGC14697	2.30	5.75
2-	417314	N68168		gb:za11c01.s1 Soares fetal liver spleen	2.30	3.12
75	433738	AI684802		ESTs	2.30	3.91
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29	3.61
	422491	AA338548	Hs.117546	neuronatin	2.29	5.66
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
00	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.28	5.14
80	401131			NM_001651*:Homo sapiens aquaporin 5 (AQP	2.27	5.62
	401205			Target Exon	2.27	2.98
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.26	3.94
	456546	AJ243662	Hs.110196	NICE-1 protein	2.26	2.52
				•		

						2.42
	443049	AI028613	Hs.132343	ESTs	2.25	3.13
	440150	BE560269	Hs.7010	NPD002 protein	2.25	4.93
	438367	N79688	Hs.204354	ras homolog gene family, member B	2.25	9.58
•	442987	AA075975		Homo sapiens clone TCCCtA00427 mRNA sequ	2.24	6.19
5	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	2.24	2.58
	447150	AI439011	Hs.86386	myeloid cell leukernia sequence 1 (BCL2-r	2.23	9.03
	450014	N41322	Hs.18441	ESTs	2.23	4.50
	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	2.22	5.64
10	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske	2.22	5.57
10	427569	BE299197	Hs.179665	cyclin-dependent kinase inhibitor 1A (p2	2.22	5.10
	444637	T19101	Hs.11494	libulin 5	2.22	6.43
	406710	AJ708347	Hs.184014	ribosomal protein L31	2.21	9.10
	424909	S78187	Hs.153752	cell division cycle 258	2.20	6.13
	407228	M25079	Hs.155376	hemoglobin, beta	2.20	11.34
15	450612	AL359946	Hs.14779	acetyl-CoA synthetase	2.20	7.03
	458568	A1769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.20	5.68
	407370	AA682384	Hs.182084	ESTs	2.20	7.00
	438942	AW875398	Hs.6451	PRO0659 protein	2.19	6.09
	400228			NM_021724*:Homo sapiens nuclear receptor	2.19	6.95
20	410185	BE294068	Hs.737	immediate early protein	2.18	11.72
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polype	2.17	7.05
	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.17	6.41
	424425	AB031480	Hs.146824	SPR1 protein	2.17	3.68
	414459	Y11525	Hs.76171	CCAAT/enhancer binding protein (C/EBP).	2.17	3.11
25	400082			Eos Control	2.16	8.40
	434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic convertas	2.16	6.B3
	439651	AF086480	Hs.56255	ESTs	2.16	3.72
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	215	3.34
	420225	AW243046	Hs.282076	Homo saciens mRNA for KIAA1650 protein,	2.14	6.20
30	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	2.14	3.42
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	2.14	9.81
	434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endoolig	2.14	6.75
	452467	AW500815		ESTs	2.13	4.66
	418226	AA424202	Hs.83834	cytochrome b-5	2.13	5.41
35	414815	AW292140	Hs.130286	ESTs	2.12	4.14
	430967	H16791	Hs.100895	ESTs	2.12	4.14
	426102	AF200496	Hs.166371	interleukin 1, zeta	2.12	3.77
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	2.11	5.30
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.11	4.01
40	427228	AA115770	Hs.174051	small nuclear ribonucleoprotein 70kD pol	2.10	5.13
	436961	AW375974	Hs.156704	ESTs	2.10	3.33
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.10	8.13
	445831	NM_006055	Hs.13351	LanC (bacterial lantibiotic synthetase c	2.08	5.42
	431593	NM_002108	Hs.276590	ESTs	2.08	4.43
45	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.92
	424389	AA339786	14.10.000	lymphocyte-specific protein 1	2.07	5.52
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.06	5.93
	400198	A2 003001		Eos Control	2.05	10.48
	426335	AI054347	Hs.2017	ribosomal protein L38	2.04	5.57
50	443652	A1080692	Hs.134229	ESTs, Weakly similar to 154401 hypertens	2.04	3.36
50	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.02	3.32
	443932	AW888222	Hs.9973	tensin	2.02	9.28
	421324	BE257515	Hs.103503	deoxyribonuclease Hike 2	2.02	5.71
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.01	5.49
55	410669	AW805749	113.103730	superoxide dismutase 2, mitochondrial	2.01	3.05
33	445193	A1279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	2.01	2.77
	400078	A121 3330	115.144030	Eos Control	2.00	11,41
	456267	AI127958	Hs.83393	cystatin E/M	1.99	3.59
	413125	BE244589	Hs.75207	glyoxalase I	1.98	6.70
60	415433	W70067	Hs.58066	ESTs	1.98	5.59
00	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.52
	417553	L09190	113.143423	trichohyalin	1.98	3.39
		LU3130		Target Exon	1,98	5.05
	403105 414081	AW969976		matrix Gla protein	1.97	8.74
65	422639	AI929377	Hs.173724	creatine kinase, brain	1.97	5.51
05	452208	AA024792	115.173724 He 31895	hypothetical protein MGC4093	1.97	5.67
	436106	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	1.97	5.75
	439265				1.96	5.09
		AL134430 BE409649	Hs.6906 Hs.227789	Horno sapiens cDNA: FLJ23197 fis, clone R mitogen-activated protein kinase-activat	1.96	5.49
70	430037 440054		Hs.6891	splicing factor, arginine/serine-rich 6	1.95	5.95
70					1.95	8.19
	417088	M54915	Hs.81170	pim-1 oncogene	1.95	5.19
	429451		Hs.202833	heme oxygenase (decycling) 1	1.95	6.78
	415274		Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.94	5.98
75	452472			ESTs, Weakly similar to C55663 oligodend	1.94	5.13
13	414860		Hs.77502	methionine adenosyltransferase II, alpha		
	437220		Hs.334305	GS1999tull	1.94	3.42 5.66
	450461		Hs.46736	hypothetical protein FLJ23476	1.94	
	424924		Hs.153834	pumilio (Orosophila) homolog 1	1.93 1.93	5.28 5.38
80	413945			CD14 antigen		5.38 5.75
οU	428193			Kruppel-like factor 4 (gut)	1.93	
	415988		Hs.78943	bleomycin hydrolase	1.92	4.65 9.79
	425783		Hs.1948	ribosomal protein S21	1.92	
	431476	BE612705	Hs.256697	histidine triad nucleotide-binding prote	1.91	7.00

	400003	A1907E10	Un 101520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.41
	456653 401846	AI807519	Hs.104520	NM_000988*:Homo sapiens ribosomal protei	1.91	5.62
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	4.00
5	400199			Eos Control	1,89 1,88	15.74 5.58
J	429367 400083	AB007867	Hs.278311	plexin B1 Eos Control	1.68	9.07
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	1.88	5.16
	400079			Eos Control	1.87	8.57
10	411807	AK000290	Hs.44033	dipeptidyl peptidase 8	1.86 1.85	5.19 2.75
10	409178 422624	BE393948 BE616678	Hs.50915 Hs.76152	katlikrein 5 KDEL (Lys-Asp-Gtu-Leu) endoplasmic retic	1.85	5.33
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membrane protei	1.85	6.01
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1,84	2.82
15	430572	U33114	Hs.245188	tissue inhibitor of metafloproteinase 3	1.83 1.83	5.10 6.48
15	426812 439927	AF105365 AA854650	Hs.172613 Hs.124597	solute carrier family 12 (potassium/chto ESTs	1.82	3.63
	415089	N25117	Hs.299465	ribosomal protein S26	1.82	6.69
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	1.82	295
20	406467	*********		Target Exon	1.79 1.79	2.65 5.24
20	426672 414088	AW270555 AW797956	Hs.171774 Hs.75748	hypothetical protein proteasome (prosome, macropain) subunit,	1.78	6.02
	433271	BE621697	Hs.14317	nucleotar protein family A, member 3 (H/	1.78	5.92
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.77	5.44
25	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.77 1.77	5.79 9.27
25	425503 429191	W92517 AF065215	Hs.158203 Hs.198161	actin binding LIM protein 1 phospholipase A2, group IVB (cytosolic)	1.77	5.44
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	1.77	6.97
	431021	A1869664		thiosulfate sulfurtransferase (rhodanese	1.77	5.23
20	432891	AF161483	Hs.279761	HSPC134 protein	1.75 1.75	5.73 5.72
30	432872 451335	Al908984 AB023192	Hs.279623 Hs.26285	selenoprotein X, 1 imidazoline receptor candidate	1.75	6.87
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase	1,74	3.01
	417824	AA084798	Hs.82646	DnaJ (Hsp40) homolog, subfamily B, membe	1.74	5.75
25	439908	AI168031	Hs.155507	ESTs	1.74 1.74	2.63 6.80
35	427349 445919	AA360154 T53519	Hs.177415 Hs.334692	Finkel-Biskis-Reilly murine sercoma viru hypothetical protein MGC14141	1.74	5.65
	427391	W60675	113.004032	hypothetical protein FLJ10350	1.73	6.13
	425299	AW505214	Hs.155560	catnexin	1.73	5.88
40	430449	AA352723	Hs.241471	RNB6	1.72 1.71	5.14 4.35
40	456766 407694	R87310 - U77594	Hs.7740 Hs.37682	oxysterot binding protein-like 1 retinoic acid receptor responder (tazaro	1.71	6.16
	412374	X01388	Hs.73849	apolipoprotein C-III	1.70	5.1B
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	1.70	7.46
45	410584	AB011112	Hs.64742	KIAA0540 protein	1.69 1.68	6.19 2.63
43	431882 441379	NM_001426 AW175787	Hs.271977 Hs.334841	engrailed homotog 1 setenium binding protein 1	1.67	7.42
	422115	AI878953	Hs.111811	microsomal glutathione S-transferase 3	1.67	6.93
	406742	AI458091	Hs.279860	turnor protein, translationally-controlle	1.66	6.26
50	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita Homo sapiens, Similar to complement comp	1.65 1.65	5.83 7.54
50	452363 446623	AI582743 AF279865	Hs.94953 Hs.15711	kinesin family member 138	1.65	5.36
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.65	12.30
	400202			NM_002795*:Homo sapiens proteasome (pros	1.64	5.70
55	401429 415166	NM_003652	Hs.78068	C14001067:gi 4126465 dbj BAA36581.1  (AB carboxypeptidase Z	1.64 1.62	3.82 5.95
,,	410169	AI373741	Hs.59384	hypothetical protein MGC3047	1.61	6.60
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.60	11.13
	453027	AI879341	Hs.539	ribosomal protein S29	1.60 1.60	10.97 5.90
60	416955 439053	AW889150 BE244588	Hs.80595 Hs.6456	NM_004552*:Homo sapiens NADH dehydrogena chaperonin containing TCP1, subunit 2 (b	1,57	5.60
•	400201	001000		NM_006156°:Homo sapiens neural precursor	1.57	5.32
	407049	X72632		NM_021724*:Homo sapiens nuclear receptor	1.57	5.42
	430775 427380	AI879186 NM_005534	Hs.250895 Hs.177559	ribosomal protein L34 interferon gamma receptor 2 (interferon	1.57 1.56	7.09 5.37
65	407143	C14076	Hs.332329	EST	1.56	6.54
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	1.56	6.35
	413559	BE155647		gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.55	5.96
	445624	AW140103	Hs.78880 2 Hs.4745	ItvB (bacterial acetolactate synthase)-I proteasome (prosome, macropain) 26S subu	1.55 1.55	4.09 5.71
70	435044 410397	NM_002802 AF217517	Hs.63042	OKFZp564J157 protein	1.54	5.14
	429071	AW794126	Hs.195453	ribosomal protein S27 (metallopanstimufi	1.54	8.70
	412915		Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	1.54	6.57
	446429 414551		Hs.201391 Hs.76394	ESTs encyl Coenzyme A hydratase, short chain,	1.53 1.53	2.87 6.07
75	406801	AW242054	Hs.190813	ribosomal protein L9	1.52	5.63
	437895	AB014568	Hs.5898	KIAA0668 protein	1.51	5.74
	413929		Hs.75617	collagen, type IV, atpha 2	1.51	6.40 7.08
	425456 409635		Hs.157850 Hs.55296	ribosomal protein L9 HLA-B associated transcript-1	1.51 1.50	5.26
80	404467		110.00230	Target Exon	1.50	5.82
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	1.50	5.25
	454098		Hs.292911	Plakophilin	1.48 1.48	3.14 6.24
	429205	A1492393	Hs. 198248	UDP-Gal:betaGlcNAc beta 1,4- galactosyli	1,40	W.E-7



	413825	BE299181	Hs.75564	CD151 antigen	1.47	5.64
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing to	1.45	6.19
	440254	A1879332	Hs.7101	anaphase-promoting complex subunit 5	1.45	5.50
5	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.42 1.42	11.24 3.18
3	423513	AF035960 D00159	Hs.129719	transglutaminase 5 gb:Homo sapiens gene for pancreatic elas	1.42	6.92
	406896 433453	BE548307	Hs.3297	ribosomal protein S27a	1.40	5.38
	405800	AA505535	TO. JEJ	gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	1.37	5.51
	421748	NM_014718	Hs.107809	KIAA0726 gene product	1.37	5.46
10	424372	AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fts, clone HE	1.36	4.06
	408250	R92918	Hs.19597	KIAA1694 protein	1.27	274
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.65
	406587			C15000544*:gij5454148 ref NP_006368.1  U	1.06 1.00	3.11 3.60
15	409574	AW419080	Hs.250645	ESTs Target Exon	1.00	3.08
13	404175 452640	AA027115	Hs.100206	ESTs, Wealdy similar to A53856 aryl-acyl	1.00	2.82
	443564	Al921685	Hs.199713	ESTs	1.00	2.51
	- 1020 1	7-00-00-				
20	TABLE 65					
20	Pkey:		ue Eos probeset iden	tifier number		
	CAT num! Accession		cluster number early accession numb	or.		
	MODESSION	. Gan	MIX SECCESSION HUMB	NA 0		
	Pkey	CAT Number	Accession			
25	407328	534268_1	A1673735 AA9780			
	427890	1373988_1	AA417099 AA435	761 AA972917 AI660387		00 AMERICANO AMERICANO DE BARNA AJARRADE AJARRAR
	444207	9172_3	BE739425 AA514	221 AAB65491 AI828293 AA470456 AI276739 AA169357 BES 94 AA513783 AI887309 AA528036 AW972006 AW873028 AI9	52464 AA3146 aanaa arosoo	40 AM162220 AM1040A6 A1524A13 A1660583 RF932521
			AI24/243 8G03339	38 AW089750 AW771461 AW089714 AI590949 AI819148 AA7	131056 RFB15	234 RF911506 AA235803 AA485373 AI735658
30			AW303133 AWA7	3080 AI707637 RE353370 RER43111 AW819036 AW393135 B	G697291 AV6	48670 AV654332 AV68753U BG566964 AIBU/43U
50			A1676072 AAR370	10 AIA52482 A1625817 AW241750 BEO48616 A1290928 AI680	714 AA48553I	D BE175687 AV648513 AW130312 AU000556 AA632893
			DE67/160 DE001	308 AAGAR166 RF176650 AA634664 AA490345 AI244948 AA6	i02956 AA483	492 AA918178 AW8U2049 BG675859 AV65887 I
			BG678060 AI5650	04 AW819026 BE843092 AV686437 AV723049 BG616948 A	911647 AI743	(90 A1091096 BE857251 A1962074 AAU40027 AVV709317
35			AA343477 AA640	112 BF876213 R82948 H26425 H82876 BE843095 BE843140 083 BF984258 AV657996 A1749532 BE758614 BE857252 BE9	80-230041 BC	501/830 AAZ3360Z BE114963 BE00000Z B134Z313 672 AVE67003 AVE67777 AV752631 RF77A97A T558A7
22			RA903144 BF338	083 BF984258 AV657996 AV749532 BE766614 BE657252 BE5 511 BE710793 BE180119 BG617338 H45942 T55897 AV6577	18 RC563497	313 N 4 0 31 3 3 N 4 0 3 1 1 1 1 1 1 1 1 2 2 3 1 2 1 1 1 1 1 1
	407102	7177_2	AUJOAST70 RED30	1005 E33652 RCASTRIR AI368018 AI421485 AI300352 AI3785	25 AI264177 A	N276281 AI245302 AI281050 AI190036 AW451438
	40/102	11/1_2	A14/2//2002 AAD10	1970 C22200 E40647 E22275 AWAZZR16 RF4457R5 AAZZ452	1 F 3 3447 CD 10	177 AW772227 F17759 H42812 R09701 AA349096
			R48772 H42892 I	142537 R47898 N28263 H25721 F32386 H43971 R48205 F21	390 H45809 A	A007629 R47897 R83734 H45844 AW983653 H43970
40			H42536 H24496 1	R48875 H42961 H22079 R86018		
	437596	2875_1	BC022398 AV743	635 AW976922 AW152652 AA910013 AA834629 BG536317	\W849807 AV	713062 AL684337 BEU44081 AA761490
	440116	454673_1		7 BF 111453 A1149320 N23160 A1446431 A1758316 AV74178	BI/91950 BM	MD3014 A1790031 MA003337 M417230 NOT217 133332
	443072	449629_1	T52179 AV734838 AI937	532 AI032318 AW749500 AA091720		
45	442679	31783_3	BC621403 BINSS	706 DCAD6376 D53718 W65356 D79357 BC434247 AA35776	9 AW978686 E	3G573200 BF132113 BF086709 AA366938 D79234
	*******	0.1.00_0	BC/0/628 AA150	3754 P.C.434311 AWQ7R6R3 AW773417 RM054667 AI799886	M433351 AH6	(1798 A1433742 BF(156186 A1281606 AWU15046 A1439565
			A1245530 A10782	67 AA807170 AA837395 W61252 AA831085 AA287371 AW76	8354 AA8906	06 AI302539 AI708575 AI673031 AI24Z260 AW514069
		٠	AA283958 AA825	5452 A1371234 AA425696 AA453422 AA827697 R23653 D202 R79358 R39136 R38800 R15089 R52937 R37502 H01021 R3	40 AA772517	740404 DC201062 DC570357 AW391045 BC496872
50				R/9358 R39136 R38800 R15089 R5293/ R3/502 R0 1021 R3	3034 (4033) /	Equate Big251002 Big510031 A11031040 Big-130012
50	424571	9758_1	H23558 RE379766 AW15	2643 AI803450 AI564343 AI092711 AI140525 AW152156 AI6	20740 AI55468	39 AI161209 AI290242 AI339745 AI374611 AI347388
	464011	3130_1	AIRSROOF AILANS	:20 Alree124 AA493912 AA406235 AA493889 A1057160 AWD	22264 AI0972	77 AI144126 AI080051 AA983529 AA860507 N53469
			AAR43767 NR111	CS AA 8866688 AA 896577 AA 983537 REOO 3004 AA 626688 AA 235	977 AI057152	A1095366 A1095356 AA458646 AW194479 AA150439
			A1375272 AW57	1777 Al359198 AA993793 BE614394 BE738239 AA127883 Al	334344 T5950	4 D81608 AA908704 AW051665 AA382785 AA3U7208
55			N24639 Al37071	5 BE244980 AAS48596 AW449675 AI191008 BF223749 N707	52 N2ZZ66 AI	191012 AAU28001 AI419100 BF 213001 DF 391340
	*****	cross 3		1968 BE858217 BF793358 AV756758 BG483603 AI093724 BF	033330 8034	2342 VI144524 132242 WW11112 BOA33121
	420787 456332	55832_7 21353_10	BE674920 AA56	9290 AA280309 10262 BG198346 BG215119 AW841716 AA228357 AW841786	i	
	418479	175360_1	DEGESTO1 DCSS	AASS REG72212 AHS1416 AISGG231 AIA175RS AI37R391 AA2	36264 AL3375	74 AI346166 AA406590 AA748618 AW771957 AA478626
60	410413	1,0000_1	AW338072 AIRR	9444 AIR10315 RE503662 RG231886 AIR88230 AI289102 BF5	94638 AW074	1094 AW512456 AA832229 AI056108 AIU25868 AI245806
			D61957 At09384	II AI721013 AI597594 AA993022 AI128620 AI285106 W37459	) W35410 N90	037 AAB903Z3 R39943 AI468/41 AA6299/6 AA4/92U1
			AI539018 AA875	875 AA448827 AW779493 Z39056 H84925 AA223923 AW517	7592 A1804400	) AAS11882 BM353143 D62885 AI457883 AI880626
			R31694 R42772	R68804 R44147 R71463 AV742540 BF966987 D12120 AF 164377 AW976054 AW662923 AW770101 AL59718	4 4 4 7 4 20 5 0 4	ACCREOMA SOLOSO LA OSLOSO A ACCREOMA ACCREOMA
65	431628	30288_1	AF1462// NM_(	112120 AF 164377 AW9/8054 AW862923 AW7/1010 AC59716 2584 BF594436 A1629024 AA311487 BG617872 AW629675 A	1000 13335 A	153668 RF171208 RF768429 RF326254 AW181992
05			AWI TRAFT AWA	72001 PC533184 AA768779 AA825697 AA808149 BF036424	AJ420469 AV	V175925 AA173981 AA557142 AW302163 AW088608
			AAR47195 AI411	RARO RM353163 AIO15673 AI357621 AI374592 AI245029 AI58	0659 AL37015	4 AA767503 AA643885 BM091307 BG496655 AW364502
			AW377222 AW3	171202 BE138896 R80586 BM090998 D25882 M85322 AI5413	63 BF675114	BG926529 AA627866 BE879221 8F594796 BF675714
70			RI086785 RG19	0411 RG217933 RG219447 RFR86143 BG403278		
70	426101	3211_1	AL049987 BG62	20667 BG571984 AW362842 BE150456 BE326465 AW872412	AA858553 AI	1724689 AA442638 AA813604 AA442648 AA663106
			AA442379 AAZ	29448 N56349 AA460220 AW971193 AA453725 A1742087 A18 6760 A1827987 A1005467 AA833517 AA563934 AA522837 AA	60142 AW/03 613876 AW/03	199 A 4 6 6 7 7 9 4 6 6 3 1 7 8 4 1 1 8 7 9 7 7 4 4 7 7 9 9 1 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
			A A 2020CC T200	184 AAC2200C DC789103 D21132 AI262026 AI216737 TR <i>8</i> 796	TRAZQA AWQ	61515 AI4597R9 RF 1(19829 BI491853 AIU84517 AW IU3030
			BE835233 A147	2712 AV741009 AASS1512 N28268 AA436880 AA447794 BEE	135410 BEB35	382 BE818325 RE818320 K04040 RE040401 W4423110
75			AA437299 BE8	18343 R95914 R31089 BF576826 AU186065 BF802058 AI217	018 AA24754	1 Al191725 BE766918
	454947		AW846590 AW	846615 AW846584 AW846592 AW846621 AW846610		
	438962		AI207343 BF81	3684 BF928775 AA828585	113734ED D**	272250 DC:057287 DE:464852 A1620722 DE:046016
	431693	1414_4	AB075855 AI79	9883 AI952039 BM313847 AW167132 AW264027 AI394192 E 74705 AW474624 AW440580 AI289435 AW002172 AI458169	MASA 193 DM.	21 2009 EGUST 201 BEHINGUZ AIGZUTZZ BENHUTTU PS609 AIGS1377 AIG31154 AI453490 AIRS735R AI469756
80			DCC02E02 AL42	NAMO ENGERE AWE1977A DESCESTO AIRSO151 AAGRS193 AIR	14417 AW298	184 H09775 AIB69379 AW207026 AI659678 AI826U/5
00			BF940660 AA7	44971 C00469 A1672560 AL045697 BF847489 BF842860 T65	400 AI863491	H24845 T54772 BE090906 BE090917 BE090877 AA152265
			BE244301 BI03	18346 B1038045 W94876 AA093121 B1523346 AW470130 N92	723 AA25887	7 R62397 BI523168

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	450515	13638_2	BE299605 AI589870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI708171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA525982 AW675471 AA010062 N80194
			H14620 H28475 H26247 RE333SR1 AWR42369 H06848 H05608 H81745 H15016 R51905 AA860423 Al860904 AA876023
5	434230 448144	41110_1 48653 1	AF 119900 NM, 018539 AA702388 N53043 BF351064 N70103 AI207469 AA561569 AW383189 W00906 W00935 N54252 BCD15871 AI521618 A471709 AW169230 BG539605 Bi058963 Bi058949 BG548398 BG952412 AW842037 AW842040 AW890573
,	453225	12287_1	AMONGET 2 DIG 204 NIA 1065 1 1 DC001018 RITSRTSR ALILESSEA ALILESSEA ALILESTE ALILES
			BE79505 AN93471 BF435179 BE797475 BG744432 BF733017 BI251710 BF435252 BE267474 BE219495 AV653212 AW248975 BI832737 BE264857 BE386198 AA773811 AI826904 BF732388 AI281977 BF732958 BF434612 AA480672 BF724595 AA058529 BG500189 AV687020 AA934427 AV696822
			RCSTASON RIDS22A7 RETARTS2 RCSSR992 RC18ITC16 RETABA54 BC876983 BE222517 W61060 BC993321 BC742061 BC696266 BC740805
10			BG688598 AA031863 AF006747 AA129619 BG745080 H29767 AA011078 T88743 BG216950 Al508941 AW166202 AA522692 A1927649 AW237367 A1935538 A1689743 AW966083 BE326704 AU147054 AW129250 BE465425 AU148980 A1242161 AW615658 AU145096 BE465120 AU159062
			AIG70410 AWA73145 RC23G394 AI292110 AI9R549G AA995R57 RF5510GG AIG32G25 AW511387 AI080003 AW243240 AI640340 AI075293 AW205957
			AIG79929 AIGB1080 AI753324 BF593137 AW337148 BE326667 AIG37787 AIG59936 F22148 AI332985 AIG50925 AW248532 BE048931 F30242 AI524808 BE939886 AI340251 AI962198 BE463831 AI347479 BE221712 AW193412 BF434502 BE939895 AI373314 AW270842 AW024782 AI772109
15			AW777775 AW767170 E75B1B AW760740 AW878580 ALS66540 AL977017 AIR21667 AL796037 AW772479 AA995455 AA470517 R00503 AL765977
			BF 196432 AW341091 AL517116 BG683520 F26241 AA160675 AU160539 BG876391 BF083008 AT795938 BF739968 AU01107 AI985556 BE792113 BI760879 BG545253 BE313692 AI339338 BF195296 AA352395 BE258769 AA160087 AA781222 AA100912 BE886334 AL534518 H02114 BG740469
			AARTINTSG HORSEA REGRESTATA REARGEST AARSCIAR RETAKININ REGRESSA WAZSIN BEG674719 AW802577 BF313256 AA188326 BFZ11944 BE489143
20			T68371 AA773564 AA470663 W42415 T61648 AA173985 AI695223 AI640567 AI915875 AI640318 AA66987 AA743161 AA834774 AA186698 AI766899 AA031697 AA129593 D25761 AA100913 AW134585 AA129330 BF434518 BE622820 AA587251 AW149318 H07926 R40908 AA011079
20			BE967287 BE253428 AI681438
	445493 417054	423456_1 12405_2	AV711317 AI809938 AI808768 AI240593 AI915771 BG533564 BG618564 AW296119 AI269233 BF508328 AW364777 AW292258 AA371049 AI452471 AI092522 BG618376 AL049080 AA631068
25	4		BGS64643 T53833 AV702544 BGS33452 AV705004 AAS88281 T28665 BGS69026 AV646874 AV647253 AV647455 AV647749 BI759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 AI435836 AI590676 AI245019 AW338243 AAS30898 D52191 AI435352 D57473 BG566952
25			AIA20505 AA0352A5 AA770A072 BC554113 AIA39237 AI287456 AV695686 AA349017
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	413659 406800	1526081_1 0_0	BE155647 ( AA505535	BE150627		
	400000	0_0	700000		•	
30	TABLE 65					
	Pkey: Ref:	Un So	idne unurpet co	rresponding to an Eos probeset  The 7 digit numbers in this column are Genhank	identifier (GI) numbers. "Dunham, et al." refers to the publication entitled	"The DNA
	rei.	se	quence of huma	in chromosome 22" Dunham, et al. (1999) Nature	102:489-495.	
25	Strand:	tno	icates DNA stra	and from which exons were predicted.		
35	Nt_positio	n: Inc	licates nucleotid	te positions of predicted exons.		
	Pkey	Ref	Strand	NL position		
	405121	8102330	Minus	35816-36004,36587-36684		
40	401203	9743387	Minus Plus	172961-173056,173868-173928 169845-170272		
40	400494 402294	9714719 2282012	Minus	2575-3000		
	404730	8389582	Plus	119832-120016,124110-124275		
	403593	6862650	Minus	62554-62712,69449-69602		
45	403710 401905	6437516 8671966	Ptus Ptus	27413-28978 153965-154441,156599-156819		
73	403108	8980955	Plus	93253-93667		
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055	i	
	402315	7381741	Minus	30728-32065 94802-94987,95804-95887,96323-96487,9759	•	
50	401131 401205	8699812 9743388	Minus Plus	167373-167433,167936-168031	•	
• •	403105	8980016	Minus	145287-145744	I	
	401846	7712190	Minus	82775-82823,82912-83022		
	406400 406467	9256298 9795551	Plus Plus	1553-1712,1878-2140,4252-4385,5922-6077 182212-182958		
55	401429	8217890	Minus	86946-87579		
	404467	8077630	Minus	24951-25853		
	406587	8189273	Minus	120577-120718 107420-107547,109625-109796		
	404175	9931117	Minus	10/420-10/54/,105025-105/50		
60						
	TABLE	6A. DISEASI	INDICATIONS	AND PREFERRED UTILITIES FOR SELECTED	GENES	
	Primeke		ease moication os probeset ide		es. These genes were identified using Eos/Affymetrix Genechip arrays.	
	ExAccn:		r Accession nu			
65	UgID:		ID number			
	UgTitte:	Unigene	tide Lindingtod for a	alaulad aran on deceribed in table 1 and abbrevia	led as follows: AWPC (androgen independent prostate diseases), arth (a	erthrific diseases), both
	Disease	thenian	nmetatic hunor	seev hoold nione. (seecasin robbeld) held. (ciselv	el diseases) FWS (bone diseases), alia (brain diseases), dreast (breast (	useases), cerv
70		Ironiro	disappael min	razih leanedansat dansa Jaaseasih letrandrat r	tes), fibro (fibrotic diseases), headok (head & neck diseases), leio (leiom	yoma uiseases), ieux
70		(leukoc)	de diseases), h	epC (liver diseases), tung (lung diseases), ovar (ov	rarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian m	ech uter (uterine
		panc (p disease		ses), pros (prostate diseases), renal (renal disease	s), mela (skin diseases), stom (stomach diseases), test (testicular diseas	caj, eta (etamo
	Utility:	preferre	o, d utilities for sel	lected gene as described in the text and abbreviate	ed as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic t	arget), mAb
75	•			arget), s.m. (small molecule target)		
75	Dimete	Ev A	lwb.	In Title	Disease	Utility
		ry Ex Acca X07820	Ug1D Hs.2258	Ug Title matrix metalloproteinase 10 (stromelysin	angio, blad, tung, cerv, ovar, headnk, esoph	mAb+diag+s.m.
	400297	AJ127076	Hs.306201	hypothetical protein DKFZp564O1278	breast, blad, coton, pros	mAb
80	400303		Hs.79136	LIV-1 protein, estrogen regulated	breast, ovar, pros, stom, uter, blad, lung, headnk	mAb s.m.
60	400843 402075			NM_003105*:Homo sapiens sortilin-related ENSP00000251056*:Plasma membrane calciu	blad im blad, tung, headnk, cerv, mela, esoph	mAb+diag
	402901			NM_025206*:Homo sapiens hypothetical pro	blad	CTL
	404287			FGENESH predicted novel CUB-domain conta	panc, lung, colon, uter, esoph	mAb+s.m.

	404682			ortholog of mouse polydomain protein	pane	diag
	404875				blad	CTL+s.m.
	404977				blad, ovar	mAb+diag
_	405033				blad	s.m.
5	405547				cerv, mela	mAb+s.m.
	406400				ovar, uter	diag diag
		M21305 AW955705	Un 62604		angio, blad, fibro glio, blad	CTL
			Hs.62604 Hs.39384		ovar, uter, cerv, panc	mAb+diag
10			Hs.40098		btad, panc, storn, uter, lung, esoph	diag
			Hs.22575	B-cell CLL/lymphoma 6, member B, zinc fi	angio	CTL
	407975	X89426	Hs.41716	endothelial cell-specific motecule 1	angio, renal	diag
			Hs.624	interleukin 8	blad, stom, headnk, cerv, hing, angio, esoph, panc	diag
15			Hs.44424	Homo sapiens orphan neurotransmitter tra	mela	mAb+s.m. mAb
13			Hs.118747 Hs.44532	SLC15A2 Solute carrier family 15 (H+/pep diubiquitin	pros, lung, fibro, uter, gfio, cerv, ovar lung, blad, headnk, panc, stom, fibro, esoph, mela	CTL
		NM_000676		adenosine A2b receptor	tung, esoph, headnk	mAb+s.m.
			Hs.31141	roundabout (axon guidance receptor, Dros	uter, fibro	mAb+s.m.
			Hs.47860	neurotrophic tyrosine kinase, receptor,	tung	mAb+s.m.
20			Hs.250822	serine/threonine kinase 15	blad, lung, headnk, storn	S.M.
			Hs.50081	Hypothetical protein, XP_051860 (KIAA119	uter, ovar, lung, colon, storn, headnk, breast, panc	CTL+diag mAb+s.m.
		W87707 AF251237	Hs.82065 Hs.112208	Interleukin 6 signal transducer (gp130,	breast, pros tung	CTL
		BE393948	Hs.50915	XAGE-1 protein kaffikrein 5	ovar, breast, mela	diag
25		BE243323	Hs.51233	turnor necrosis factor receptor superfami	angio, renal, colon, storn	mAb+s.m.
		AI401535	Hs.146090	ESTs	renal, glio	mAb+s.m.+CTL
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	glio	mAb+diag
	409420	Z15008	Hs.54451	taminin, gamma 2 (nicein (100kD), kalini	tung, headnk, panc, stom, cerv, esoph, blad	diag
20	409632		Hs.55279	serine (or cysteine) proteinase inhibito	lung, blad, headnik	diag mAb+s.m.+CTL
30		AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (		CTL
	409063	AI743750 AA077391	Hs.98306	KIAA1862 protein gb:7B14E12 Chromosome 7 Fetal Brain cDNA	renal ovar, renal	mAb+s.m.+CTL
	409757		He 123114	cystatin SN	panc, stom, lung, blad,	diag
		AW247090	Hs.57101	minichromosome maintenance deficient (S.	tung, cerv, blad, test, esoph	CTL+s.m.
35		AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	breast, panc, ovar, colon, headnk, lung, blad, esoph	diag
	410001	AB041036	Hs.57771	kallikrein 11	ovar, pros, uter, cerv, tung	diag
	410055		Hs.58241	gene for serine/threonine protein kinase	renal	s.m. CTL
		BE311926	Hs.15830	hypothetical protein FLJ12691	renal, blad	CTL
40		AA381807	Hs.61762	hypoxia-inducible protein 2 alpha-2,8-sialyltransferase III	lung, renai panc	s.m.
40	410309 410407	BE043077 X66839	Hs.278153 Hs.63287	carbonic anhydrase IX	renal, lung, colon, storn, ovar, uter, blad	mAb+s.m.
		D31382	Hs.63325	transmembrane protease, serine 4	colon, blad, lung, ovar, panc, headnk	mAb+diag+s.m.
	411274	NM_002776		kallikrein 10	colon, ovar, uter, cerv, headk, panc	diag
	411411	AA345241		ESTs, Weakly similar to KIAA1330 protein	renal	mAb+s.m.
45	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	ovar	diag
	412078	X69699	Hs.73149	paired box gene 8	ovar	CTL s.m.
	412140		Hs.73625	RAB6 interacting, kinesin-like (rabkines	tung, blad, headnk, breast, ovar, panc, angio, test, mela mela	mAb+s.m.+CTL
	412580 412609		Hs.17901 Hs.74124	similar to CABLES [Homo sapiens] ocular albinism 1 (Nettleship-Falls)	meia meia	s.m.
50	412628		Hs.306051	hypothetical protein MGC2648	pros	diag
50	412709		Hs.74518	KIAA0027 protein	glio	mAb+s.m.
	412719	AW016610	Hs.816	ESTs	lung, headnk, blad, glio, cerv	s.m.
	412959	D87458	Hs.75090	KIAA0282 protein	glio	CTL+s.m.
5.5		X81120	Hs.75110	cannabinoid receptor 1 (brain)	glio	mAb+s.m. mAb
55	413048	M93221	Hs.75182	mannose receptor, C type 1	fibro, panc	diag
	413063 413278	AL035737 BE563085	Hs.75184 Hs.833	chitinase 3-like 1 (cartilage glycoprote interferon-stimulated protein, 15 kDa	glio, ovar, blad, hung panc, tung, blad, breast, cerv, ovar, headnk, esoph, meta, stom	CTL+s.m.
	413324		Hs.75294	corticotropin releasing hormone	blad	diag
	413385		Hs.840	indoleamine-pyrrola 2,3 dioxygenase	blad, lung, mela, fibro, uter	s.m.
60	413554	AA319146	Hs.75426	secretogramin II (chromogramin C)	panc, glio	diag
	413719		Hs.75498	small inducible cytokine subfamily A (Cy	panc, lung, headnk, cerv, colon, uter, stom, esoph	diag CTL effect
	414577		Hs.72116	hypothetical protein FLJ20992 similar to	angio	CTL+diag
	414774		Hs.77274	plasminogen activator, urokinase	lung, blad, headnk, panc, stom, ovar, esoph breast, blad, lung, fibro, panc, colon, headnk,	diag
65	414812	X72755	Hs.77367	monokine induced by gamma Interferon	cerv, storn, renal, ovar, test, mela, esoph	diag
05	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	glio, lung, renal, esoph, panc, headnk, arth	mAb+s.m.+CTL
	414883		Hs.348669	CDC28 protein kinase 1	tung, ovar, storn, colon, cerv, headnk, test	ş.m.
	414907		Hs.77597	polo (Drosophia)-like kinase	blad, lung, ovar, test	s.m.
70	414945		Hs.77667	lymphocyte antigen 6 complex, locus E	mela	mAb+s.m.
70	415138		Hs.295944	tissue factor pathway inhibitor 2	angio, panc, stom, lung, uter	CTL+diag mAb+s.m.+CTL
	415511		Hs.182362	ESTs	blad, over, renai	mAb+s.m.
	415539 415668		Hs.72472 Hs.306814	BMP-R1B Homo sapiens lysyl oxidase-like 4 (LOXL4	breast, uter, pros meta	diag
	415669		5 Hs.78589	serine (or cysteine) proteinase inhibito	lung	mAb+diag+s.m.
75	415817		Hs.78867	protein tyrosine phosphatase, receptor-t	lung, glio, headnk, cerv, mela, esoph, fibro	mAb+s.m.
	415910		Hs.78913	chemokine (C-X3-C) receptor 1	glio	mAb+s.m.
	415929	AA724373	Hs.304950	Homo sapiens mucolipin-3 (MCOLN3)	mela	mAb
	415989		Hs.351201	ESTs	pros, ovar, blad, tung, headnk, panc, colon, stom	mAb+s.m.+CTL
80	416091			defensin, bela 3	headrik, esoph, mela	CTL+diag CTL+s.m.
ου		AA236776		MAD2 (mitotic arrest deficient, yeast, h Kremen 2	lung, headnk, colon, uter, stom esoph, lung, cerv, ovar	mAb+s.m.
	416250 416350			phospholipase A2, group IID	esoph, lung, cav, oval test, mela, fibro	CTL
	416530		Hs.79361	kallikrein 6 (neurosin, zyme)	ovar, uter	diag
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					

	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	breast, panc, uter, mela n	nAb+s.m.
			Hs.79432			fiag
		D54745	Hs.80247	cholecystatinin		Siag .
e			Hs.292453		<b>9</b>	nAb+s.m. Jiag
5		NM_006183 U65590	Hs.80962 Hs.81134			fiag
			Hs.42146			CTĹ
		D13168	Hs.82002	endothelin receptor type B		mAb+s.m.
10	417389	BE260964	Hs.82045			mAb+diag mAb
10	417433	BE270266	Hs.82128			mAb+diag
	417542 417771	J04129 AA804698	Hs.82269 Hs.82547			mAb
	417866	AW067903	Hs.82772		tung, panc, breast, ovar, headnk, stom	ÇTL
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)		diag
15	417933	X02308	Hs.82962	thymidylate synthetase		s.m. mAb+diag+s.m.
	418007 418030	M13509 BE207573	Hs.83169 Hs.83321	matrix metalloproteinase 1 (interstitial neuromedin B		diag
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	mela	diag
••	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9		CTL+diag
20	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me		s.m. mAb+diag
	418506 418526	AA084248 BE019020	Hs.372651 Hs.85838	Unknown protein for MGC:29643 (formerly solute carrier family 16 (monocarboxylic		mAb+s.m.
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	esoph, headrik	s.m.
	418678	NM_001327		cancer/testis antigen (NY-ESO-1)	and, ever ever the every every every	CTL
25	418830	BE513731	Hs.88959	hypothetical protein MGC4816		CTL s.m.
	418857	D31771 AF147204	Hs.89404 Hs.89414	msh (Drosophila) homeo box homolog 2 chemokine (C-X-C motif), receptor 4 (fus		mAb+s.m.
	418870 419080	AF147204 AW150835	ns.69414 Hs.18878	hypothetical protein FLJ21620	renal, uter, lung	CTL
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	tung, esoph, headnk, blad	diag
30	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	tung	mAb+s.m.
		AW338625		ESTs: similar to TRANSMEMBRANE 4 SUPER		mAb+s.m. CTL+s.m.
	419183 419216	U60669 AU076718	Hs.89663 Hs.164021	cytochrome P450, subfamily XXIV (vitamin small inducible cytokine subfamily B (Cy	blad, lung, headnk, panc panc, lung, stom, cerv, pros, headnk, esoph	diag
	419235	AW470411	Hs.288433	neurotrimin	panc, fibro, headnk, lung	mAb+diag
35	419452		Hs.90572	PTK7 protein tyrosine kinase 7	ovar, pros, lung, breast, uter, lest, panc, storn	mAb+s.m.
-	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	glio, ornuc, storn, tung, panc, colon, renal, uter	mAb+s.m.
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	lung, fibro, test	mAb+diag CTL+s.m.
	419704 419723	AA429104 AL120193	Hs.45057 Hs.339810	ESTs longevity assurance (LAG1, S. cerevisiae	glio glio	mAb+diag
40	419741		Hs.93002	ubiquitin carrier protein E2-C	blad, lung, colon, ovar, test, esoph, mela	CTL+s.m.
	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	blad, stom	mAb
	420162		Hs.95577	cyclin-dependent kinase 4	lung, mela	s.m. CTL
	420208		Hs.95972	silver (mouse homolog) like	mela blad	mAb
45	420370 420440		Hs.97234 7 Hs.97644	uroplakin 2 mammaglobin 2	ovar, uter, cerv	diag
73	420602		Hs.99236	regulator of G-protein signalling 20	headrik, glio, cerv, mela	CTL+s.m.
	420610		Hs.99348	distal-less homeo box 5	uter, endo, lung	CTL
	420737		Hs.99899	CD70; tumor necrosis factor (ligand) s	renal	mAb+s.m. mAb+s.m.+CTL
50	420789 420876		Hs.199882 Hs.177744	ESTs FGENES predicted novel protein containin	renal panc, blad	s.m.
50	421066		Hs.101408	branched chain aminotransferase 2, mitoc	blad, lung	CTL+s.m.
	421110		Hs.1355	cathepsin E	blad, panc, storn, fung, fibro, ovar, esoph	sm+diag
	421340		Hs.1369	decay accelerating factor for complement	angio, panc, stom	diag n diag
55	421379 421471		Hs.103982 Hs.327179	small inducible cytotine subfamily B (Cy solute carrier family 17 (sodium phospha	breast, panc, headrik, lung, stom, blad, cerv, colon, fibro, lest, mela, esopt renal	mAb+s.m.
))	421474		Hs.104637	solute carrier family 1 (glutamate trans	tung	mAb+s.m.
	421508		3 Hs.105115	absent in melanoma 2	blad, esoph, lung, mela	mAb+s.m.+CTL
	421524			GDNF family receptor alpha 1	breast	mAb+s.m. diag
60		AF026692		secreted frizzled-related protein 4 defensin, beta 2	breast, ovar, panc, cerv, uter, pros, lung, stom, headnk headnk, lung	CTL+diag
UU		AJ000152 AI910275	Hs.105924 Hs.350470	trefoil factor 1 (breast cancer, estroge	breast, panc, lung, omuc	diag
	421666			endothelin 3	mela	mAb+diag
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	tung	mAb+s.m.
45	421817			ATP-binding cassette, sub-family C (CFTR	lung, cerv, headnk, blad	mAb+s.m. mAb+s.m.
65	422033 422048		5 Hs.110903 15 Hs.288126	claudin 5 (transmembrane protein deleted spondin 2, extracellular matrix protein .	glio panc, pros	diag
	422109		Hs.1473	gastrin-releasing peptide	pane, tung, colon, fibro	diag
		L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	headnix, blad, tung, cerv, storn, esoph	diag
70		3 AF027208		prominin (mouse)-like 1	colon, breast, fibro	mAb+s.m. s.m.
70		2 AA305159		fis485	mela colon, omuc, stom, panc	mAb+diag
		0 AA315993 2 AF019225		regenerating gene type IV applipoprotein L	blad, lung, headnk, renal	diag
		3 AW41130		CDC45 (cell division cycle 45, S.cerevis	lung, blad, test, cerv, headnk, esoph	s.m.
-		9 U79745	Hs.114924	solute carrier family 16 (monocarboxylic	mela	mAb+s.m.+CTL
75		0 D30783	Hs.115263	epiregulin	panc, colon, blad	mAb+diag CTL+s.m.
	42239	7 AJ223366 4 AJ186431		MYEOV Myeloma overexpressed gene (in a s prostate differentiation factor	panc, stom, colon, esoph, renal, blad blad, panc, pros, angio, colon, stom, lung, meta	diag
		7 BE33685		transforming growth factor, beta-induced	colon, renal	mAb+diag
		5 AW40970		baculoviral IAP repeat-containing 5 (sur	lung, blad	s.m.
80	42280	9 AK00137	Hs.121028	hypothetical protein FLJ10549	blad, cer, lung, uter, angio, storn, test	s.m.
		7 L32137	Hs.1584	cartilage oligomeric matrix protein (pse	breast, ovar, pros, panc, lung, colon, uter ovar, blad, panc , lung, headnk, colon, storn	diag CTL+s.m.
	42295 42316				ovar, mad, panc, rung, neadink, colon, storii renal, ovar, blad	mAb+s.m.
	42310		19.124110	companies annual a fal areas		

	422104	W4 004430	Un 1624	ephrin-A1	pros, panc, renal	mAb+s.m.
		NM_004428   Al039402		DEME-6 protein	breast, renal, ovar, pros. colon	CTL
				NY-REN-24 antigen	glio	mAb
_		AW604297			renal, colon	mAb
5	423583			KtAA1028 protein	pros	s,m. diag
				heparin-binding growth factor binding pr	lung, blad, headnk, panc blad, lung, headnk, ovar, panc, colon, storn, uter, cerv, esoph, test	mAb+diag+s.m.
				matrix metalloproteinase 12 (macrophage achaete-scute complex (Drosophila) hornol	colon, stom, ovar	CTL
				periostin (OSF-2os)	breast, colon, blad, lung, fibro, panc, headnk, ovar, mela	mAb+diag
10				putative chemokine receptor, GTP-binding	blad, headrik, stom, cerv, esoph	mAb+s.m.
				serine (or cysteine) proteinase inhibito	headnk, lung, cerv	diag
			Hs.143811	hypothetical protein FLJ20513	colon, stom	mAb+s.m.+CTL s.m.
			Hs.1765	tymphocyte-specific protein tyrosine kin	mela, fibro lung, coton, test	S.M.
15		AA285249 NM 005209	Hs.146329	protein kinase Chk2 (CHEK2) crystallin, bela A2	panc	s.m.
13		AF242388	Hs.149585	lengsin	lung	s.m.
	424503	NM_002205		integrin, alpha 5 (fibronectin receptor.	panc, pros, angio, blad, tung	mAb+s.m.
	424620		Hs.151254	katlikrein 7 (chymotryptic, stratum com	ovar	diag
00	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	headrik, panc, lung, blad, uter, cerv, colon, stom, test, mela	diag CTL+s.m.
20	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	blad, breast mela	CTL+s.m.
	424825 424905	AF207069 NM_002497	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio NIMA (never in milosis gene a)-related k	ovar, blad, tung, headnk, panc, storn	s.m.
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	renal, fibro	mAb+s.m.
	425071	NM_013989		deiodinase, lodothyronine, type II	pros, colon, storn, uter, cerv, headnk, esoph, panc	diag
25	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	gijo, mela	mAb+s.m.+CTL mAb+s.m.
	425115	R44564	Hs.123956	downstream of: G protein-coupled recept	glio breast, ovar, lung, colon, panc, headnik, stom, uter, cerv, blad, esoph	mAb+diag+s.m.
	425247	NM_005940 U63630		matrix metalloproteinase 11 (stromelysin protein kinase, DNA-activated, catalytic	lung, headrik	s.m.
	425322 425535	AB007937	Hs.155637 Hs.158287	syndecan 3	mela, glio	mAb+s.m.
30	425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	tung, headnk, cerv, esoph, blad	mAb
-	425721	AC002115	Hs.159309	uroplakin 1A	blad	mAb
	425723		Hs.159311	dickkop! (Xenopus laevis) homolog 4	endo, uter, colon	CTL+diag s.m.
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidaling monooxyg	lung	mAb+diag
35	425776	U25128 AI587490	Hs.159499	parathyroid hormone receptor 2 NK-2 (Orosophila) hormolog B	ovar, uter, tung panc, glio	s.m.
33	425842 425852		Hs.159623 Hs.159651	death receptor 6, TNF superfamily member	blad, lung, headnk	mAb+s.m.
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322		mAb
	425921		Hs.162211	solute carrier family 6 (neurotransmitte	stom, panc	mAb+s.m.
40	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	renal	mAb+s.m. mAb+diag
40	426028		Hs.172028	a disIntegrin and metalloproteinase doma	blad breast, lung, renal, colon, ovar, uter	mAb+diag
	426215 426227	AW963419 U67058	Hs.155223 Hs.154299	stanniocalcin 2 Human proteinase activated receptor-2 mR	panc, lung, colon, esoph, storn	mAb+s.m.
	426322		Hs.2012	transcobalamin I (vitamin B12 binding pr	panc, blad, storn	diag
	426344		Hs.322469	transcriptional activator of the c-fos p	glio	CTL+s.m.
45	426427		Hs.169840	TTK protein kinase	ovar, tung, headrik, cerv, colon, uter, stom, test	CTL+s.m. s.m.
	426451		Hs.169946	GATA-binding protein 3 (T-cell receptor	blad, breast	mAb+diag
	426514 426600		Hs.170195 B Hs.171014	bone morphogenetic protein 7 (osteogenic VGF nerve growth factor inducible	ovar, colon, blad, tung, cerv mela	diag
	426761		Hs.172089	PORIMIN Pro-oncosis receptor inducing me	lung, esoph, pros, uter, panc, colon, ovar, headnk	mAb+s.m.
50		AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	renal ,	mAb+s.m.
	426890		Hs.41294	ESTs	renal, colon, ovar, uter, storn	CTL CTL+s.m.
	427239		Hs.356512	ubiquitin carrier protein	tung, blad, test, mela	CTL
		AA448542	Hs.251677 Hs.176977	G antigen 7B	hing, headrik, blad, mela, esoph glio	CTL+s.m.
55	427722	AI880044 AKD00123		protein kinase C binding protein 2 hypothetical protein FLJ20116	colon, stom, panc	CTL
23	427747			serine/threonine kinase 12	blad, lung, ovar, stom, test, esoph	s.m.
	427923			FGENESH predicted 11 TM protein	mela	mAb mAb+diag
	427969		3 Hs.2230	epidermal growth factor (beta-urogastron	panc	CTL
60	428093			ESTs	ovar, panc glio	mAb+s.m.
00	428141 428179		Hs.182611 Hs.279696	solute carrier family 11 (proton-coupled serum/glucocorticoid regulated kinase-ti	breast	s.m.
	428187		Hs.285529	G protein-coupled receptor 49	ovar, uter, colon, stom	mAb+s.m.
	428242		Hs.2250	leukemia inhibitory factor (cholinergic	ovar, panc, , lung	diag
	428296		58 Hs.183572	solute carrier family 22 (organic cation	renal	mAb+s.m. mAb+diag+s.m.
65	428330		Hs.2256	matrix metalloproteinase 7 (matrilysin,	uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela, stom	diag
	428368		Hs.83326 Hs.2265	matrix metalloproteinase 3 (stromelysin secretory granule, neuroendocrine protei	headnk, storn, esoph, colon panc	diag
	428393 428456		91 Hs.184339	KIAA0175 gene product	ovar, cerv, panc, lung, blad, mela	s.m.
	428479		Hs.334562	cell division cycle 2, G1 to S and G2 to	lung, blad, colon, uter, ovar	s.m.
70	42848			solute carrier family 7 (cationic amino	lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela	mAb+s.m.
	42848			pancreatic polypeptide	panc	diag diag
	42850			chromogranin 8 (secretogranin 1)	panc, fung mela, panc, stom, headnk	mAb
	42851			plexin C1 G protein-coupled receptor 64	ovar, EWS, uter	mAb+s.m.
75	42857 42866		56 Hs.184942 6 Hs.189095	similar to SALL1 (sal (Drosophila)-like	blad, ovar, pros, tung, stom, test	CTL+s.m.
,,	42869			KIAA1866 protein	breast, colon, lung, panc, stom, headnk, ovar, EWS	mAb
	42874	8 AW59320	6 Hs.98785	Ksp37 protein	tung	diag
	42875	8 AA43398	8 Hs.98502	CA125 antigen; mucin 16	ovar, cerv, lung, panc, stom, renal	diag mAb+s.m.
90	42877				ovar	mAb+s.m.
80	42878		Hs.193470		glio, mela renal	mAb+s.m.+CTL
	42884 42895				cerv, panc, colon, stom, headrik, renal	mAb+diag
	42896				lung, cerv	diag

		05020004	11- 104504	antimals and indused 2 (DAIO4).	ton area calca our	mAb+s.m.
			Hs.194691 Hs.197962			mAb+s.m.
			Hs.198249			mAb+s.m.
_			Hs.198396		ung	mAb+s.m.
5			Hs.198612		a Brat a seal Bra	mAb+s.m.
			Hs.335891			mAb+s.m. diag
		AW009166 AB024937	Hs.99376 Hs.211092			mAb+diag
		AL134197	Hs.93597			s.m.
10		NM_000867			leio	mAb+s.m.
		R60704	Hs.234434		glio	s.m.
		AA361258	Hs.237868		mela, lung, panc, stom, esoph, headnk	mAb+s.m.+CTL CTL
		NM_001922			mela bung, blad, headnik, cerv, esoph	mAb+s.m.
15	430486 430822	BE062109 AJ005371	Hs.241551 Hs.248017		mela	s.m.
1.5	430890	X54232	Hs.2699		glio, lung, cerv, blad, esoph	mAb+s.m.
	431053	S40369	Hs.249141		glio	mAb
	431130	NM_006103			ovar, uter	diag diag
20	431462				panc, tung, glio, test ovar, pros, tung, blad	mAb+s.m.
20	431515 431620	NM_012152 AA126109	Hs.264981		esoph, cerv	CTL+s.m.
	431629	AU077025	Hs.265827		panc, uter, cerv, stom, esoph, mela	mAb•diag
	431630	NM_002204		integrin, alpha 3 (antigen CD49C, alpha	ovar, panc, blad, headnk, mela, renal	mAb+s.m.
25	431840	AA534908	Hs.2860		test, renal, blad	CTL mAb+diag
25	431846	8E019924	Hs.271580		lung, blad, headnik, uter, cerv, stom, ovar renal	mAb+s.m.+CTL
	431870 431939	AW449902 AW008061	Hs.105500 Hs.231994	ESTs	renal, colon	mAb+s.m.+CTL
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	lung, blad, cerv, headnik, ovar, colon, pros, panc, breast, esoph, test, mela	
••	432196	AW300888		hypothetical protein FLJ10830	renal	CTL
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	breast, colon, ovar, stom, panc, uter, cerv, tung	mAb+diag+s.m. CTL
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	renal panc, breast	diag
	432596 432606	AJ224741 NM_002104	Hs.278461	matrilin 3 granzyme K (serine protease, granzyme 3;	renal, breast, lung, storn, hepC, fibro	CTL
	432800	BE391046	Hs.278962	AIM-1 protein	mela, pros	mAb+s.m.
35	432829	W60377	Hs.57772	ESTs	blad	CTL+s.m.
	432867		Hs.233364	ESTs	stom, colon	mAb+s.m.+CTL diag
	432874	W94322	Hs.279651	melanoma inhibitory activity	panc, stom, mela pros, renal	mAb+s.m.
	432990 433001	AL036071 AF217513	Hs.279899 Hs.279905	tumor necrosis factor receptor superfami clone HQ0310 PRO0310p1	colon, breast, tung, blad, cerv, uter, test, meta	s.m.
40	433447	U29195	Hs.3281	neuronal pentraxin II	mela, esoph, colon, renal	diag
	433848	AF095719	Hs.93764	carboxypeptidase A4	headnk, esoph, lung	S.M.
	433867		Hs.3618	hippocalcin-like 1	renal	CTL CTL+s.m.
	434206		Hs.362915 Hs.93605	ESTs, Wealdy similar to S69890 mitogen i	storn, colon mela	S.M.
45	434276 435013		Hs.110024	leucine zipper, putative tumor suppresso NM_020142:Homo sapiens NADH:ubiquinone o		CTL
	435472		Hs.283022	triggering receptor expressed on myeloid	glio	mAb
	435505	AF200492	Hs.211238	interleukin-1 hornolog 1	lung, headnk	diag
	435869		Hs.54650	junctional adhesion molecule 2	angio, glio	mAb mAb+s.m.
50	436456 436480		Hs.248122 Hs.87469	melanin-concentrating hormone receptor ( putative acid-sensing ion channel	mela, glio glio	mAb+s.m.
50	435481		Hs.5199	HSPC150 protein similar to ubiquitin-con	lung, blad, colon, ovar, uter, headnk, test	s.m.
	436576		Hs.77542	ESTs	renat, panc, headnik, lung	mAb+s.m.
		AA628980	Hs.192371	down syndrome critical region protein DS	blad, lung	CTL+s.m. mAb+s.m.
55	436895		Hs.5338	carbonic anhydrase XII	breast, renal, ovar, glio tung, panc, renal, uter, colon	CTL
33	436961	AW375974 AB018305		ESTs spondin 1, (f-spondin) extracethular mat	ovar, fibro	diag
		AU076916		guarrine monphosphate synthetase	tung, blad, cerv, esoph, headnk	s.m.
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	headnk, cerv, tung, blad, breast, pros, ovar, stom, esoph	CTL
60	437100		Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	panc, renal	mAb+s.m.+CTL mAb+s.m.+CTL
00		A1765021 AI581344	Hs.210775 Hs.127812	ESTs ESTs, Wealdy similar to T17330 hypotheti	renal, uter, ovar lung	CTL
	437852			putative GPCR	blad, lung	mAb+s.m.
	437938		Hs.369628	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapie		mAb+s.m.+CTL
65	438380		Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	glio, mela	diag CTL+diag
65	438549		Hs.21858 Hs.93522	trinucleotide repeat containing 3	mela renal	mAb+s.m.+CTL
	438859 438929			Homo sapiens mRNA for KIAA1647 protein C	renat	mAb+s,m.+CTL
	438960			gb:EST391184 MAGE resequences, MAGP He		mAb+s.m.+CTL
<b>5</b> 0	439018	8 AW30088	7 Hs.26638	membrane-spanning 4-domains, subfamily A	uter, stom, pros. libro	mAb
70		3 AW23829		UL16 binding protein 2	lung, headnk, cerv, esoph, blad, colon	mAb mAb+s.m.
	43947		Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G CEGP1 protein	lung breast, AWPC, pros, blad	diag
	439569 43960		6 Hs.222399 Hs.58561	G protein-coupled receptor 87	lung, blad, headnk, cerv, esoph	mAb+s.m.
	43973			sema domain, immunoglobulin domain (lg),	blad, lung, cerv, renal	mAb+s.m.
75	43975	9 AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	coton, storn, panc, lung	mAb+s.m.+CTL
		9 AW60029		hypothetical protein FLJ10430	renal, cerv, pros, headrik, colon, test	mAb s.m.
		6 AK00051 5 W03476	7 Hs.6844 Hs.266331	NALP2 protein; PYRIN-Containing APAF1-li Horno sapiens Fc receptor homolog express	blad, ovar, lung, headnk, test mela	diag
	44006 44022			tumor necrosis factor receptor superfami	meia glio	mAb
80	44030				renal, colon, blad	mAb+s.m.
	44031	1 AI733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN!	renal	mAb+s.m.+CTL
	44051		Hs.161	cadherin 2, type 1, N-cadherin (neuronal MAD1 (mitotic arrest deficient, yeast, h	glio, ovar, uter, renal, hepC	mAb+diag s.m.
	44067	£ 77'00381	1 Hs.7345	HAND I CHINANG BLOOM GENERALLY RESOLD II	meta	

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			Hs.23044 Hs.222119	RAD51 (S. cerevisiae) homolog (E coli Re ESTs, Weakly similar to S30433 keratin 1	tung, blad, headnik, test, mela, esoph renal	s.m. mAb+s.m.+CTL
			Hs.222119 Hs.372210	ESTs, Wealdy similar to S72482 hypotheti	fibro, angio	mAb
			Hs.128899	ESTs; hypothetical protein for IMAGE:447	breast, tung, blad, panc, headnk, storn, ovar, pros	mAb+s.m.
5		AW874138	Hs.129017	ESTs; type la transmembrane protein	ovar, uter	mAb mAb+s.m.+CTL
		AA995998	11- 0004		uter, ovar, renal	mAb+diag
	443105	A96/53 A1128388	Hs.9004 Hs.143655	chondroitin sulfate proteoglycan 4 (mela ESTs	mela btad, ovar, tung, headnk, stom	mAb+s.m.+CTL
		BE614387	Hs.333893	c-Myc target JPO1	coton, tung, blad, panc	CTL
10	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	colon, lung, blad, storn, test, mela	CTL
		AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	renal	diag
		AI085198	Hs.164226	Thrombospondin 1	angio, panc, uter glio, uter, ovar	diag mAb+s.m.+CTL
		AW449952 NM_013409		basic-helix-toop-helix-PAS protein folilistatin	lung, cerv, headnk, blad, esoph	diag
15	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	renal	mAb+s.m.
		BE395085	Hs.10086	type I transmembrane protein Fn14	panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv	mAb
	444371	BE540274	Hs.239	forkhead box M1	tung, headnk, blad, glio, test, mela	s.m.
	444381	BE387335	Hs.283713	hypothetical protein BC014245	breast, colon, blad, lung, panc, headrik, ovar, stom, uter, renal, angio, test, mela, esoph	diag
20	444488	AW192879	Hs.355660	ancient conserved domain protein 4	renal	mAb+s.m.
20	444527	NM_005408		small inducible cytokine subfamily A (Cy	fibro, esoph	diag
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	tung, blad, headrik, cerv	mAb+diag
	444783		Hs.62180	anillin (Drosophila Scraps homotog), act	ovar, lung, blad, headnik, panc, cerv, storn, utar, colon, esoph	CTL+s.m. mAb+s.m.
25	444809	BE207568 NM_000677	Hs.208219	oculospanin adenosine A3 receptor	meia glio, renal	mAb+s.m.
LJ	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	panc, headnk, stom, lung, esoph	diag
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	ovar, blad, uter, breast, lung, headrik, renal, fibro, panc, cerv	mAb+diag
	445891	AW391342		DPCR1 protein	stom, panc, esoph, omuc, esoph	mAb
30		D29954	Hs.13421	KIAA0056 protein	pros . colon, breast	CTL mAb+diag
30	446051 446163	BE048061 AA026880	Hs.37054 Hs.25252	ephrin-A3 protactin receptor	breast, cerv, uter	mAb+s.m.
		AI281848	Hs.194691	retinoic acid induced 3	storn, panc, colon, ovar	mAb+s.m.
	446341		Hs.310735	FGENESH prediction similar to multidrug	mela	mAb+s.m.
25	446619		Hs.313	secreted phosphoprotein 1 (osteopontin,	ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter	diag
35	446650	AB016625	Hs.15813	solute carrier family 22 (organic cation	renal breast, panc, headnk, lung, libro, mela	mAb+s.m. diag
	446921 447004	A8012113 AW296968	Hs.16530 Hs.157539	small inducible cytokine subfamily A (Cy FGENESH predicted secreted protein	glio	mAb+diag
	447033		Hs.157601	Predicted gene: Eos cloned; secreted w/V	colon, pros, fibro, breast, ovar, lung, panc	CTL+diag
40	447072		Hs.17279	tyrosylprotein sulfotransferase 1	glio, panc	CTL+s.m.
40	447131		5 Hs.17466	retinoic acid receptor responder (tazaro	renal, breast, stom, lung, mela, ovar	mAb+s.m. CTL+diag
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	esoph, stom, colon renal	CTL
	447269 447342		1 Hs.17958 Hs.19322	cerebroside (3-phosphoadenylylsulfate:g Homo sapiens, Similar to RIKEN cDNA 2010	colon, blad, pros, tung, storn, AWPC, ovar	CTL
	447400			hypothetical protein FLJ20315	colon, pros, stom, uter	CTL
45	447674		Hs.19192	cyclin-dependent kinase 2	mela	S.M.
	447835			ESTs, Weakly similar to 138022 hypotheti	renat, ovar, uter	mAb+s.m.+CTL mAb+s.m.
	447937 448105		Hs.20034 Hs.298241	Homo sapiens mRNA full length insert cDN Transmembrane protease, serine 3	mela breast, panc, colon, lung, ovar, stom	mAb+s.m.+CTL
	448243			integrin, beta 8	ovar, uter, lung, stom, headnk, glio, panc	mAb+s.m.
50	448321		3 Hs.20912	adenomatous polyposis coli like	glio	mAb+s.m.+CTL
	448499			p53-regulated DOA3	glio /	CTL+s.m. mAb+s.m.
	448595			KIAA0644 gene product	breast, glio mela	diag
	448610 448733		7 Hs.21602 9 Hs.187958	nel (chicken)-like 1 solute carrier family 6 (neurotransmitte	tung, renal	mAb+s.m.
55	448844		Hs.177164	FGENESH predicted novel cell surface pr	pane, lung, stom, omuc	mAb+s.m.
-	449048		Hs.22920	similar to S68401 (cattle) glucose induc	panc, ovar, uter, glio, headnk, lung	mAb
	449444			solute carrier family 16 (monocarboxylic	renal, panc	mAb+s.m. mAb+s.m.
	449523		9 Hs.54443 Hs.288708	chemokine (C-C motif) receptor 5 hypothetical protein FLJ21562	tung, panc, renal, storn, hepC, fibro, meta colon	CTL
60	449720 449722			cyclin B1	headrik, blad, lung, panc, angio, test, meta, esoph	ş.m.
	450001			solute carrier family 6 (neurotransmitte	renal	mAb+s.m.
	450375			a disintegrin and metalloproteinase doma	breast, ovar, headnk, panc, tung, esoph, colon	mAb+diag+s.m. CTL
	450531			(BC017500) Similar to hypothetical prote	colon lung, headnk, panc, breast, storn, ovar, esoph, colon	mAb+diag
65	45070° 450720		Hs.288467 0 Hs.355462	hypothetical protein XP_098151 (leucine- HUMPSPBA Human pulmonary surfactant-as		s.m.
-		1 N25156	Hs.25648	tumor necrosis factor receptor superfami	lung, renal	mAb+s.m.
	45098			ERO1 (S. cerevisiae)-like	blad, lung, ovar, panc	diag
	45109		Hs.25954	interleukin 13 receptor, alpha 2	glio, fibro, mela	mAb+s.m. CTL
70	45131			Human DNA sequence from clone RP3-447F transmembrane 4 superfamily member 7	3 colon, panc renal	mAb
70	45152 45153		Hs.26518 Hs.26550	retinoid X receptor, gamma	mela	CTL+s.m.
	45166		Hs.326444	cartilage acidic protein 1	blad, ovar, tung	mAb+diag
		9 U80456	Hs.27311	single-minded (Drosophila) homolog 2	pros	CTL
75		9 F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX).	angio	CTL+s.m. CTL
75		8 AF263921 7 AB00236		papillomavirus regulatory factor PRF-1 a disintegrin-like and metalloprotease (	renat ovar	mAb+s.m.+diag
	45209 45219	7 ABW236 0 H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRN		mAb
		4 Al694413			stom, panc, renal, colon, mela, fibro	mAb+s.m.
00	45220	3 X57522	Hs.352018	transporter 1, ATP-binding cassette, sub	cerv, esoph, blad, stom, mela, renal	mAb+s.m.
80	45228		Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL		diag mAb+s.m.
		5 N54926	Hs.29202 115 Hs.29352	G protein-coupled receptor 34 turnor necrosis factor, alpha-induced pro	giio, fibro, panc blad, breast, panc, headnk, storn, lung, arth, renal, esoph	diag
		1 U88879	Hs.29499	toll-like receptor 3	renal, hepC	mAb
				•		

	452747	BE153855	Hs.61460	lg superfamily re	ceptor LNIR		dnk, ovar, stom, uter, panc	mAb
			Hs.18878	hypothetical prof		renal, headnk, colon, h		mAb+s.m.+CTL
		U65011	Hs.30743		pressed antigen in mela	tung, ovar, breast, met		CTL mAb+diag
5			Hs.8687		sintegrin-like and metallo	neauni, oreasi, colon, renal	arth, lung, blad, esoph, storn	CTL
,	453195 453496	BE241876	Hs.32352 Hs.33084		tein DKFZp434K1210 mily 2 (facilitated glu	renal, pros		mAb+s.m.
	453642		Hs.34074	dipeptidytpeptid		glio		mAb+s.m.
	453837		Hs.256126		repeat-containing 7 (liv	renat, meta		s.m.
		AL080235	Hs.35861		nescence 1 (RIS1)	glio, lung, uter, headni	k, cerv, panc, pros	mAb+s.m.
10	453968	AA847843	Hs.62711	High mobility gr	oup (nonhistone chromoso	tung, uter, blad, test		CTL+s.m.
		AI690321	Hs.203845		ium channel, subfamily K, m	ovar		mAb+s.m. CTL
		NM_002448			a) homeo box homolog 1 (fo	uter, ovar		mAb+s.m.
		BE259150	Hs.127792	delta (Drosophi	a)-like 3 n rat sarcoma 2 viral on	glio, lung panc		s.m.
15		M54968 A1693815	Hs.351221 Hs.127179	cryptic gene	II (8) SECONIS Z VII SI UN	panc, pros, lung		diag
1.5		AA331517	Hs.286055	chimerin (chima	enial 2	glio		mAb+s.m.
		AI796870	Hs.54277		similar to RIKEN cDNA 28100	meta, fibro		mAb
	458435	AJ418718	Hs.144121	ESTs. Wealdy	similar to T46916 hypotheti	glio		mAb+s.m.+CTi.
00	458627	AW088642	Hs.97984	SRY (sex deter	mining region Y)-box 17 (S	ovar, uter, test		CTL
20		_						
	TABLE 66		alaura Para arab					
	Pkey: CAT num		ene cluster nur	eset identifier nun nhor	10s			
	Accession		enbank access		,			
25								
	Pkey		CAT Nurr	ber Accession				
	409745	MH1944_5	5 BI030997	AA921874 AW18	18822 BI027862 AI347618 AI36	1453 A1088754 AW2074	91 AA077391 BG012775 BG997382	AZ86833 AA1507ZZ BIUU/625
			B1027864	B1009100 B10062	275 B1006270 B1031000 B10298	864 B1006277 B1007627 (	B1006266 B1006991 B1006990 B100776	23 81001 105 90331311
30	400000	4040500			'818 BG015789 BI033807 AA34	41445	•	
30	438966 442438	1242593_ 24590_1	1 AW9790	74 AA834841 AA8 5 AH1477222 AH2	12003U 14945 AU13214AA FA7756 AW97	9025 AAR2R595 AAR2R5	77 BE935573 AA829588 A1743616 B	E315309 BE047365 AI761053
	442430	24330_1	AW1689	50 AA833900 BG	79419 BE171071 BF034368 B	F754297 R61781 F0814	9 F07647 T77332 AA897461 AI82971	4 Al376820 Al809991
			AW6618					
2.5								
35	TABLE 6							
	Pkey:	Ļ	totque number	corresponding to	an Eos proceset whom in this column are Cooks	nt Identifier (CI) number	s. "Dunham, et al." refers to the public	ation entitled The DNA
	Ref:		equence of his	nan chromosoma	22' Dunham, et al. (1999) Natu	re 402:489-495.	5. Danian, 615. 1515-15 15 15 part	
	Strand:				exons were predicted.			
40	NL positi			tide positions of p				
	_							
	Pkey	Ref	Strand	Nt_position		17		
	400843	9188605 8117407	Plus Plus		7653-7784,8892-9023,9673-980 035,122804-122921,124019-12			
45	402075 402901	8894222	Minus	175426-175		410		
73	404287	2326514	Ptus	53134-5328				
	404682	9797231	Minus	40977-4115				
	404875	9801324	Ptus	96588-9673	2,97722-97831			
50	404977	3738341	Minus	43081-4322				
50	405033	7107731	Minus	142358-142				
	405547 406400	1054740 9256298	Plus Plus		1520,124914-125050 1878-2140,4252-4385,5922-60'	77		•
	400400	3230230	1 103	1335-1712,	1010-2140,4202-4000,0322-00	.,		
55	TABLE							
	Pkey:			beset identifier n				
	ExAccn Unigene		Unigene numb		enbank accession number			
	Unigene		Unigene gene					
60	Seq ID				linking the information in Table	67 to the sequences in T	able 68	
							C (D.)	
	Pkey	ExAccn		UnigenelD	Unigene Title	interetifiat	Seq 1D No Seq ID No 1 & 199	
	418007			Hs.83169 Hs.83169	matrix metalloproteinase 1 ( matrix metalloproteinase 1 (	interstitial	Seq ID No 2 & 200	
65	418007 428368			Hs.83326	matrix metalloproteinase 3 (		Seq ID No 3 & 201	
0,5	417856		_	Hs.82772	collagen, type XI, atpha 1		Seq ID No 4 & 202	
	444381			Hs.283713	hypothetical protein BC0142	245	Seq ID No 5 & 203	
	452281	T93500		Hs.28792	Homo sapiens cDNA FLJ11	041 fis, clone PL	Seq ID No 6	
70	428698			Hs.334838	KIAA1866 protein		Seq ID No 7 & 204	
70	452862			Hs.8687	ADAMTS2 (a disintegrin-lik		Seq ID No 8 & 205	
	432201			Hs.298241	Transmembrane protease, s ESTs, Weakly similar to S6	Semie J 0900 mitoson i	Seq ID No 9 & 206 Seq ID No 10 & 207	
	434206 422260			Hs.362915 Hs.105484	regenerating gene type IV	was untaffell t	Seq ID No 11 & 208	
	409041			Hs.50081	Hypothetical protein, XP_05	51860 (KIAA119	Seq ID No 12 & 209	
75	443426			Hs.9329	chromosome 20 open readi		Seq ID No 13 & 210	
-	44321	I AI1283	38	Hs.143655	ESTs	•	Seq ID No 14	
	42866			Hs.189095	similar to SALL1 (sal (Dros	ophila)-like	Seq ID No 15 & 211	
	41327			Hs.833	interferon-stimulated protein	n, 15 kDa	Seq ID No 16 & 212 Sea ID No 17 & 213	
80	45240			Hs.29352	turnor necrosis factor, alpha turnor necrosis factor, alpha		Seq ID No 18 & 214	
30	45240 40838			Hs.29352 Hs.44532	diubiquitin		Seq ID No 19 & 215	
	41620			Hs.79078	MAD2 (mitotic arrest deficie	ent, yeast, h	Seq ID No 20 & 216	
	40975			Hs.123114	cystatin SN		Seq ID No 21 & 217	
		-			•			

				1.00	Can ID No 22 8 218
	425921 452194	NM_007231 AI694413	Hs.162211 Hs.373599	solute carrier family 6 (neurotransmitte olfactory receptor, family 2, subfamily	Seq ID No 22 & 218 Seq ID No 23 & 219
	452194	Al694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 24 & 220
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	Seq ID No 25 & 221
5	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	Seq ID No 26 & 222
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No 27 & 223
	415989	AI267700	Hs.351201	ESTs	Seq ID No 28
	415989	A1267700	Hs.351201	ESTs	Seq ID No 29 Seq ID No 30 & 224
10	424252 424252	AK000520 AK000520	Hs.143811 Hs.143811	hypothetical protein FLJ20513 hypothetical protein FLJ20513	Seq ID No 31 & 225
10	432867	AW016936	Hs.233364	ESTs	Seq ID No 32
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	Seq ID No 33
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	Seq ID No 34 & 226
1.0	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 35 & 227
15	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 36 & 228
	428953	AA306610	Hs.348183 Hs.348183	tumor necrosis factor receptor superfami tumor necrosis factor receptor superfami	Seq ID No 37 & 229 Seq ID No 38 & 230
	428953 428953	AA306610 AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 39 & 231
	452203	X57522	Hs.352018	transporter 1. ATP-binding cassette, sub	Seq ID No 40 & 232
20	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	Seq ID No 41 & 233
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	Seq ID No 42 & 234
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA.	Seq ID No 43 & 235
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	Seq ID No 44 & 235 Seq ID No 45 & 237
25	435472 418870	AW972330 AF147204	Hs.283022 Hs.89414	triggering receptor expressed on myeloid chemokine (C-X-C motif), receptor 4 (fus	Seq ID No 46 & 238
2.5	415511	A1732617	Hs.182362	ESTs	Seq ID No 47
	440304	BE159984	. Hs.125395	hepatitis A virus cellular receptor 1	Seq ID No 48 & 239
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	Seq ID No 49 & 240
20	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	Seq ID No 50
30	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 51 & 241 Seq ID No 52 & 242
	410153 410153	BE311926 BE311926	Hs.15830 Hs.15830	hypothetical protein FLJ12691 hypothetical protein FLJ12691	Seq ID No 53 & 243
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 54 & 244
	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 55 & 245
35	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 56 & 246
	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospha	Seq ID No 57 & 247
	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	Seq ID No 58 & 248
	426890	AA393167	Hs.41294	ESTs ESTs	Seq ID No 59 & 249 Seq ID No 60
40	437212 438966	Al765021 AW979074	Hs.210775	gb:EST391184 MAGE resequences, MAGP Homo	Seq ID No 61
40	440311	A1733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN!	Seq ID No 62
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 63
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 64
A.F	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	Seq 1D No 65 & 250
45	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	Seq ID No 66 & 251 Seq ID No 67 & 252
	443595 443595	AF169312 AF169312	Hs.9613 Hs.9613	PPAR(gamma) angiopoletin retated protein PPAR(gamma) angiopoletin retated protein	Seq ID No 68
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No 69 & 253
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	Seq ID No 70 & 254
50	420737	L08096	Hs.99899	CD70; tumor necrosis factor (ligand) s	Seq ID No 71 & 255
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	Seq ID No 72 & 256
	420789	AI670057	Hs.199882	ESTS	Seq ID No 73 Seq ID No 74
	420789 441392	A1670057 AW451831	Hs.199882 Hs.222119	ESTs ESTs, Weakly similar to S30433 keratin 1	Seq ID No 75 & 257
55	452431	U88879	Hs.29499	toll-like receptor 3	Seq ID No 76 & 258
	431870	AW449902	Hs.105500	ESTs	Seq ID No 77
	431870	AW449902	Hs.105500	ESTs	Seq ID No 78
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	Seq 1D No 79 & 259 Seq 1D No 80
60	409745	AA077391	Hs.93522	gb:7814E12 Chromosome 7 Fetal Brain cDNA Homo sapiens mRNA for KIAA1647 protein,	Seq ID No 81
00	438859 409637		Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 82 & 260
	409637		Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 83
	409348		Hs.146090	ESTs	Seq ID No 84
	447269		Hs.17958	cerebroside (3-phosphoadenylylsulfate:g	Seq ID No 85 & 261
65	453195		Hs.32352	hypothetical protein DKFZp434K1210	Seq ID No 86 & 262 Seq ID No 87
	428841		Hs.104935	ESIS	Seq ID No 88
	428841 428841		Hs.104935 Hs.104935	ESTs ESTs	Seq ID No 89
	409663		Hs.98306	KIAA1862 protein	Seq ID No 90 & 263
70	409663		Hs.98306	KIAA1862 protein	Seq ID No 91 & 264
	431939		Hs.231994	ESTs	Seq ID No 92 & 265
	432606		Hs.3066	granzyme K (serine protease, granzyme 3;	Seq ID No 93 & 266
	411411		Hs.55950	ESTs, Weakly similar to KIAA1330 protein	Seq ID No 94 & 267
75	433867		Hs.3618	hippocalcin-like 1 hippocalcin-like 1	Seq ID No 95 & 268 Seq ID No 96 & 269
13	433867 437938		Hs.3618 Hs.369628	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	Seq ID No 97
	432579		Hs.278439	nucleolar protein 3 (apoptosis repressor	Seq ID No 98 & 270
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No 99 & 271
00	432196	6 AW300888	Hs.273230	hypothetical protein FLJ 10830	Seq ID No 100 & 272
80	432198		Hs.273230	hypothetical protein FLJ 10830	Seq ID No 101 & 273 Seq ID No 102
	438929		Hs.253177	ESTs	Seq ID No 102 Seq ID No 103 & 274
	410059 446650		Hs.58241 Hs.15813	gene for serine/threonine protein kinase solute carrier family 22 (organic cation	Seq ID No 104 & 275
	******		13,13010	and a series in tall the for forme agence.	



	426812 447131	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo retinoic acid receptor responder (tazaro	Seq ID No 105 & 276 Seq ID No 106 & 277
	449444	NM_004585 AW818436	Hs.17466 Hs.351306	solute carrier family 16 (monocarboxylic	Seq ID No 107 & 278
_	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No 108 & 279
5	444488 450931	AW192879 N25156	Hs.355660 Hs.25648	ancient conserved domain protein 4 tumor necrosis factor receptor superfami	Seq ID No 109 & 280 Seq ID No 110 & 281
	409220	BE243323	Hs.51233	tumor necrosis factor receptor supertami	Seq ID No 111 & 282
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfami	Seq ID No 112 & 283
10	425998 425998	AU076629	Hs.165950 Hs.165950	fibroblast growth factor receptor 4 fibroblast growth factor receptor 4	Seq ID No 113 & 284 Seg ID No 114 & 285
10	425009	AU076629 X58288	Hs.154151	protein tyrosine phosphatase, receptor t	Seq ID No 115 & 286
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	Seq ID No 116 & 287
	432990 436576	AL036071 Al458213	Hs.279899 Hs.77542	tumor necrosis factor receptor superfami ESTs	Seq ID No 117 & 288 Seq ID No 118 & 289
15	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	Seq ID No 119 & 290
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No 120 & 291
	410274	AA381807	Hs.61762 Hs.110024	hypoxia-inducible protein 2 Empirically selected from AFFX single pr	Seq ID No 121 & 292 Seq ID No 122 & 293
	125218 436961	H91923 AW375974	Hs.156704	ESTs	Seq ID No 123
20	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	Seq ID No 124 & 294
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	Seq ID No 125 & 295 Seq ID No 126 & 296
	419508 431840	AW997938 AA534908	Hs.90786 Hs.2860	ATP-binding cassette, sub-family C (CFTR POU domain, class 5, transcription facto	Seq ID No 127 & 297
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	Seq ID No 128
25	447835	AW591623	Hs.164129	ESTs, Weakly similar to 138022 hypotheti	Seq ID No 129 Seq ID No 130 & 298
	429276 448595	AF056085 AB014544	Hs.198612 Hs.21572	G protein-coupled receptor 51 KIAA0644 gene product	Seq ID No 131 & 299
	440516	842303	Hs.161	cartherin 2, type 1, N-cartherin (neuronal	Seq ID No 132 & 300
30	456759	8E259150	Hs.127792	delta (Drosophila)-like 3	Seq ID No 133 & 301 Seq ID No 134 & 302
30	447004 425088	AW296968 AA663372	Hs.157539 Hs.169395	FGENESH predicted secreted protein hypothetical protein FLJ12015	Seq ID No 135 & 303
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	Seq ID No 136 & 304
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like transcriptional activator of the c-fos p	Seq ID No 137 & 305 Seq ID No 138 & 306
35	426344 419704	H41821 AA429104	Hs.322469 Hs.45057	ESTs	Seq ID No 139 & 307
	412959	D87458	Hs.75090	KIAA0282 protein	Seq ID No 140 & 308
	448499	BE613280	Hs.77550	p53-regulated DDA3 ESTs, Wealdy similar to T46916 hypotheti	Seq ID No 141 & 309 Seq ID No 142 & 310
	458435 443785	AI418718 AW449952	Hs.144121 Hs.190125	basic-helix-loop-helix-PAS protein	Seq ID No 143 & 311
40	427343	AI880044	Hs.176977	protein kinase C binding protein 2	Seq ID No 144 & 312
	416857	AA188775	Hs.292453	FGENESH predicted TM containing protein	Seq ID No 145 & 313 Seq ID No 146 & 314
	429149 418030	AW193360 BE207573	Hs.197962 Hs.83321	Homotog of mouse ADP-ribosylation factor neuromedin B	Seq ID No 147 & 315
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	Seq ID No 148 & 316
45	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	Seq ID No 149 & 317 Seq ID No 150 & 318
	430147 453642	R60704 Al370936	Hs.234434 Hs.34074	hairy/enhancer-of-split related with YRP dipeptidytpeptidase VI	Seq ID No 151 & 319
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No 152 & 320
50	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucose induc	Seq ID No 153 & 321 Seq ID No 154 & 322
50	418506 416636	AA084248 N32536	Hs.372651 Hs.42645	Unknown protein for MGC:29643 (formerly solute carrier family 16 (monocarboxylic	Seq ID No 155 & 323
	421508	NM_004833	Hs.105115	absent in melanoma 2	Seq ID No 156 & 324
	421379	Y15221	Hs.103982 Hs.193470	small inducible cytokine subfamily B (Cy	Seq ID No 157 & 325 Seq ID No 158 & 326
55	428784 431958	Y12851 X63629	Hs.2877	purinergic receptor P2X, ligand-gated to cadherin 3, type 1, P-cadherin (placenta	Seq ID No 159 & 327
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	Seq ID No 160 & 328
	418678	NM_001327	Hs.167379 Hs.167379	cancer/testis antigen (NY-ESO-1) cancer/testis antigen (NY-ESO-1)	Seq ID No 161 & 329 Seq ID No 162 & 330
	418678 420208	NM_001327 BE276055	Hs.95972	silver (mouse homolog) like	Seq ID No 163 & 331
60	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	Seq ID No 164 & 332
	438549 412580	BE386801 AA113262	Hs.21858 Hs.17901	trinucteotide repeat containing 3 similar to CABLES [Homo sapiens]	Seq ID No 165 & 333 Seq ID No 166 & 334
	417166	AA431323	Hs.42146	Paired box protein Pax-3	Seq ID No 167 & 335
65	428513	BE220806	Hs.184697	plexin C1	Seq ID No 168 & 336
65	447937 447937	AL109716 AL109716	Hs.20034 Hs.20034	Homo sapiens mRNA full length insert cDN Homo sapiens mRNA full length insert cDN	Seq ID No 169 & 337 Seq ID No 170 & 338
	446341	AL040763	Hs.310735	FGENESH prediction similar to multidrug	Seq ID No 171 & 339
	446341	AL040763	Hs.310735	FGENESH prediction similar to multidrug	Seq ID No 172 & 340
70	458079 415668		Hs.54277 Hs.306814	Homo sapiens similar to RIKEN cONA 28100 Homo sapiens lysyl oxidase-like 4 (LOXL4	Seq ID No 173 & 341 Seq ID No 174 & 342
,,	447674		Hs.19192	cyclin-dependent kinase 2	Seq ID No 175 & 343
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	Seq ID No 176 & 344
	440065		Hs.266331 Hs.77667	Homo sapiens Fc receptor homolog express lymphocyte antigen 6 complex, locus E	Seq ID No 177 & 345 Sea ID No 178 & 346
75	414945 440672		Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	Seq ID No 179 & 347
	412609	Z48804	Hs.74124	ocutar albinism 1 (Nettleship-Falls)	Seq ID No 180 & 348
	453837 453837		Hs.256126	bacutoviral IAP repeat-containing 7 (liv bacutoviral IAP repeat-containing 7 (liv	Seq ID No 181 & 349 Seq ID No 182 & 350
	434276		Hs.256126 Hs.93605	leucine zipper, putative tumor suppresso	Seq ID No 183 & 351
80	408367	AK001178	Hs.44424	Homo sapiens orphan neurotransmitter tra	Seq ID No 184 & 352
	444809 415929		Hs.208219 Hs.304950	oculospanin Homo sapiens mucolipin-3 (MCOLN3)	Seq ID No 185 & 353 Seq ID No 186 & 354
	421666		Hs.1408	endothelin 3	Seq ID No 187 & 355

5	425535 AI 451537 RS 430280 A	B007937 56631 A361258	Hs.1765 Hs.158287 Hs.26550 Hs.237868 Hs.83384	syndecan 3 retinoid X receptor interteukin 7 rece			Seq ID No 188 Seq ID No 189 Seq ID No 190 Seq ID No 191 Seq ID No 192
	448610 N 432800 B 416350 A 405545	M_006157 E391046 F188625	Hs.21602 Hs.278962 Hs.189507	nel (chicken)-like AIM-1 protein phospholipase A Target Exon	1 2, group tiD		Seq ID No 193 Seq ID No 194 Seq ID No 195 Seq ID No 196
10	432874 W	72755 194322	Hs.77367 Hs.279651	monoxine induce metanoma inhibi	ed by gamma inter tory activity	reron	Seq ID No 197 Seq ID No 198
15	Seq ID No Nucleic	sequences as descri D: 1 DNA sequ Acid Accessio	ence in 8: NM_00242	21.2			
	Coding B	equence: 11		31	41	51	
20	î	i		ī	ĭ	ĩ	
	CCAGCGAC TACTACAA	CT TTCCTCCACT TC TAGAAACAC CC TGAAGAATG AT TGAAGCAAA	GCTGCTGCTG AGAGCAAGAT ATGGGAGGCAA	CTGTTCTGGG GTGGACTTAG GTTGAAAAGC	TCCAGAAATA GGAGAAATAG	CCTGGAAAAA TGGCCCAGTG	60 120 180 240
25		CC TGAAGGTGA					300
		TG AGGGGAACC					360
	TACACGCC	AG ATTTGCCAA	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACTC	420
		TG TCACACCTC					480 540
30		TG TCAGGGGAG TG CTTTTCAAC					600
50		GA CCAACAATT					660
	GGCCATTC	TC TTGGACTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
		TG GTGATGTTC					780
35	GGACGTTC	CC AAAATCCTG	r CCAGCCCATC	GGCCCACAAA	CCCCAAAAGC	ATGTGACAGT	840 900
"	TTCTACAT	GC GCACAAATC	CTTCTACCCG	GAAGTTGAGC	TCAATTTCAT	TTCTGTTTTC	960
•	TGGCCACA	AC TGCCAAATG	G GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
		CA AAGGGAATA					1080
40		ICA TCTACAGCT					1140 1200
70		TA AACGATCTA					1260
	GGAATTGG	CC ACAAAGTTG	A TGCAGTTTTC	ATGAAAGATG	GATITITCTA	TTTCTTTCAT	1320
		AC AATACAAAT		ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380
45	AATAGCTC	EGT TCAACTGCA	G GAAAAATTAG				
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50	i	i.	i	í	ì.	î	
	ATGCACAG	SCT TTCCTCCAC	T GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
		CTC TAGAAACAC ACC TGAAGAATO					120 180
		AAT TGAAGCAA					240
55		CCC TGAAGGTGA					300
		CTG AGGGGAACG					360
		CAG ATTTGCCA/ ATG TCACACCTO					420 480
		TTG TCAGGGGAG					540
60	CTTGCTC	ATG CTTTTCAAG	C AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
		GGA CCAACAAT					660
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	GGACGTT	CCC AAAATCCT	T CCAGCCCATC	GGCCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
65	AAGCTAA	CCT TTGATGCT	AT AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
	TTCTACA	TGC GCACAAAT	CC CTTCTACCCG	GAAGTTGAGC	TCAATTTCAT	TICTGTTTTC	960
		AAC TGCCAAAT TCA AAGGGAAT					1020 1080
		ACA TCTACAGO					1140
70	CTTTCTG	AGG AAAACACT	GG AAAAACCTAC	TTCTTTGTTG	CTAACAAAT!	CTGGAGGTAT	
		ATA AACGATCT					
		GCC ACAAAGTT GAC AATACAAA					
		GGT TCAACTGC			· IIIIGACIC	COMMOCI	1300
75	Seq ID	NO: 3 DNA s	equence				
		: Acid Access sequence: 64		724.4	•		
	1	11	21	31	41	51	
80	1	1	1	1	1	1	4.5
		AGGC AGGCAAGA					
		AGA GTCTTCCA GGAG CTGCAAGG					
		TACG ACCTCAAA					

	GTTGTTAAAA A	VAATCCGAGA	AATGCAGAAG	TTCCTTGGAT 1	GGAGGTGAC C	GGGAAGCTG	300
	GACTCOGACA C	TCTGGAGGT	GATGCGCAAG	CCCAGGTGTG C	AGTTCCTGA T	TGTTGGTCAC	360 420
	TTCAGAACCT T	PROCEGGAT	CCCGAAGIGG .	RUGARARUCC F	TCTTCACAIA	AGGATTOTG	480
5	GTCTGGGAAG	AGGTGACTCC	ACTCACATTC	TCCAGGCTGT A	TGAAGGAGA	GCTGATATA	540
•	ATGATCTCTT 1	TTGCAGTTAG	AGAACATGGA	GACTTTTACC (	TTTTGATGG	ACCTGGAAAT	600
	GTTTTGGCCC A	ATGCCTATGC	CCCTGGGCCA	GGGATTAATG (	GAGATGCCCA (	CTTTGATGAT	660
	GATGAACAAT (	GGACAAAGGA	TACAACAGGG	ACCAATITAT 1	TCTCGTTGC '	TGCTCATGAA	720
• •	ATTGGCCACT (	CCCTGGGTCT	CTTTCACTCA	GCCAACACTG A	AAGCTTTGAT	GTACCCACTC	780
10	TATCACTCAC	TCACAGACCT	GACTCGGTTC	CCCCLCLCLC 1	AAGATGATAT	AAATGGCATT	840
	CAGTCCCTCT	ATGGACCTCC	CCCTGACTCC	CCTGAGACCC	CCCTGGTACC	CACGGAACCT	900 960
	GTCCCTCCAG AGCACTCTGA	AACCTGGGAC	GCCAGCCAAC	TGTGATCCTG	CTTIGICCTT	CARATOCIGIC	1020
	AGCACTCTGA	GGGGAGAAAT	CCIGATOTT	TCTTCATTTT	CCCATCTCT	TOTTCAGGC	1080
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50	Nucleic Ac. Coding sequilar I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGAAT AAACCTACAG GTCTGTCTGC TTTCAGAATA CTATCCTGG TTTTCAGAATA	id Accessionence: 15 11	m #: EOB Bet 001 21 	31   GOCCCAGCAG GACGACATCA GTTCTGGAAA AAGGGGAAT AAACCTGATTC GGCAAAATGA GAAAACTTGA GCCTACCAC GTTCCTCCAAACC GTTCCTCCAGC GTCCTCAAACC GCCTGGATGGTCT GGCCTGGACGGACT GGCCTGGACGGACG GCCTGGGACC	ACTACAGAGT ACTACAGAGT AACAGAAGAA TGGCCAGGTC CAGACACTGT ACGTCAGT ACGTCAGT ACGTCAGT TCACCACCAT CCACCATT CCACCAGT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATTT CTTCCAAAGA AGTCAATGAC AGCCAAATCA AAGTCCCTCA	120 180 240 300 360 420 480 540
50 55	Nucleic Ac. Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGAAT AAACCTACAG GTCTGTCTGC TTTCAGAAT TTTTCAGAAT TCGCTATGCAT ATGCTATGCCAT TTGCATATCCAGAT TTGCATATCCAGAT	id Accessionence: 15 11	m #: EOS Ber  001 21	31   GCCCCAGCAG GACGACATCA GTTCTGGAAA AAGGGGGAAT AACCTGATTC GGCAAAACTTGA GGCTACCAG GTTTCCTCCT CTCTCAAACC TGGATGGTCT GCCTGGAGGAC CAGAAGGAT	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGTC CAGACACTGT GTACGTCAGT ACGTCAGGC AGACTCAGC AGACTCAGC CTCCACCATC GCAGCCTGGC TCCACCATC TCCACCATC TCCACCAGT TCAGTCAGC TCCACCAGT TCAGTCGGC TCCACCAGT TCAGTTGTC TCAGTGGGC TCAGTGGCC TCAGTGGCC TCAGTGGCC TCAGTGGCC TCAGAGGGAGC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGG GTATGAATT CTTCCAAAGA AGTCCATCAA GAAGGCAATCA AAGTCCCTCA GAAGGCTATC AGCCTTACTG GAGCTTACCTG TAGCTTACCTG TAGCTTACCTG	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Ac. Coding sequilar I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGAAT AAACCTACAGA TTTTCAGAATAA CTTATCCTGG TTTTCAGAATA TCGGTATGCG ATCGATATCCC CCATGTTTTC	id Accessionence: 15 11	m #: EOB Ber  001 21	31	ACTACAGAGT ACTACAGAGT ACTACAGAGA TGGCCAGGT CAGACACTG GTACGTCAGT ACGTCAGC TCCAACCATC ATTTGGAGC TCCACCAGC TCACCCCAC TCAGTCTGCC TCACCCAAC TCAGTTGTC TGGAAGGAA ATTGGGGGCT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GATCAATGCC GAAAGTGAAATCA GAAGTCAATCA AAATCCCTCA AAATCCCTCA GGAAGTGATA CGCCTTCATTG AGCTTACCTG AGCTTACCTG AGCTTACCTG AGCTTACTTG AGCTTACTTG AGCTTACTTG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAT AAACCTACAG GTCTGTGCTGC GTTTCAGAATA CCTATCCTGG TTTTCAAAAT TCGCTATGCC ATCGATATCC CATGTTTTC ATGGATATCC	id Accessionence: 15 11	m #: EOS Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAGAGA TGGCCAGGTC CAGACACTGT GTACGTCAGGC AGACTGAGC AGACTGAGC AGACTGAGC TCCAACCATT CATTGAGGC GCAGCCTGC TCACTCCAA TCAGTGGT TCAGTGGT TCAGTGGT TCAGTGGT ATTGGGGGCT	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCCTCA GAAAGTGAAA GGCCTAATCA GAACGCTATC GCCTTAACCT GTATTACCTC TAGCTTACCTC TAGCTTACCTC TAGCTTACCTC TAGCTTACCTC TAGCTTACCTC TAGCTTACCTC TACCTTCATT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT ACCTATCCTGGC ATTGCTAAAAT TCGCTATGCC ATGGTTTTC ATGGCTATGC CCAGTATTTC ATGGCTATGC CCTTCCTCACC CCTCTCCTCACC	id Accessio uence: 15 11	m #: EOS Ber  021	31	ACTACAGAGT GGGTCGGGT AACAGAAGA TGGCCAGGT GTACGTCAGT GTACGTCAGT ACGTCAGC TCCAACCATC ATTTGGAGGC TCCACCAGC TCAGTCAGC TCAGTCAGC TCACCAAC TCAGTGGCC TCACTCAA TTGAGGGGA TTGAGGGGAA ATTCTTTAA GGAAACCCG GGAACCTCTG ACCCTCTG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATCATTGCC GGAAGTGAAATCA GAAGTCCCTCA AAATCCCTCA GGACTTATCC GCCTTCATTG AGCTTACCTG TGCTTCATTG ATCTGTTCATT ATCTGTTGCA AAAAACCTGAG GCCTGCTTCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
50 55 60	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT ACACCAGAAT ACACCAGAAT ACACCAGAAT CCTATCCTGG TTTCAGAATA CCTATCCTGG TTTTCAAAAT CCTATCCTGG ATCGATATCC CCATGTTTTC GCCATGTATGCC CCTTCCTCACC CCCCAAGGGA	id Accessionence: 15  11    CANANCTANC AGGACGANTT TTGTGCTG ACACGGTGCG ACAGGCGTGT TTTCACAGGG CTGCCCTAC TTGTCGCTGC CATTCTTCA AGACACACT AGACACACT AACAGAGATT AAGACCAAACA AACAGACT ATTCTACT AAGACCAACA AACAGACT AACAGACACAC AACAGACCAACAC CTTCTCCCAC AGAATTCTCCCAC AGAATTCTCCCAC AGAATTCTCCCAC	m #: EOS Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGT CAGACACTGT GTACGTCAGT ACGTCTGGCG ACGACTGAGC ACTACTGGCG CTCAACCATT TCAGTCAGT TCAGTCAGT TCAGTCAGT TCAGTCGGC TCACTCCAA TCAGTCGGC TCAGTCGGC TCAGTCGGC TCAGTCGGCGCT TCAGTCGGCGCT ATTCTTAA GGAAACCCG ACCCCTCTG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGATGCAATCA GAAGGGAAATCA GAAGGCTATC GGAAGGTAATC GGAAGGTAACCT GACCTTCATTG TAGTTACCTG TGTTTTTGGA TTCCTTCATT ATCTGTTGCA AAAACCTGAG GCCTGCTTCT ATTGGCTAAT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	Nucleic Ac. Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGAAT AAACCTACAG GTCTGTCTGG TTTTCAGAAT TCGCTATGCC ATGGATATCC CATGTTTTC ATGGCTATGCC CCTGGTCTTC CCCAGGTAGGCC CCCCAAGGGA GGTGGGGCCC	id Accessionence: 15 11	m #: EOB Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGT CAGACACTGG AGACTCGGC AGACACTGGC AGACTCAGC ACGCTCAGCC ACGCTCAGCC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCACC TCCACCCAC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATTATAAG GGATGAATGC GGAAGTGAAA AGTCCCTCA GGACCTTACTG AGCTTACTG TATCCTTATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTT ATCTTCATT AACCTGAG AAAACCTGAG CCCTCCTCATTT AACCTGATG TATCCTTCATT TATCGTTACT TATCGTTACT TATCGTTACAT TATCGTTACAT TATCGTTACAT TATCGTTACAT TATCGTTACAT TATCGCTAAT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
50 55 60 65	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT ACCTATCCTGGC ATGGCTATCGCC ATGGATATCCC CCATGTTTTC ATGTGCTATGGCCATCAGGGA GCTGCGCGCCC CCTCCTCAC CCCCAAGGGAA	id Accessionence: 15  11	m #: EOS Ber  021	31	ACTACAGAGT GGGTCGGGT AACAGAAGA TGGCCAGGT GTACGTCAGT GTACGTCAGT GTACGTCAGT TCCAACCATC TCCAACCATC TCAGTCTGAGC TCAGTCAGC TCAGTCAGC TCAGTCAGC TCAGTCTGAC TTCAGTGGGA TTCAGTGGGC TCACTCAA TTCAGTGTGC TGGAAGGGAA TTGGGGGCT AATTCTTTAA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATCAATGCC GAAAGTGAAATCA AGTCCATCA AGCTCACTCA AGCTTACTCA GGCTTCATTG AGCTTACTTG ATCTGTTGCA ATCTGTTGCA ATCTGTTGCA ATCTGTTGCA TTCCTTCATT ATCTGTTGCA TTCCTTCATT ATCTGTTGCA GCCTGCTTCT TATTGGCTAAT GGATCTTCACTG CCTGCTTCT TATTGGCTAAT GGATCTTCAG CCTGCTTCATT AGGATCTTCAG CCATGTCACCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
50 55 60	Nucleic Ac. Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC TCAAGACAGT GCAGTCCGTA ACACCAGAAT ACACCAGAAT TTTTCAGAAT TGCTATCCTGG TTTTCAGAAT TGCTATGCC ATGGATATCC CCAGGTTTTC AGGCAGGCC CCCCAAGGGG GGTGGGGCCC TCGACAGAAAT TCAGACACCC TTGACAGAACCC CCCCAAGGCAG GGTGGGGCCC TCGACAGAAAT TCAGACACCC GTTGCTCCCC	id Accessionence: 15 11	m #: EOB Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGT CAGACACTGG AGACTCGGC AGACACTGGC AGACTCAGGC ACGCTCAGCC ACGCTCAGCC TCCACCAT TCAGCCTGGC TCAGCCTGGC TCAGCCTGGC TCAGCCTGGC TCAGCCTGGC TCAGCCTGGC TCAGCCTGGCGCT ACGCCTCGGC ACCCCTCTG AGACACAG AGACACAG AGACACAG AGACACAG AGACACAG GCAGACCGG AGACACAG GCAGACCGG AGACACAG GCAGACACG AGACACAG GCAGACACG AGACACAG GCAGACACG GCGCCCCC GCCGCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGG GTATGATGT CTTCCAAAGA AAGTCCATCA GAAGGCTATC AGCATTACTAG GAAGGCTATC AGCTTACTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATT ATCCTTCATT ATCCTTCAT ATTAGCTAAT ATGGATCTCAG CATCTCGTG AAGGGAAGGC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1250 1320
50 55 60 65	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACTACTAGGCA ACACTACTAGG GTCTGTGTGC TTTCAGAATA CCTATCCTGG TTTTCAGAATA CCTATCCTGG ATCGATATGGC ATCGATATGGC ATCGATATGGC CCATGTTTTC AGTTATGG GCCAGTAAGG GGTGGGGCGC CCTCGCAGGAA TCAGACACC GTTGGTTAGG GTGGTGGCGGC GTGGTGGTGGCGGG GTGGGCGCG GTGGAGAAA	id Accessioner: 15  11	m #: EOS Ber  021	31	ACTACAGAGT GGGTCGGGT AACAGAGAA TGGCCAGGT CAGACACTG GTACGTCGG AAGATGAGG AGACTGGGC AGACTGGC ATTGGGCGGCT TCAGACGAGT TCAGCACATG ATTGGAGGAGGAG TCAACACATG ATTGGTCAG ATTCATTTAA GGAAACCGG ACTCTAA ATTCTTTAA GGAAACCGG ACCCTCTG AAGAACAAA GCAAGGAGC AGACTGGC CAGGGGGCC CAGGGGGCC CAGGGGGCC CAGGGGGCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCCTCA GAAGTGAAA TGCCAAATCA GAAGCCTATC GCTTCATTG AGCTTACCTG TGTTTTTGGA AAAACCTGAG GCCTGCTTCATT ATCGCTAAT ATCGCTAAT TGCCTAAT ATCGCTAAT ATCGCTAAT CGCTTCATT ATCGCTAAT GGATCTTCAG CATGTCACC CCACTCGGTG CAAGGGAAGGC CCCCTCGGCT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 11080 1140 1260 1320 1380
50 55 60 65	Nucleic Ac Coding sequil I I I ATGCCAGGCA ACCTCTCANG CAGTCTGTGC CAGATCGCTA ACACCAGATA ACACCAGATA ACACCAGAT TTCCAGATCA CTTTCAAAATCC CATGTTTTCAAAATCC CATGTTTTCAAAATCC CCATGTTTTCAAAAT GCCAGTATACC GCCAGGATAAGG CCTTCCTCAC GCTGCCAGGAGGA GGTGGGGCGC TCGACAGGAA TCAGACACC GTTGCTCCC GTAGATAAGC	id Accessionence: 15  11    CANANCTANC AGGACGANTT TTGTGTCCTG ACAGGGGTGT TTTCACAGGG CTGCCCCTAC TTGTGCTGC CATCTTTCA AGACACACA AGACACACAC AACAGACACAC TTTTCACACGG CANTCTTTCA AGACACACAC TTTTCACTGC AACACACACAC TTTTCACTGC AACACCACAC TTTTCTACTTC CCGGCCACAC CCGGAAAACC TTTTCTCCCAC CGGATGTTCC CCGGAAAACC TTACTCGCGG AAGACCAGAA CCAGGACTGC CCGGCTTTTC CCGGCTTTTC CCGGCTTTTC CCTGCCTTTTC CCTGCCTACC CCTGCCTACC CCTGCCTACC CCTGCCCACC CTGCCCACC CCACCCACC CCACCCCCC CCACCCACC CCACCCACC CCACCCACC CCACCCACC CCCCCC	m #: EOS Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGT CAGACACTGT GTACGTCAGG ACGCTGGCC AGACACTGT CATTGGAGC CTCAACCATT CTGGAGCGT CTGAACGATT CTGGAGGGGGAGCT CAGAAGAAAAA GCGAACACAC AGAACAAAAA CCGGAGCCGCCC CAGGGGGGGCGC CCAGGGGGGCGC CCCAGGGGGGCGCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCA GAAGTGAAA AAGTCCATCA GAACGCTATC GTATGATCA AAGTCCTCATTC TACTTTCCATTC TACTTTCCATTC TACTTTTCCATCAT AACACCTCATT TACTTGTTCATT ATCTGTTGCA AAAACCTGAG GCCTGCTTCT TATTGGCTAAT GGATCTTCAC GCTGCTTCT GCTGCTCTCCT GCCTCCTGCT GCCTCCTGCT GCCCTCGGCT TCCCTCCGCC TCCCTCGCCT TTCCCTGCCT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500
50 55 60 65 70	Nucleic Ac. Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAAT AAACCTACAG GTCTGTCTGGC TITTCAGAATAT CCTATCCTGG TITTCAGAATAT CCCATGTTTTC ATGCTATGCC ATGGATATCC CCCAGGTAGC CCCCAAGGGA CCCCCAAGGGA TCAGACACC CCCCAAGGGA TCAGACACC CTTGCTCCCC GTTGCTCCCC GTTGCTCCCC GTTGCTCCCC GTTGCTCCCC GTTGCTCCCC GTAGATAAGG TCGGCCTCTCC GCCAGCTTGG	id Accessionence: 15  11    CANANCTANC AGGACGANT TTGTOTCCTG ACACGGTCCTG ACACGGTCCTG TTGTCACAGGG CTGCCCCTAC TTGTCACAGGG CTGCCCCTAC AGACACAGG CATTCTTCA AGACACAGG AAAACCAAACA CCCGAAAACC CCCCGAAAACCAGA CCCGGAAAACC ATCACTGGGG AAGACCAGAA CCCGGAAAACC CCCGGAAAACC CCTGCCTTTTC CCCGGCTTTTC CCCGGCTTTTC CCCGGCTTTTC CCCGGCTTTTC CCCGGCTTTTC CCCGGCTTTTC CCCGCCCACC CCGGCTTTTC CCCGCCCACC CCCGCAAAACCAGAAACCAGAAACCAGAAAACGAAAACAGAAACAGAAACAGAAACAGAAACAGAAACAGAAACAGAAACAGAAAACAGAAAACAGAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAGAAAACAAAACAAACAAACAAAACAAAACAAAACAAAACAAAA	m #: EOB Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGT CAGACACTGG CAGACACTGGC AGACACTGGC AGACACTGGC ACGCTCGGCC ACGCCTGGCC TCCACCACA TCGACCAT TCAGCGGCT TCAGCGGGCT TCAGCGGGCT ACTCCTCGA AGACACAG ACGCAGCGGCC ACCCCTCTG AGAACACAG GCAGACCCG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGAATT CTTCCAAAGA AGTCCCTCA GAAGTGAAA TGCCAAATCA GAAGCCTATC GCTTCATTG AGCTTACCTG TGTTTTTGGA AAAACCTGAG GCCTGCTTCATT ATCGCTAAT ATCGCTAAT TGCCTAAT ATCGCTAAT ATCGCTAAT CGCTTCATT ATCGCTAAT GGATCTTCAG CATGTCACC CCACTCGGTG CAAGGGAAGGC CCCCTCGGCT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 11080 1140 1260 1320 1380
50 55 60 65	Nucleic Ac Coding sequil I I I ATGCCAGGCA ACCTCTCANG CAGTCTGTGC CAGATCGCTA ACACCAGATA ACACCAGATA ACACCAGAT TTTCAGAATA CCTATCTGG TTTTCAAAATCC CCATGTTTTCAAAAT GCCAGTATGCAGG GCCAGTAGGC GTGGCAGGAGGCG TCGACAGGAGGCG TCGACAGGAG	id Accessionence: 15  11    CANANCTANC AGGACGANTT TTGTGTCCTG ACAGGGGTGT TTTCACAGGG CTGCCCCTAC TTGTGCTGC CATCTTTCA AGACACACA AGACACACAC TTTTCACAGGG CATCTTTCA AGACACACAC TTTTCACAGGG CATCTTTCA AGACACACAC TTTTCACAGGG CAATCTTTCA AGACACACAC TTTTTCACTGGG AACACCAACAC TTTTCTCCCAG CGAATACC CCGGAAAACC AACACCAGAAC CCGGACCACC CTGCCTTTTC CCGGCTTTTC CCGGCTTTTC CCGGCTTTTC CCTGCCTTTTC CCTGCCTACC AAGACCAGAACG AAGACCAGAACG AAGACCAGAACG AAGACCAGC CTGCCCACC ATGACAACG ATGACAACG AAGGCCACC ATGACAACG ATGACAACG ATGACAACG ATGACACG ATTCCCCGCG TTTCTCCCACC ATGACACG ATGACACG ATTCCCCACC ATGACACG ATTCCCCGCG TTTCTCCCCGCG TTTCTCCCCCGCG TTTCTCCCCGCG TTTTCTCCCCGCG TTTTCTCCCCGCG TTTTCTCCCCCGCG TTTTCTCCCCCGCG TTTTTCTCCCCCGCG TTTTTCTCCCCCGCCC TTTTTCCCCCCGCG TTTTTCTCCCCCGCG TTTTTCTCCCCCGCG TTTTTCTCCCCCGCCC TTTTTCCCCCCGCCCCT TTTTCTCCCCCGCCCCT TTTTTCTCCCCCCGCCCCT TTTTTCTCCCCCGCG TTTTTCTCCCCCCCC	m #: EOS Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGAA TGGCCAGGT CAGACACTGT GTACGTCAGG ACAGCTCGGCGT ACGTCTGGCCGT ACGTCTGGCCGT CATTGGAGCCTGGCCT CAGACACATGT CTGCAACATGT CTGCAACATGT CTGCAACATGT CTGCAACATGT CTGCAACATGT CTGCAAGGAGCCGCAACACACACACACACACACACACACA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTCCATCA GAAGTGAAA AAGTCCATCA GACGCTATC GTATGATCA AAGTCCTCATTG TATCTTCATTG TATCTTCATTA AACACTGAG GCTTCTTCATT ATCTGTTGCA AAAACCTGAG GCCTGCTTCT ATTGGCTAAT GGATCTACCC GCACTTCACCC CCACTCGGCTC TTCCCTGCCT TTTGGGCTCC TTTGGGCTCC TTTGGGCTCC CTTTGGGCTCC CTTTGGGCTCC CTCGCCCAGTCC CCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1200 1140 1320 1380 1440 1560 1560
50 55 60 65 70	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGC CAGATCGCTA ACACCAGAT AAACCTACCAGAT AAACCTACCAGAT AAACCTACCAGAT TTTCAGAATA TCGCTATCCTGG ATCGATATGCC ATCGATATGCC ATCGATATGCC CCCAGGAGAT TCAGACACCC CCCCAAGGGAT TCAGACACCC GTTGCTCCCC GTAGATAAGC CTCCCCCCCCCC	id Accessionerce: 15  11	m #: EOS Ber  21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGT CAGACACTGGC AGACACTGGC AGACACTGGC AGACACTGGC ACGCTCAGCG ACGCTCAGCG ACGCTCAGCG TCCACCAT TCAGCCTGGC TCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGGGCT CAGAGAGAGAGGGGCT ACGCAGAGAGAGGGAGCCGG ACGCAGAGGGCCG ACGCAGGGCCGC CAGGGGCGC CAGGGGCGCC CAGGGGCGC CTCATCGTC CTCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GTTCCCCCCAG GCGCAAAGGC TCCCACAGGCCGC CCGCAAAGGC CCCACAGGCCGC CCCACAGGCCGC CCCCCAAGGCCGC CCCCCAAGGCCGC CCCCCAAGGCCGC CCCCCAAGGCCGC CCCCCCAAGGCCGC CCCCCCAAGGCCGC CCCCCCAAGGCCGC CCCCCCCAG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGC GGATTATAGC GGATGTCATCG GGAAGTGAAA AGGTCCTCA GGAAGCCTATC AGCTTACTGG TATGTTGTGA AAGACCTCATG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATT ACTTGTTGCA AAAACCTGAG CCTGCTTCT TATCGCTAAT ATTGGCTAAT AGGATCTTCAG CCTCGGCT TCTCCTGGCT TTCCCTGGCT TTCCCTGCCT CCAGCCTCCC CAGCCTCCCC CAGCCTCCCC	120 180 240 300 480 480 600 600 720 780 840 1020 1120 1260 1320 1440 1560 1620 1620
50 55 60 65 70	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGGC CAGATCGCTA ACACTACTAGG GTCTGTGCTGC GTCTGTGCTGC GTTTTCAAAAT CCTATCCTGG TTTTCAAAAT CCTATCCTGG ATGGCTATGGCATATGGCATATGGCATATGCC ATGTTTTCAAAAT CCCCAAGGGA GCCAGGATAAGG CCTTCCTCAA CCCCAAGGGA TCAGACACCC GTTGGTCCCCC GTAGATAAGC TCGGCCTTCG GCAGCTTGG CCTCCCCCC CCGTCCAGC GTGGTCAGCA TCGGCCTCCCCCC CCGTCCAGC GCGCCGAGGAGA TCAGACACTTCG CCTCCCCCC CCGTCCAGC GCCGCCGAGGGT CAAGACTTT	id Accessionence: 15  11    CANANCTANC AGGACGANTT TTGTGCTG ACAGGCGTGT TTTCACAGGG CTGCCCTAC TTGTCCTGC TTGTCCTGC ACAGGCGTGT TTGTCCTGC ACAGGCGTGT TTTCACAGGG CATTCTTTCA AGACACAGC ANCACACAC ANCACACACAC CATTCTTCACTG AAGACCANC CANTCTTCACTG AAGACCANC CTTCTCCCAC CANTCTCCCAC CANTCTCCCAC CANTCTCCCAC CATCTTTCCCAC CANACC TTCTCCCAC CATCTCCCCAC CATCTCCCCAC CATCTCCCCCCCTTC CTTCCCCCCCTTC CTTCCCCCCCTTC CTTCCCCCC	m #: EOS Ber  21    CCGAACAGGC GGATTACCT GGTGGATCCT CTATCGAGGG GCTGATTGAG GCTGATTGAG TCAAAGAGGAT ACTGTTTTCC ATCTTGGGAT ACTGCCCG TCTGCCCCG TCTGCCCCG TCTGCCCCG AACAGGAGACACC AGTTATAAA GCAGCTCT AGGCCCCACC AGGACCACC AGGACCACC AGGACCACC AGGACCACC AGGACCACC ACGAGCACC ACGAGCACC ACGAGCCCACC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGCCCCACC ACGAGAGCCCC ACGAGACCCC ACGAGACCCC ACGAGCCCCACC ACGAGACCCC ACGAGACCCC ACGAGACCCC ACGAGCCCCC ACGAGACCCC ACGAGACCCC ACGAGACCCC ACGAGACCCC ACGAGAGCCCC ACGAGCCCC ACGAGACCCC ACGAGAGCCCC ACGAGAGCCCC ACGAGAGCCCC ACGAGAGCCCC ACGAGAGCCCC ACGAGACCCC ACGAGCCCCC ACGAGCCCCC ACGCCCCACCC ACGCCCCACCC ACGAGCCCCC ACGCCCCACCC ACGCCCCCC ACGCCCCC ACGCCCCCC ACGCCCCCC ACGCCCCCC ACGCCCCCC ACGCCCCCCCC	31	ACTACAGAGT GGGTCGGGT AACAGAGAGA TGGCCAGGT CAGACACTG GTAGGTCGGGT AGACTGGC AGACTGGC AGACTGGC AGACTGGC AGACTGGC AGACTGGC ATTGGAGGC TCACTCCAA TCAGTGGC TCACTCCAA ATTGTTGTC TGGAGGGGT ATTGGGGCT AGACCATG AGACCAGG GGAACCCG AGACCAG CAGGGGGC CCAGGGGGC TCACTGCCAA GGGGGCG TGTCCCCA GGGGCGCC TGTCCCCCA GGCGAAGG	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GGATATTGATT CTTCCAAAGA GAAGTGAAAT GGAAGTGAAA GGCCTCATTG GACCTCATTG GACTTTTCGATG GAAGCCTATC GCTTCTTTGAA AAAACCTGAG GCTTCATTG ATTGCTCATT ATTGTTGCA AAAACCTGAG GCTCCTCT ATTGGCTAAT GGATCTTCAG CATGTCCCC CCCCTCGGCT CTTCCCTGGCT CTTCCCTGGCT CTTCCCTGGCT CTTCCCTGGCT CTTCCCTGGCT CTTCCCTGCCT CTTCCCTGGCT CTTCCCTGGCT CTTCCCTGCCT CTTCCCTGCCT CCCCCCAGTCC CAGCCCAGCC	120 180 240 300 360 420 480 540 660 660 720 780 900 960 1020 1140 1260 1320 1320 1440 1500 1620 1680 1740
50 55 60 65 70	Nucleic Ac. Coding sequil I I ATGCCAGGCA ACCTCTCANG CAGTCTGTGC CAGATCGCTA ACACCAGATA ACACCAGATA ACACCAGATA ACACCAGAT TTTCAAAATCC CATGTCTTGAAATA CCTATCCTGG TTTTCAAAAT CCTATCCTGG GCAGTATCCCAGGATA GCCAGTATCCCCCAGGATA GCCAGTATCCCCCCCCCC	id Accessionence: 15  11    CANANCTANC AGGACGANT TTGTGTCCTG ACACGGTCCTG ACACGGTCCTG CTGTCCCCTAC TTGTGCTGTC AGACCACAC TTGTGCTGC AGACCACAC CATTCTTCA AGACCACAC AACACACAC TTTTCACTTC AACACCACAC CTTCTCCCAC CCGGANACC ATTCTCCCACCC TTTCCCCACCC TTTCCCACCC TTTCCACCC TTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTTCCAACCC TTTTCCAACCC TTTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTTCCAACCC TTTTCCAACCC TTTCCAACCC TTTTCCAACCC TTTTCAACCC TTTTCA	m #: EOS Ber  001 21	31	ACTACAGAGT GCGTCCGGGT AACAGAAGA TGGCCAGGT CAGACACTGT GTACGTCAGG ACGCTCGGCC ACGCCTCGGCC ACGCCTCGGCC ACGCCCCCCC GCGCCAGCCCCCC GCGCCAGCCCCCCCGGCCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATTAGC GGATTATAGC GGATGTCATCG GGAAGTGAAA AGGTCCTCA GGAAGCCTATC AGCTTACTGG TATGTTGTGA AAGACCTCATG TATCCTTCATTG TATCCTTCATTG TATCCTTCATTG TATCCTTCATT ACTTGTTGCA AAAACCTGAG CCTGCTTCT TATCGCTAAT ATTGGCTAAT AGGATCTTCAG CCTCGGCT TCTCCTGGCT TTCCCTGGCT TTCCCTGCCT CCAGCCTCCC CAGCCTCCCC CAGCCTCCCC	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1200 1140 1320 1380 1440 1560 1560 1680 1740 1860
50 55 60 65 70	Nucleic Ac Coding sequil I I I ATGCCAGGCA ACCTCTCAAG ACGTCTGTGGC TCAAGACAGT CAGATCGCTA ACACCAGAT AAACCTACAG GTCTGTGTGC GCAGTCTGTGCTGC TTTCAGAATA CCTATCCTGG TTTTCAAAAT TCGGTATGGC ATGGATAGGC ATGGATAGGC GCAGTAGGG GCTGGAGGAGAAT TCAGACACCC GTTGCTCCCC GTAGATAGCC GTAGATAGGG GCGGGGGGCGGGGGGCGAGGAGAAT TCGGCCTCAAGGAT TCGGCCTCCCC GCGCGGAGGGG GCGCGGAGGAGTTCAGACCCC CCGTCCAGCCGGGGGGGGGG	id Accessionence: 15  11  11  12  CANANCTANC AGGACGANTT TTGTOTCCTG ACAGGCGTGT TTTCACAGGG CTGCCCCTAC TTGTCGCTGC AGACCAACA TTGTCGCTGC AACACACACA AACAAACA AACAAACA CCCGAAACC TTTTCCCCAC AGACTCCCCAC AGACCACAC TTCTCCCAC AGACCACAC TTCTCCCAC AGACCCACC ATACACACC TTCTCCCACC AGACCCCCCCTTCC TTCCCCACC ATACACACC TTCTCCCCACC ATACACCCCCCCTTC TTCCCCACC TTCCCCCCCC	m #: EOS Ber  101 21	31	ACTACAGAGT GGGTCGGGT AACAGAGAA TGGCCAGGT CAGACACTG GTACGTCGG AACAGAGAA TGGCCACGT ACTGGCC AGACACTG GTACGCC ACACCAC TCCAACCATG TCAGCCACCAC TCACCACCAC TCACCACCAC TCACCACCAC TCACCACCACCACCACCACCACCACCACCACCACCACCAC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTGCAATCA GGAAGTGAAA GGCCTCATTG AGCTTATTCGA TGCCAAATCA GAAGCCTATTC AGCCTTCATTG TATTTTCGA TTCCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCAT TATTCCTTCATT TATTCCTCCT TGTGGGCTCC CCCCTCGGCT CTTTCCCTGCCT CTTTCCCAACCCTG CAGGAACACCTG CAACTCCCAAC ATAGGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGGAAGAC ATAGGAAGAC ATAGGAAC ATAGGAAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGA	120 180 240 300 360 420 480 540 660 720 980 1020 1140 1200 1320 1380 1560 1740 1560 1740 1860 1790
50 55 60 65 70	Nucleic Ac. Coding sequil I I I ATGCCAGGCA ACCTCTCANG CAGTCTGTGG CAGTCGTGTG CAGATCGCTA ACACCAGATA ACACCAGATA ACACCAGAT TTCAGAATA CCTATCCTGG TTTTCAGAATA CCTATCCTGG CCTAGGCTA GCAGTATCC CCTAGGTTTCCACAGA GCTGGCAGGAG GGTGGGGCGC GTGGCAGGAG GGTGGGGCGC TCGACAGGAT CCCCAAGGGA GGTGGGGCGC GTAGATAAGG CTCCACCGG TCGACGGAG CTCGACGGAGGAG CTCACCCG GCAGGTTAGC CCCTCACCCG CCGTCAGGC GCCGGAGGG CCGCAGGAGGG TCAAGACTT AGCTCTCCAC GCCCATCAG GCCCCATCAG GCCCCATCAG GCCCGATCAG GCCCGCATCAG GCCCGCATCAG GCCCGCATCAG GCCCGCATCAG GCCCGCATCAG GCCCGCAAGGG GCCCGCAACAG GCCCCCATCAG GCCCGCAACAG GCCCGCACCAG GCCCGCAACAG GCCCGCAACAG GCCCGCAACAG GCCCCCAACAG GCCCCCAACAAC GCCCCCAACAG GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCCAACAAC GCCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCAACAAC GCCCCCCCAACAAC GCCCCCCAACAAC GCCCCCAACAAC GCCCCCCAACAAC GCCCCCCCC	id Accessionence: 15  11    CANANCTANC AGGACGANT TTGTGTCCTG ACACGGTCGT ACACGGTCGT CTGTGCCCTAC TTGTGCTGTG CAGCACAGG CTGCCCCTAC TTGTGCTGC AGACACAGC CATTCTTCA AGACACACT AACAGACACT TTTTCACTTC AACACCACAC AACACCACAC CCGGACACAC CCGGACACAC CCGGACCACC ATGCCTTCC CTTCCCACC ATGCCTTTC CTCCCACCC TTTCCCACCC TTTCCAAGGC GGACGCACCACC GGACCCACCC TTTCCCACCC TTTCCAAGGC GGACCGCACCC TTTCCAAGGC GGACCGCACCC TTTCCAAGGC GGACCGCACCC TTTCCAAGGC GGACCGCACCC GGACCCCCACCC GGACCCCCACCC CGACCC GGACCCCCACCC CGACCC CGACCCCCACCC CGACCC CGACCC CGACCCC CGACCC CGACCC CGACCC CGACCC CGACCC CGCACCC CGCCC CGCACCC CGCC CCC CGCC C	m #: EOS Ber  001 21	31	ACTACAGAGT GGGTCCGGGT AACAGAAGAA TGGCCAGGT CAGACACTGT GGAGCTGGCC AAGACACTGT GGAGCTGGCC ACAGCACTGT CTGCACCATT TCGCGGCT TCGCAGGAGCCGC CAGACACACGGGCGC CAGACACACGGGCGCC CAGACACGCCCCCCGGCCAGCCA	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATATT CTTCCAAAGA AGTCCATCC GGAAGTCAATCA AGACCTCATC GCCTCATTC TATCCTTCATTC TATCCTTCATTC TATCCTTCATT ACTCTTCATTC AAAACCTGAG GCCTCCTCCC TATCCACCC TATCCACCC TATCCACCC TATCCACCC TATCCACCC TATCCACCC TTCCCTCCC	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1140 1320 1340 1560 1680 1740 1860 1920 1920
50 55 60 65 70	Nucleic Ac Coding sequil I I ATGCCAGGCA ACCTCTCAAG CAGTCTGTGGC CAGTCGTAG CAGATCGCTA ACACTACAG GTCTGTGCG TTTCAGAATA CCTATCTGGG TTTTCAGAATA CCTATCTGG TTTTCAGATATCCAG GTCATAGC ATGGATATGC ATGGATATGC CATGTTTC CAGACAGCA CCCAGGATAGGG GGTGGGGGC CTTCCTCAC CCCAAGGAA TCAGACACCC GTAGATAAGC TCGGCCTTCG CCGCCCCCC CCGTCCAGC GCGCGGAGGA TCAAGACTT AGCTCTCAC GCCGCACCAG GCGCGATCAG GCCCATCAG GCCCATCAG GCCCATCAG GTCTCTCACCC GTCACCCC CCGTCCAGC GCCCCATCAG GCCCCATCAG GCCCCATCAG GTCTCTCACC GTCCACCC GTCCACCC CCGTCCAGC GCCCCATCAG GCCCATCAG GTCTCTGAC GTCTCCACC GTCCACCC TCAAGACTTT	id Accessionence: 15  11  11  12  CANANCTANC AGGACGANT TTGTGCTG ACAGGCGTGT TTTCACAGGG CTGCCCCTAC TTGTCACTGG CATTCTTCA AGACATACT AGACACTACT AGACACTACT AGACACTACT AGACACTACT AGACACTACT CCGGGCCACA AGACACTACT CCGGGCCACA AGACACTACT CCGGGCCACA AGACACTACT CCGGGCCACA AGACACACAC CCTCTCCCAC AGAAACCAACAC CCTCTCCCACACAC CCGGAAACC CCTCTCCCACACACC CCGGAAACC CCGGAAACC CCGGAAACC CCGCAACACC CTGGCCACC CCGGACTTC CCGCCACC CCGCCACT CCCCCCCTTTCCACAC CCGGCCCACT CCCCCCCCCTTTCCACACC CGGCCCACCACC CGGCCCACCACC CGGCCCACCACC CGGCCCACCACC CGGCCCACCC CGCCCCC CCCCCC CCCCC CCCCCC CCCCCC CCCCCC	m #: EOS Ber  21	31	ACTACAGAGT GGGTCGGGT AACAGAGAGA TGGCCAGGT CAGACACTGT GTACGTCGGGT AGACACTGT GTACGTCAGG AGACTGAGG AGACTGAGG TCCCAACCATT TCAGGTGGC TCACACCATT TCAGGTGGCT ATTGGAGGAGGAG ATTCAGTTTAA AGACCAGGAGGAG AGACCAGG CAGGAGGAG CCCCAGCAG GCCCAGCAG GCCCAGCAG CCCCAGCAG CCCCAGCAC CACCCCGCCTG CAGGGGGGC CTCATCGTC CAGGGGGGC CTCATCGTC CAGGGGGGC CTCATCGTC CAGGGGGGC CTCATCGTC CAGGGGGGC CTCATCGTC CAGGGGGGC CCCCAGCAGC CCCCAGCCAC CCCCAGCCAC CCCCCGCCTG CAGCCCGCCTG CAGCCCGCCCC CAGCCCGCCTG CCCCCGCCTG CCCCCGCCTG CCCCCGCCTG CCCCCGCCTG CCCCGCCTG CCCCGCCTG CCCCCGCCTG CCCCCCCC	GATATTGAAG TATGTCATCT AGTTGTTGCA GGATTATAAG GTATGATTT CTTCCAAAGA AGTGCAATCA GGAAGTGAAA GGCCTCATTG AGCTTATTCGA TGCCAAATCA GAAGCCTATTC AGCCTTCATTG TATTTTCGA TTCCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCATT ATCTTCTTCAT TATTCCTTCATT TATTCCTCCT TGTGGGCTCC CCCCTCGGCT CTTTCCCTGCCT CTTTCCCAACCCTG CAGGAACACCTG CAACTCCCAAC ATAGGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGGAAGAC ATAGGAAGAC ATAGGAAC ATAGGAAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGAC ATAGGAAGA	120 180 240 300 360 420 480 660 780 900 960 1020 1140 1220 1380 1440 1560 1620 1680 1890 1680 1890 1890 1890 1980 2040

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	GGAGACGAGG A	GGATGAGAA G	CCGCTTCCT (	SCCACOGTTG 1	CAATGACCA (	CGTGCCTTCC	2280
	TCCTCCAGGC A GCCAGCCTGC A						2340 2400
_	CATCCTCAGG G	CAAGTACTC (	TCCCTGGCC	TCCAAGGCTC /	AGGATGTTCA	ACAGAGCACA	2460
5	GACGCGGACA C	GGAGGGTCA 1	TCTCCCAAA	GCACAGCCAG (	GTCCACAGA		2520
	TCCCCTGCTC G	TCCTCCCGC A	AGCACGGTCA	CAGCAGCATC (	CAGTGTTCC	CAGAAGGATG	2640
	CCGGGACCCC A	GAGCAGAGA (	CCCCCCTCCC	TCACCTTCCC /	AGCCCAGGCT	CTCACTGACC	2700
10	CAGGCCGGGC G	SCCCCCCCCCC (	CACGTCGCAG	GGCCGCTCCC /	ACTECTECTC -	GGACCCTTAC	2760
10	ACGGCGAGCT C	CAGAGGGAT (	CTCCCCACG	GCCCTCCAGA (	ACCAGGACGA ATGTGCGGC	CCATGCCCAG	2820
	GCCGCGCGCG C	CAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
	ACAGGCGCAG C	GCCAGGTGG (	CGACCACAGG	TCCCAGCGCG	GACATGCGGC	CTCCCCCCCCC	3000
15	AGGCCCAGCC O	GACCCGGCGG (	CCCCCAGTCC	CCCCCCCCCC	TCCCCAGCAG	GGCAGCGCCG	3060 3120
13	GCCGAGGACG A	AGGAGGAGGA	GGACGCGGGG	TTTTTTTAAAG	GCGGGAAAGA	AGACCTTCTG	3180
	TCTTCCTCTG 1	TGCCAAAGTG	CCCCTCTTCC	TCCACTCCCA	GGGGCGCAA	AGACGCCGAT	3240
	GGGAGCCTCG C	CCAAGGAAGA	GAGGGAGCCT	GCCATCGCGC	CTCCCCTCG	CCCACCGACC	3300 3360
20	GTCCCTTCCC (	GACCGCCGCC	TCGCAGCGCT	GCCACCGTGA	GCCCCGTCGC	GGGCACCCAC	3420
	CCCTGGCCGC (	GGTACACCAC	GCGCGCCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGCGCC AGACCCTCTT	AGAGGATGAT	GCATGCCAGA	TTCCGTAACC	TAGAAGGGAA	ACAGCCTGCC	3540 3600
	GGTAGTAATG	GAAAACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
25	GTTGTGGACC '	TTGATCGTGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAAATC	CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC CCACTCTTTG	GAACCATIGI	AGATCTGGAA	3780 3840
	CCTCTGGCCA	ATGCCCAAGA	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
20	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
30	ACGACGCCCC	TGCCTACCAC	CCCTACCACT	AGGCCCACCA ACACCGAGGC	CTGCCACCAC	CATGUAGUCU	4020 4080
	CGCACGACCA	CCAGGCGTCC	<b>AACAACCACA</b>	GTCCGAACCA	CTACGCGGAC	AACCACCACC	4140
	ACCACCCCCA	AACCCACCAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	
35	GACGATGATG	GCAACCTGAT	AATGAGCTCC	GCAGTACCTA	CAGAGTGCTA	CGCTGAAGAA CTACGTTATA	4320
33	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCCAGAG	GAAGGCGCCA	TCAGTTCCTT	TCCTGAAGAA	4440
	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GCACTGGATC	ACCIGACGIA	CCTAAATAAA	4500 4560
40	GATGAAATCA	TCCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACTCATTTG	TCATTGTGGA	TTGGGACAAA	4680
	GCCACCCCAG	GAGATTTGGT	CACAGGTTAT	TIGGTTTACA	ACTTGCCCAT	TGAGAACCTA	4740 4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
45	ATCAGCCCTT	CGGTCTCATT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCCC	4920
	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	CTTCCTCCAGC	TACACGGACT GTTGTTCTTT	4980 5040
	GTAATTCACT	GAGGTATAAA	ATCTACCTCA	GTGACAACCT	GAAAGATACA	TTCTACAGCA	5100
50	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
50	GAAGAACAGG	GCCTCAGTCC	ACCTTTCCC	ACATOGGOTT	CGGAACCCC	TACTATCGCC TACTATG	5220 5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAAGTG	GTAATCACAC	GACCGTCATG	5340
	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCA	CTAAGTCGCA	CTAGGGGCTC	TGAGCAAAGA	5400
55	CAGCCAGCAT	GCTCAGCCCC	GGAACTCAG	CCCACTTCTT	GCCTGGAC	r ggacactggc A atgaacagga	5460 5520
55	TTCAGTTTTG	CTGTTAACTT	TGCTTCTCT	A CTTTTTTTTC	TTTGTTTGT/	A ATAGCACATC	5580
	CCAGAGACAT	CAGAAACCAG	CAACTGATTO	AGTGTGATTT	CCCAGACTT	TTAGGCATGA	5640 5700
	AATTCGGACA	TTTCTGTTTT	TCCAGGAAT	GCATATGCAC	AAACTAACT	CTTCATGGAA AATTTAAGCT	5760
60	TCAGGTCCCT	TTGTATGCAG	TAGAAAGGA	AAAATTATT A	CACCACCAA	A GAAAATAAAT	5820
						TATCAAATC	
						A TATCCACACT A AAAAAAAAAA	
	AAAAAA						
65		0 DUS 0					
		: 8 DNA Sequiid Accessio		4244			
		mence: 1					
70	1	11	21	31	41	51	
70	ATGGATCCG	CGGCGGGAG	c cccrcccc	C CTGCTCTGC	c ccccccrcc	T GCTGCTGCTC	60
	CTGCTGCTGC	c ceceeceec	r ccrecceco	CCCCCCCCC	C CCGCGAACG	C CAGGCTCGCC	120
	GCCGCCGCCC	ACCCCCCAG	G CGGGCCCCT	G GGGCACGGA	G CGGAGCGCA	T CCTGGCGGT(	3 180 240
75						C AGCTACGTCO	
	AACGAGGAGG	G AGCCTGGCA	G TCACCTCTT	C TACAATGTC	A CGGTCTTTG	G CCGAGACCT	360
						T GGAGTGGCAG	
	GTGGCCGGC	C TAGCCGAAG	C CTCCTCTG1	G GCGCTCAGC	A ACTGCGATC	'A CGTCGGAGAI G GCTGGCTGG	
80	CTGATCCGG	A TGGAGGAGG	A GGAGTTCTT	C ATCGAACCC	T TGGAGAAGO	G GCTGGCGGC	G 600
	CAGGAGGCT	G AGCAAGGCC	G TGTGCATGT	G GTGTATCGC	C GGCCACCCA	IC GTCCCCTCC IA CAGCCTCAG	I 660 C 720
	CGCGCCCTG	G GCGTCCTAG	A GGAGCACGC	C AACAGCTCG	A GGCGGAGGG	C ACGCAGGCA	T 780
	GCTGCAGAC	G ATGACTACA	A CATCGAGGT	C CTGCTGGG	G TGGATGACT	C TGTGGTGCA	G 840
						630	
						<b></b>	

	TTCCACGGGA A	AGGAGCACGT	ACAGAAGTAC	CTGCTGACAC	TCATGAACAT	rgt caatgaa	900
	ATCTACCATG A	ACGAGTCCTT	GGGTGCCCAC /	ATCAACGTGG	TCCTGGTGCG (	CATCATCCTC	960
	CTGAGCTATG C	GAAAGTCCAT	GAGCCTCATC (	GAGATCGGGA AAGCCAGACA	ACCCCTCTCA (	GAATACCAC	1020 1080
5	GATCACGCCA T	CTTCCTCAC	ACGGCAGGAC	TTTGGGCCTT	CCGGCATGCA	AGGCTATGCT	1140
_	CCTGTCACCG (	GCATGTGCCA	TCCGGTCCGC .	AGCTGCACCC	TGAACCATGA	GGACGGCTTC	1200
	TCCTCAGCGT	TTGTGGTGGC	CCATGAGACT	GGCCACGTGC	TGGGCATGGA	GCACGACGGG	1260 1320
	CAGGGCAACC (	GCTGTGGCGA	CGAGGTGCGG	TOCACCAGCA	AGGAGCTGAG	CCGCTACCTG	1380
10	CACTCCTATG						1440
	CTCCCGGGAC '	TGCACTACTC	CATGAACGAG	CAATGCCGCT	TTGACTTCGG	CCTGGGCTAC	1500
	ATGATGTGCA	CCCCCTTCCC	GACCTTTGAC	CCCTGCAAGC	AGCTGTGGTG	CAGCCATCCT	1560
	GACAACCCCT	ACTITICCAA	BACCAAGAAG	ATCTOCCTCA	CACCTGACAT	CCTCAAACGG	1620 1680
15	GACGGCAGCT	GGGGCGCTTG	GAGTCCGTTT	GGCTCCTGCT	CACGTACCTG	TGGCACGGGC	1740
	GTGAAGTTCA	GGACCCGCCA	GTGTGACAAC	CCACACCCGG	CCAACGGGGG	CCGCACCTGC	1800
	TCGGGCCTTG	CCTACGACTT	CCAGCTCTGC	AGCCGCCAGG	ACTGCCCCGA	CTCCCTGGCT	1860
	GACTTCCGCG	AGGAGCAGTG	CCGCCAGTGG	GACCTGTACT	TCGAGCACGG GATGCCACCT	GTACTGCGAG	1920 1980
20	TOTAGGGAGA	CCGGGGGAGGT	GGTGTCCATG	AAGCGCATGG	TGCATGATGG	GACGCGCTGC	2040
	TCCTACAAGG	ACCCCTTCAG	CCTCTGTGTG	CGCGGGGACT	GCAGGAAGGT	GGGCTGTGAC	2100
	GCTGTGATCG	GCTCCAGCAA	GCAGGAAGAC	AAGTGTGGCG	TGTGCGGAGG	GGACAACAGC	2160
	CACTGCAAAG	TGGTCAAGGG	CACGTTCACA	CGGTCACCCA	AGAAGCATGG AGGAGGTAGA	CCCCACCAGC	2220 2280
25	CACCATCTGG	CCCTCAAGAA	CCTGGAGACA	GGCAAGTTCA	TCTTAAATGA	AGAGAATGAC	2340
	GTGGATGCCA	<b>GTTCCAAAAC</b>	CTTCATTGCC	ATGGGCGTGG	AGTGGGAGTA	CAGAGACGAG	2400
	GACGGCCGGG	AGACGCTGCA	GACCATGGGC	CCCCTCCACG	GCACCATCAC	CGTTCTGGTC	2460
	ATCCCGGTGG	GAGACACCCG	GGTCTCACTG	GACGACTICTO	ACATGATCCA TGGTCTACGA	CTCCCCCCTC	2520 2580
30	AAGAAGTGGT	CTCCGTGCTC	CAAGCCCTGT	GGCGGAGGGT	CCCAGTTCAC	CAAGTATGGC	2640
•••	TGCCGCCGGA	GGCTGGACCA	CAAGATGGTA	CACCGTGGCT	TCTGTGCCGC	CCTCTCGAAG	2700
	CCCAAAGCCA	TCCGCAGAGC	GTGCAACCCA	CAGGAATGCT	CCCAGCCAGT	GTGGGTCACA	2760
	GGCGAATGGG	AGCCATGTAG	CCAGACCTGT	ACCOGCTCCC	GCATGCAGGT TGCACGCCAA	CCACTCCAAT	2820 2880
35	GACGCCCGGC	CCGAGAGCCG	CCGGGCCTGC	AGCCGCGAGC	TCTGCCCTGG	TCGTTGGCGA	2940
	GCCGGGCCCT	GGTCCCAGTG	CTCAGTAACC	TGTGGCAACG	GCACCCAGGA	GCGGCCAGTG	3000
	CCCTGCCGCA	CCGCGGACGA	CAGCTTCGGC	ATCTGCCAGG	AGGAGCGTCC	TGAGACAGCG	3060
					ATCCCTCCAA	CTCGTCAAAG	3120 3180
40					AAGTCTTGTC		3240
	TCCATCCCAG	GCTACAACAA	GCTGTCCTGC	AAGTCCTGTA	ACCTGTACAA	CAACCTCACC	3300
					ACGACATTGA		3360
	CCTACCCTCC	CAGTGCCCAC	TGTAGCCATG	GAGGTGCGGC	CATCACCAAG ATCACCCAGA	AACCAATGCC	3420 3480
45	GTAGATGAAC	CCTACAAAAT	CCATGGCCTG	GAAGATGAAG	TCCAGCCACC	CAACCTAATC	3540
	CCTCGACGAC	CGAGCCCCTA	TGAAAAGACC	AGAAACCAAA	GAATCCAAGA	GCTCATTGAT	3600
	GAGATGCGGA	AGAAAGAGAT	GCTCGGAAAG	TTCTAA			3636
	Sea ID NO:	9 DNA sequ	ence				
50			n #: NM_024	022			
		nence: 202	1563				
	1	11	21	31	41	51   ·	
	ACCGGGCACC	GGACGGCTC	GGTACTTTCC	   TICTTAATT/	GTCATGCC	GTGTGAGCCA	60
55	GGAAAGGGCT	GTGTTTATG	G GAAGCCAGTA	ACACTGTGG	CTACTATCT(	TTCCGTGGTG	120
	CCATCTACAT	TTTTGGGAC	r CGGGAATTA1	GAGGTAGAG	G TGGAGGCGGA	GCCGGATGTC	180
	AGAGGTCCTG	AAATAGTCA	CATGGGGGA	AATGATCCG	C CTGCTGTTG/	AGCCCCCTTC ACCAGATGCA	240 300
	CATTCCCAT	CGCITTIG	2 CCTIONION	i iiowwwiiw			
60		CTGCACAGA	T CCTGTCACT(	CTGCCATTG	A AGTTTTTTC	AATCATCGTC	360
	ATTGGGATCA	TTGCATTGA	f ATTAGCACTO	GCCATTGGT	A AGTTTTTTC	AATCATCGTC CTTCGACTGC	360 420
	ATTGGGATCA TCAGGGAAGT	TTGCATTGAT ACAGATGTO	f ATTAGCACTO G CTCATCCTT	GCCATTGGT AAGTGTATC	A AGTTTTTTC C TGGGCATCC G AGCTGATAG	AATCATCGTC CTTCGACTGC TCGATGTGAC	420 480
	ATTGGGATCA TCAGGGAAGT GGAGTCTCGC	TTGCATTGA ACAGATGTO ATTGCAAAG	F ATTAGEACTO G CTCATCETT A CGGGGAGGAO	GCCATTGGT AAGTGTATO GAGTACCGC	A AGTTTTTCC C TGGGCATCC G AGCTGATAG T GTGTCCGGG	AATCATCGTC A CTTCGACTGC C TCGATGTGAC F GGGTGGTCAG	420 480 540
	ATTGGGATCA TCAGGGAAGT GGAGTCTCGC AATGCCGTGC	TTGCATTGA ACAGATGTO ATTGCAAAG TCCAGGTGT	T ATTAGEACTO G CTCATCCTT A CGGGGAGGA T CACAGCTGC	GCCATTGGTO CAGTGTATO CGAGTACCGC CTCGTGGAAG	A AGTTTTTCC C TGGGCATCC G AGCTGATAG T GTGTCCGGG A CCATGTGCT	AATCATCGTC CTTCGACTGC TCGATGTGAC GGGTGGTCAG CGATGACTGG	420 480
65	ATTGGGATCA TCAGGGAAGT GGAGTCTCGC AATGCCGTGC AAGGGTCACT GATAACCTCA	A TTGCATTGA T ACAGATGTO G ATTGCAAAG C TCCAGGTGT T ACGCAAATG A GAGTGAGCT	T ATTAGEACTY G CTEATECTT A CGGGGAGGA T CACAGETGE T TGEETGTGE C GETGGAGGG	GCCATTGGTO AAGTGTATCC GAGTACCGC TCGTGGAAG CCAACTGGGT GCAGTTCCGG	A AGTTTTTCC C TGGGCATCCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT G AGGAGTTTG	AATCATCGTC CTTCGACTGC TCGATGTGAC GGGTGGTCAG CGATGACTGG ATGTGAGTTCA GTCCATCGAT	420 480 540 600 660 720
65	ATTGGGATCA TCAGGGAAGT GGAGTCTCCC AATGCCCTGC AAGGGTCACT GATAACCTCC	A TTGCATTGA T ACAGATGTO G ATTGCAAAG C TCCAGGTGT T ACGCAAATG A GAGTGAGCT C CAGATGACA	T ATTAGEACTO G CTCATECTT A CGGGGAGGA T CACAGETGE T TGCCTGTGC C GCTGGAGGGG A GGTGACTGC	GCCATTGGT AAGTGTATO GAGTACCGC TCGTGGAAG CCAACTGGGT GAGTTCCGG ATTACACCAC	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCTT G AGGAGTTTG G AGGAGTTTG T CAGTATATG	AATCATCGTC CTTCGACTGC TCGATGTGAC GGGGGGTCAG CGATGACTGG A TGTGAGTTCA TGTCCATCGAT GAGGGAGGGA	420 480 540 600 660 720 780
65	ATTGGGATCA TCAGGGAAGT GGAGTCTCCC AATGCCGTGC AAGGCTCACT GATAACCTCA TGTGCCTCTC	A TTGCATTGA T ACAGATGTO G ATTGCAAAG C TCCAGGTGT T ACGCAAATG A GAGTGAGCT C CAGATGACA G GCCACGTGG	TATTAGCACTO CTCATCCTT CGGGGAGGA CACAGCTGC CTGCTGTGCC CGCTGGAGGG AGGTGACTGC TACCTTGCA	GCCATTGGT AAGTGTATO GAGTACCGC TCGTGGAAG CCAACTGGGT GCAGTTCCGG ATTACACCAC GTGCACAGCC	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT G AGGAGTTG T CAGTATATG T CAGTATATG T GTGGTCA A	AATCATCGTC CTTCGACTGC TCGATGTGAC GGGGGGTGTCAG CGATGACTGG A TGTGAGTTCA TGTCCATCGAT GAGGGAGGGA AAGGGGCTAC	420 480 540 600 660 720 780 840
65	ATTGGGATCA TCAGGGAAGT GGAGTCTCCC AATGCCGTGC AAGGGTCACT GATAACCTCAC TGTGCCTCTC AGCTCACGCC	TTGCATTGA' ACAGATGTO ATTGCAAAG TCCAGGTGT ACGCAAATG AGAGTGAGCT CAGATGACA GCCACGTGG TCGTGGGTG	f ATTAGCACTO G CTCATCCTT A CGGGGAGGA T CACAGCTGC T TGCCTGTGGC C GCTGGAGGGG A GGTGACTGC T TACCTTGCA G AAACATGTC	GCCATTGGT AAGTGTATC GAGTACCGC TCGTGGAAC CCAACTGGGT GCACTCGGA TTACACCAC GTGCACAGCC TTGCTCTCG	A AGTTTTTCC C TGGGCATCCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT; G AGGAGTTTG T CAGTATATG T GTGGTCA C AGTGGCCCT	AATCATCGTC ACTICGACTGC TCGATGTGAC GGGTGGTCAG CGATGACTGG ATGTGAGTTCA GGCCATCGAT GAGGGAGGGA GAAGGGCTAC GCAGGCCAGC	420 480 540 600 660 720 780
65 70	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCACG AATGCCGTGG AAGGGTCACTC CACCTCTTGG TGTGCCTCTC AGCTCACGCI ACTGCTGCACACCI ACTGCTGCACCI ACTGCTCACCI ACTGCTGCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTGCACCI ACTGCTCACCI ACTGCTGCACCI ACTGCTCACCI ACTGCTCACCACCI ACTGCTCACCI ACTGCTCACCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTCACCI ACTGCTCA	TTGCATTGA' ACAGATGTO ATTGCAAAG TTCCAAGGTGT ACGCAAATG AGAGTGACCT CAGATGACA GCCACCTGG CCACCTGGG ATCGTGGGGC ACGCGTACCC	T ATTAGCACTO C CTCATCCTTT C CCGGGAGGA T CACAGCTGC T TGCCTGTGC C GCTGGAGGGA A GGTGACTGC T TACCTTGCA T TACCTTGCA A CACAGCTG A CCTGTGCGG A TGACTTGTA	GCCATTGGT AGGTACGC TGGGTACGC TCGGGAG CCACTGGGT GCACTGGGT GCACAGCC TTGCACAGCC TTGCTCTGG GGGCTCTGTC CCTCCCCAAGC CCTCCCCAAGC	A AGTTTTTCC TGGGCATCCL G AGCTGATAG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT G AGGAGTTTG T CAGTATATG T GAGTATATG C AGTGGCCCC AGTGGCCCC T CATGGACCA	ATTCATCGTC CTCGACTGC CTCGACTGC CTCGATGTGAC CGGTGGTCAG CGGTGACTTCA TGTCCATCGAT GAGGGAGGGA AAGGGCTAC GTGGATCATC GTGGATCATC GTGGATCATC CCAGGTGGGT CCAGGCCAGC CTCGATCATC CCAGGTGGGT	420 480 540 600 660 720 780 840 900 960 1020
	ATTGGGATCH TCAGGGAAGT GGAGTCTCCC AATGCCGTGG AAGGGTCACT GATAACCTCC CACCTCTTGG TGTGCCTCTT AGCTCACGCI CTTCAGTTCC ACTGCTGCC ACTGCTGCC ACTGCTGCC	TIGCATTGA' T ACAGATGTO ACAGATGTO TOCAGGTGT ACGCAAATG ACGCAAATG ACGCAAATG ACGCAAATG ACGCACTGG TCGTGGGTG ACGCCTACC CACTGGGTACC	T ATTAGCACTY G CTCATCCTTT G CTGATCCTTT G CGGGGGAG T CACAGCTGCT T TGCCTGTGCC G GTGAAGGG T TACCTTGCA G AAACATGTC A CCTGTGCGA C TGACTTGTA A TCCAGCCCC	GCCATTGGT AGTGTATO GGAGTACCGC TCGTGGAAG CCAACTGCGT ATTACACCAC GTGCACAGCC CTTGCTCTGG GGCTCTGTC CCTCCCCAAG A TCCCACTGA	A AGTTTTTCC C TGGGCATCCU G AGCTGATAGG T GTGTCCGGG A CCATGTGCTT T CCCAAGCTT G AGGAGTTTG T GTGGTC\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\	ATCATCGTC CTCGACTGC CTCGATGTGAC GGGTGGTCAG CGGTGATCACTGG CGGTGATCACTGG GTCCATCGAT GTCCATCGAT GAGGGAGGGA AAGGGGCTAC GGCAGGCTAC GGCAGGCTAC GCAGGTGGT TCCAGGTGGGT TTGCATCACCAC	420 480 540 600 660 720 780 840 900 960 1020
	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCACC AATGCOGTGC AAGGGTCACC GATAAACCTCI CACCTCTTGG TGTGCCTCTT AGTTCAGGCI ACTGCTGCACC ACTGCTGCACC ACTGCTGCAACTACC AGCAAGTACC AGCAAGTACC AGCAAGTACC AGCAAGTACC	TIGCATTGA' TACAGATOTO A CAGATOTO A CAGATOTO A CAGTOATO A CAGTOATO A CAGTOACCT C CAGATOACCA G GCCACGTGG A TCGTGGGTA C CAGGCTACC C CAGGCTACC C TGTTGGACA A AGCCAAAGA	T ATTAGEACTY C CTCATCCTTT A COGGGAGGA T CACAGCTGC T TGCCTGTGCC G GTTGGAGGGG A GGTGACTGC T TACCTTGCA G AAACATGTC A CCTGTGCGG A TGACTTGTA A TCCAGCCCC G GCTGGCCA	G GCCATTGGT:  AAGTGTATO G GAGTACCGC T TCCTGGAAG C CAACTGGGT G CAGTTCCGG G TGCACAGCC C TTGCTCTGG G GGCTCTGTC C GGCTCTCCCAAG A TCCCCCAAG A TCCCACATTG	A AGTTITTO C TGGGCATCC G AGCTGATAGG T GTGTCCGG A CCATGTGCT T TCCCAAGCT T GCGTATATG T CAGTATATG T GTGGTC A TCACGCCC T CATGGACCA C TGAGGACA C TTATGAAGC TTATGAAGC	ATCATCGTC CTTCGACTGC TTCGATGTGAC TGGGTGTCAG TGTGAGTTCA TGTGAGTTCA TGTCATCGAT GAGGGAGGA AAGGGCTAC GTGAGTCAGC TGTGAGTCAGT TGTGAGTTCA TGAGGAGGA AAGGGCTAC TGGAGCAGC TGGATCATC TGTGATCATC TGCCGGCCA TGGCCGGCCAC	420 480 540 600 660 720 780 840 900 960 1020 1080 1140
70	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCACC AATGCCGTGG AAGGGTCACT GATAACCTCT GGCTCACGCI CTTCAGTTCC ACTGCTGCACCT ACTGCTGCACCT ACTGCTGCACCT ACTGCTGCACCT ACTAGCTTCC ACTAGCTTCC AGCAGTTACC CTCACCTTC	A TTGCATTGA' ACAGATGTO ATTGCAAAG TCCAGGTGT ACGCAAATG CAGATGACA CAGATGACA CAGATGACA GCCACGTGG A TCGTGGGTG CAGATGACA CAGAGCTACC CACTGTGTTT CTGTTGGACA AGCCAAAGA AAGCAAAAGA AATGAAAATGA	T ATTAGEACTY C CTCATCCTT A COGGGAGGA T CACAGCTGC T TGCCTGTGC C GCTGGAGGG A GGTGACTGC T TACCTTGCA GAACATGTC A CCTGTGCG A TGACTTGTA A TCAGCCCC G GCTGGCAG T CCAGCCCCT T CCAGCCCTT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCT T CCAGCCCT T CCAGCCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCCT T CCAGCCT T CCAGCCT T CCAGCCT T CCAGCCCT T CCAGCCT T CCAGCCCT T CCAGCCT T CCACCCT T CCAC	G GCCATTGGT:  AAGTGTATO  GAGTACCGC  T TCGTGGAAG  C CAACTGGGT  A TTACACCAC  G TGCACAGCC  C TTGCTCTCG  G GGCTCTGTC  C CTCCCCAAG  A TCCACTTG  T GACATCGCC  G TGCCTGCC  G TGCTGCCC  C TGCCCCAAG  C TGCCCCAAG  C TGCCCCAAG  C TGCCCCAAG  C TGCCCCCAG  C TGCCCCCAG  C TGCCCCCAG  C TGCCCCCCCCCC  C TGCCCCCAG  C TGCCCCCCCCC  C TGCCCCCCCC  C TGCCCCCCCCC  C TGCCCCCCCCC  C TGCCCCCCCCCC	A AGTTITTOM C TIGGEOATCO G AGCTGATAGG G AGCTGATAGG T GTGTCCGG A CCATGTGCT T TCCCAAGCT G AGGAGTTG T CAGTATATG T GTGGTCC\(\lambda\) C AGTGGCCCT A TCACGCCCC T CATGAACA G TGGAGAAGA C TTATGAAGC A ACTCTGAAG A ACTCTGAAG A	ATTCATCGTC CTCGACTGC CTCGATGTGAC CGGTGGTCAG CGGTGGTCAG CGGTGGTCAG CGGTGGTCAG CGGGGGGGAGGGGA	420 480 540 600 660 720 780 840 900 960 1020
	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCTCGG AATGCGTGG AAGGGTCACT GATAACCTCI CACCTCTTGG TGTGCCTCTC AGCTCAGGCI CTTCAGTTCC AGCAGAGTACC CTCACGTTCC GATGGAAAAA	A TTGCATTGA' T ACAGATGTC T ACAGATGTC T ACAGATGTC T ACGCAAATG A GAGTGAGCT C CAGATGACA T CCAGGTGC T CCAGTGCC C AGGGCTACC C ACTGGTTC C TGTTGGACA A GCCAAAGA A AGCCAAAGG T TGTCCTGGA T TGTCTGGACA	### ATTAGEACTY ### COGGGAGGA ### COGGGAGGAG ### COGGGAGGAG ### COGGGAGGAG ### COGGGAGGAGA ### COGGGAGGAGA #### COGGGAGGAGA #### COGGGAGGAGA #### COGGGAGGAGA #### COGGGAGGAGA #### COGGGAGGAGAGAGGAGAGAGGAGAGGAGAGGAGAGGAG	G GCCATTGGT: T ANGTGTATO C GAGTACCGC T TCGTGGAAG G CAACTGGGT G TGCACACCC TTGCTCTGG G GGCTCTGTC C CTCCCCAAG A TACACCCT T GACATCGC G TGCACTGC G TGCACTGC G TGCACTGC G TGCACTGC G TGCACTGC G TGCACGCC G TGCACGCC G TGCACGCC G TGCACCCCACG G GGGGCCACA	A AGTTITTO C TOGGCATCO G AGCTGATAGG T GTGTCCGG T CAGTGTCT T TCCCAAGCT G AGGAGTTTO T CAGTATATO C AGTGCCCC A TCAGGCCCC G TGGAGAAGA C TTATGAAGC A ACTCTGAAG G AGATGAAG G	ATCATCGTC CTTCGACTGC TTCGATGTGAC TGGGTGTCAG TGTGAGTTCA TGTGAGTTCA TGTCATCGAT GAGGGAGGA AAGGGCTAC GTGAGTCAGC TGTGAGTCAGT TGTGAGTTCA TGAGGAGGA AAGGGCTAC TGGAGCAGC TGGATCATC TGTGATCATC TGCCGGCCA TGGCCGGCCAC	420 480 540 600 720 780 840 900 960 1020 1080 1200 1200
70	ATTGGGATCA TCAGGGAAGT GGAGTCACC AATGCCGTGG AAGGGTCACC GATAACCTCTGG TGTGCCTCTAGTTCC ACTCTGCGC CTTCAGTTCC ACTGCTGCACC CTAGTTTCC AGCAAGTAAC CTCACCTTC GATGGAAAAA CCTGTCCTG GTGACAGTTAC GTGACAGTTCC GATGGAAAAA CCTGTCCTG	A TTGCATTGA' T ACAGATGTO ATTTGCAAAG T TCCAGGTGT ACGCAAATG AGGGTGAGCT CCAGTGGT AGGCAACGGG ATCGTGGGT CAGGCTACC ACTGGTTT CTGTTGGACA AGCCAAAGA ATGCAAAATGA TGTGCTGGA AGCCAACGG GGATCACCGGG AGGCAACT GGGGAAATCAAGCGG AGGCAACT GGGAAATCAAGGG GGATCATCT	### ATTAGEACTY  ### COGGGAGGA  ### COGGGCAA  ### COGGCCAA  ### COGGCCCAT  ### COCCCTCCAA  ##	G GCCATTGGT  T ANGTGTATO  GAGTACCGC  T TOTTGGAAG  C CACTGGGT  G TGCACAGCC  C TTGCTCTGG  G GCCTCTGC  C TTCCCCAAG  A TCCACTTG  G AGCATCGCC  G TGCACTGGCC  G TGCCTGCCC  G GGGCCACA  G TTCCACG  G TGCTGCCC  G GGGCCACA  G TTCCCACG  G TTCCCACC  G TTCCCCACC  G TTCCCCC  G TTCCCCC  G TTCCCCC  G TTCCCACC  G TTCCCCC  G TTCCCCC  G TTCCCCC  G TTCCCCC  G TTCCCCC  G TTCCCCC  G TTCCCC  G TTCCC  G TTCCCC  G TTCCCC  G TTCCCC  G TTCCC  G TTCCC  G TTCCCC  G TTCCCC  G TTCCC	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT G AGGAGTTG T CAGTATATT T CAGTATATAT T CAGGCCC A TCACGCCCC T CATGACA G TGGAGAAGA C TTATGAAGC A ACTCTGAAG G AGGATCGGA G GGAATCTGGA G GCTACCTGA	ATCATCGTC CTCGACTGC CTCGATGTGAC TGGGTGTCAG TGTGAGTTCA TGTCGATTCA TGTCCATCGAT GAGGGGGGA GAAGGGCTAC GGCAGCCAGC TGTGGATCATC TCCAGGTGGT TGTCTACCAC TGCCGGGCCA AGACTTCCCC GTGACCCTCC CACACAGGAC CGGGGCAC CCACAGGGAC CGGGGCAC CGGGGCAC CGGGGCAC CGGGGCAC CGGGGCAC CCACAGGGAC CGGGGCAC CGGTGGCGTGC	420 480 540 660 720 780 840 900 1020 1080 1140 1200 1320 1380
70	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCTCGG AATGCGTGG CACCTCTTG GGTCACCTCT AGCTCAGTCC ACTCTCAGTCC ACTGCAGCA CTAGGTTCCC AGCAAGTACC CTCACGTTCC GATGGAAAAA CCTGCTCCTG GGTGACGGC GTGACGGC GACGACAGC GACGAAAAA	A TTGCATTGA' T ACAGATGTC T ACAGATGTC T ACAGATGTC T ACCAGATGTC T ACGCAAATG A GAGTGACA T CCAGGTGT C CAGATGACA T CCAGGTACC C ACGGTACC C ACTGGTTC T GTTTGGACA A AGCCAAAGG A ATGAAATGA A TGTAAATGA T GTTTGGACA C G GCATCATCT C TGTTTGGACA C G GCATCATCT C TGTTGGACA C ACAGGGGGC C G GCATCATCT C AGGGGGACA C AGGGGGACA C AGGGGGACA C AGGGGGACA C ACAGGGGGCAC C AGGGGGACA C ACAGGGGGCAC C AGGGGGACA C ACAGGGGGACA C ACTGAATGAT C AGGGGGACA C ATTGAATGAC C AGGGGGACA C AGGGGGACA C ATTGAATGAC C AGGGGGACA C ATTGATGATGAC C AGGGGGACA C ATTGATGATGATGAC C AGGGGGACA C ATTGATGATGATGATGATGATGATGATGATGATGATGATG	### ATTAGEACTY ### CONTROL OF THE PROPERTY OF	G GCCATTGGT: T ANGTGTATO C GAGTACCGC T TCGTGGAAG G CAACTGGGT G TGCACAGCC C TTGCTCTG G GGCTCTGTC C CTCCCCAAG A TACACCACT G TGCACTGCC G TGCACTGCC G TGCTGCC G TGCTGCC G TGCTGCC G TGCTGCC C TCGCGC C CTCGCGC C CTCGCGC C CTGGGTGC C CTGGGTGC C CTGGTGTC C CTGGTGCC C CTGGTGTGT	A AGTTITTOO C TOGGCATCO G AGCTGATAGG T GTGTCCGGG A CCATGTCCT T TCCCAAGCT G AGGAGTTTO T CAGTTATAT G TGGGTCC A TCAGGCCCC T CATGGACA G TGGAGAAGA C TTATGAACC A CTCTGAAG G AGGATGGAC A ACTCTGAAG G AGGATGGAC A AGTCTGCA G GCTACCTGA C C AAGAGAGA C TAACACCC AAGAGAGAGA C AAGAGAGAGA C AAGAGAGAGA	ATCATCGTC ACTTCGACTGC TOGATGTGAC TOGATGTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTCAC TOGATCACC TOGATCACCAC TOGACCACAGGAC TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACAGGACA TOGACACACAGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGACA TOGACCACAGACA TOGACCACAGACA TOGACCACAGACA TOGACCACACACACACACACACACACACACACACACACACA	420 480 540 660 720 780 840 900 960 1020 1140 1260 1380 1440
70	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCATCA AATGCOTTGG AATGCCTCTTGG TGTGCCTCTTG AGCTCACGCI CTTCAGTTTCA ACTGCTGCAC CTAGTTTCCA GGAGAAAATAC CTCACGTTCC GATGGAAAAA CCTGTCCTG GTGTACGGT TTAGTGCGGA	A TTGCATTGA' T ACAGATGTO ATTGCAAAG TTCCAAAG TTCCAAAG TTCCAAAG AGAGTGAC GGCAACGCG ACTGTGGTG CAGGCTACC CACTGGTT CTGTTGGACA AGCCAAAG AAGCCAAAG AAGCCAAAG AAGCCAAG CGGACAAG AAGCCAAGG GGCAACG GGCAACG GGCAACG GGCAACG GGCAACG GGCAACG GGCAACG GGCAACG GGCACACG GGCACACG GGCACACG GGCACACG GGCACACG GGCACCAGC GCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GGCACCAGC GCACCAGC GCACCACC	### ATTAGEARTY  ### CONTROL OF THE C	G GCCATTGGT: I ANGTGTATO GAGTACCGC T TCOTGGAAG G CAACTGGGT G CAGTTCCGG G TGCACAGCC C TTGCTCTGG G GGCTCTGT C CTCCCCAAG A TCCCACTG G GGCCCACG G TGCACGCC G GGGCCACA G ATTCCACG G CTCCGCGC G CTGCCCGCC G CTGCCCGCCC G CTGCCCGCCCCCCCCCC	A AGTTTTTCC C TGGGCATCC G AGCTGATAGI T GTGTCCGGG A CCATGTGCTT T TCCCAAGCT T TCCCAAGCT T CAGTATATG T GTGGTCC A TGAGGCCT T CATGAGCCC T CATGACCA G TGAGACACA C TTATGAACC A ACTCTGAAG G AGGATGAG A AGATCTGC A AGATCTGC A AGAGAGGA G TGAACAACC A AGAGAGGA G TGAACAACC A AGACAACC A TGAACAACC A TGAACAACC A TGAACAACC A TGAACAACC A GATCTGCA A GATCACAACC A TGAACAACC A TGAACAACAACC A TGAACAACAACC A TGAACAACAACC A TGAACAACAACAACC A TGAACAACAACAACC A TGAACAACAACAACC A TGA	ANTORTOGIC CTCGACTGC CTCGACTGC CTCGACTGC CGGTGGTCAG CGGTGGTCAG CGGTGGTCAG CGGTGGTCAG CGGTGGTCAG CGGCGCAG CGGCGCAG CGGCGCAG CGGCCAG CGCGCCCCC CGCGCCAG CCCCCCCC	420 480 540 660 720 780 900 960 1020 1080 1240 1320 1320 1340 1500
70	ATTGGGATCA TCAGGGAAGT GGAGTCACCG AATGCCGTGG AATGCCTCTG GATAACCTCT CACCTCTTGG TGTGCCTCTAGTTCC ACTGCTGCA ACTGCTGCAC CTAGTTTCCC AGCAGTAAC CTCACCTCC GATGGAAAAA CCTGTCCTG GTGACGGCA GTGACGGCA GACAGCTGC TTAGTGCGGAAAAAAAAAA	A TTGCATTGA' T ACAGATGTO ATTTGCAAAG T TCCAGGTGT ACGCAAATG AGGGTGAGCT CCAGTGGT AGGCAACAG ATCGCGGGG ATCGTGGGG ATCGTGGGG ATCGTGGGA AGCCAAAG AGCCAAAG ATGAAATGA ATGAAATGA GTGCTGGGA ACCCAGGGG ACGCGGGACAGGT CCAGCAGGGGACAGGT CAGCCAGGCAACAGCG AGCACAGCT CAGCACAGCA	### ATTAGEACTY  ### COGGGAGGA  ### COGGCAGGA  ### COGGCAG  ### COGGGGAG  ### COGGGGAG  ### COGGGGAG  ### COGGGGAG  ### COGGGGGGGC  ### COGGGGGGGC  ### COGGGGGGGC  ### COGGCAGGAG  ### COGGGGGGCC  ### COGGCAGGAG  ### COGGC	G GCCATTGGT  T ANGTGTATO  GAGTACCGC  T TOTTGGAAG  C CACTGGGT  G TGCACAGCC  C TTGCTCTCG  G GGCTCTGC  C TCCCCAAG  A TCCACTTC  G GGGCCACA  G TGCACTCCC  G TGCACTCCC  G TGCCCCAC  G TGCCTGCCC  G TGCCTGCCC  C TCCCCACC  C TCCCCACC  C TGCCCCACC  C TGCCCCACC  C TGCCCCACC  C TGCCCCCC  C TGCCCCCC  C CTCCCCCCCC  C CTCCCCCCCC  C CCCCCCCC	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT G AGGAGTTG T CAGTATATG T CAGTATATG T CAGTATATG T GTGGTCC A TCACGCCCC T CATGACAG G TGGAGAGA G TGGAGAGA G TGGAGAGA G TATGAAGG C TATGAAGG G AGATCTGA G AGATCTGA G GCTACCTG G GCTACCTG G GCTACCTG G GAGAAGA G TGAACAGG G TAAACAGG G TAAACAGG G TGAACAGG G TGAACG G TGAACAGG G TGAACAGG G TGAACAGG G TGAACAGG G TGAACAGG G TGAACAGG G TG	ATCATCGTC ACTTCGACTGC TOGATGTGAC TOGATGTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTCAC TOGATCACC TOGATCACCAC TOGACCACAGGAC TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACCACAGGACA TOGACCACAGGACA TOGACACACAGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGGACA TOGACCACAGACA TOGACCACAGACA TOGACCACAGACA TOGACCACAGACA TOGACCACACACACACACACACACACACACACACACACACA	420 480 540 660 720 780 840 900 900 1080 1140 1200 1320 1380 1440 1560
70 75	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCATCG AATGCCTCTG GATAACCTCT AGCTCACGC AGCTCACGC AGCTCACGC AGCTCACGC AGCAGTACC CTAGTTTCC AGCAGGTAC CTAGCTTCC GATGGAAAA CCTGTCCTG GACAGGTAC CTGGTACGGT TAGTGCGA ACCCGTGCA TTAGTGGAA ACCCGTGCA TTAGTGGAA ACCCGTGCA TTAGTGGAA ACCCGTGCA TCACCTTGCA TGAAGAGGA TCCCTGGAA	A TTGCATTGA' T ACAGATGTO ATTGCAAAG TTCCAAGGTT T ACGCAAATG A GAGTGAGCT C CAGATGACA A TCGTGGGTG C AGGGCTACC C ACTGTGTT C TGTTGGACA A AGCCAAAGA A ATGCAAATGA A ATGCAAATGA G GGACAAGA C CAGGGGGACA C CGGCCAGC C CAGGGGGACA C CGGCCAGC A CCTCCTTCC A CGGGCACAC C CGGCCAGC C CGACCAGCT C CTCCCTGT/	### ATTAGEACTY A COGGGAGGA T CACAGCTGC* C GCTGGAGGG A GGTGATGC G AACATGTC A CTGTGCGG A TGACTTGTA A TCAGCCCC G GCTGGAGGC A TGACTTGTA C TCAGCCCC C GCTCGGCAA C GCTCGCAG C GCTCGCTT C CCCCTCCAT G GGGGGGGC T GGACTGGAT GGACTGGAT GGACCTGGT GGACCTGGAT GGACCTGCAT GGACCTGGAT GGACCTGCAT GCACCTGCAT GCACCTCCAT GCACCTCAT GCACCTCCAT GCACCTCAT GCACCTCCAT GCACCTCAT GCACCTCCAT GCACCTCCAT GCACCTCCAT GCACCTCCAT GCACCTCCAT GCACCTCCAT GCACCTCCAT GC	G GCCATTGGT I ANGTGTATO G GAGTACCGC I TCOTGGAAG C CAACTGGGT G CAGTTCCGG G TGCACAGCC C TTGCTCTGG G GGCTCTGTC C CTCCCCAAG A TCCCCTGG G TGCACTGG G TGCACTGG G TGCCTGGCC G GGGCCAAG C CTTGGCCC G GGGCCAAG C CTTGGCCC C CTGGGCC C CTGGTGTGT C TGCCAGAG C CACGAGCAC ACGAGCAC ACGACCAC ACCAC ACCA	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGG A CCATGTGCT T TCCCAAGCT T TCCCAAGCT T CAGTATATG T GTGGTCC T CATGGACCA G TGGAGACA G TGGAGACA ACTCTGAAG G AGGATGGA AGATCTGC C AGGAGAGA G AGGATGAG G AGGATGAG G AGGATGAG G AGGATGAG G AGGATGAG G AGGATGAG G TGAACAAG G TGAACAAG TGAAGAGG TGAACAAG C TGATGAGAG C C ACCTTGA	ATCATCGTC ACTTCGACTGC TCGATGTGAC TGGGTGTCAG TGGGGTGTCAG TGTCATCGAT TGAGGAGGAG AAGGGCCAGC TGTGATCATC TGTCATCATC TGCAGGCCAGC GCAGCCAGC TGGGGTCAC AGACCTCCC GCAGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CCACAGGGCCAGC CGCGGCCAGC CGCGGCCAGC CCACAGGGCC CGGGTGGCAGC CGGGTGCAGC CTGGGGTTAC CCACACCCGATC CCACACCCGATC CCCACCCGATC CCCACACCCCACC CCCACACCCCACC CCCACCCCACC CCCACCCACC CCCACCCCACC CCCACCCACC CCCACCCCACC CCCCACCC CCCACCCCACC CCCACCCCACC CCCCACC CCCCACCCCACC CCCCACCC CCCCACC CCCACCCCACC CCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCC CCCCACCCCACC CCCCCACCC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCCACCC CCCCACC CCCCCACCC CCCCCACC CCCCCACC CCCCACCC CCCCCACC CCCCCC	420 480 540 660 720 840 900 1020 1080 1140 1260 1320 1320 1440 1500 1660
70 75	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCACCG AATGGCTCAC GATAACCTCT GATAACCTCT CACCTCTTGG TGTGCCTCACGCT CTCAGTTCC ACTGCTGCAC ACTGCTGCAC GGAGAAAAA CCTGTCCTG GATGGAAAAA CCTGTCCTG GATGGAAAAA CCTGTCCTG TCAGCGCACCAC TCAGGAGAAAA CCCGTTCC TCAGGGAAAAA CCCGTTCC TGAGGGAAAAA CCCGTCC TCAGGGAAAAA CCCGTCC TCAGGGAACAC CGGCACCAG	A TTGCATTGA' T ACAGATGTO ATTTGCAAAG T CCCAGGTGT' ACGCAAATGA AGAGTAGACT CCAGTGTT' CCAGTGTGT' CCAGTGTGT' CCAGTGGTGA' ATCGTGGGTGA' ATCGTGGTGTG' CCACTGGTTGCAAAATGA' AGCCAAAGA AGCCAAAGA' AGCCAAAGA' CCGCAGGGGACAAGC' ACGCCGGCAGGCTACC' ACGCCGGCAAGACAACT ACGCCGCAGGCAAGC' ACCCCGTGT' AGCAGGGCAAACT AGCAGCGCCAGGT' AGCACGAGCT' AGCCCCGTGT' AGCAGGCCAGCT' AGCAGGCCAGGCT' AGCAGGCCAGCT' AGCAGGCCAGCT' AGCAGGCCAGGCT' AGCAGGCCAGCT' AGCAGGCCAGCT' CCCGTGTT' CCAGGCCAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCG	### ATTAGEACTY  ### COGGGAGGA  ### COGGCAGGA  ### COGGCAG  ### COGGGAGG  ### COGGCAG  ### COGGCAG  ### COGGCAG  ### COGGGAGG  ### COGGCAGG  ### C	G GCCATTGGT  T ANGTGTATO  G GATTACCGC  T TOTTGGAAG  G TGCACAGCC  T TGCTCTCG  G GGCTCTGTC  C TCCCCAAG  A TCCACTTC  G GGGCCACA  A TCCACTTC  G GGGCCACA  C TCGCCGCC  G TGCTGCCC  G TGCTGCCC  G TGCCTGCCC  G TGCTGCCC  C TGCCAAG  A TCCCACTTC  C TGCCAAG  A TCCCACTTC  C TGCCAGAC  C TTTCCACAC  C CTGCGCC  C CACGAGCAC  A TTCCTACC  C ACGAGCAC  C ACGAGCAC  C CCTCCATC  C CCTCCCATC  C CCTCCATC  C ACGAGCAC  C ACGAGCAC  C CCTCCCATC  C CACCAGCACC  C CCTCCCATC  C C CTCCCATC  C C C C C C C C C C C C C C C C C C	A AGTTTTTCC C TGGGCATCC G AGCTGATAGG T GTGTCCGGG A CCATGTGCT T TCCCAAGCT G AGGAGTTG T CAGTATATG T CAGTATATG T CAGTATATG C ATGGCCC T TATGACCA G TGGAGAGA G TGGAGAGA G TATGAGG C TATGAGG C TATGAGG G GCTACCTG AGACAGG G GCTACCTG G TGAACAGG C TGATGAGAGA G TGAACAGG C TGATGAGAGA C TGAGAGAGA G CTACCTG C AAGAGAGG G TGAACAGC C AGACAGC C TGATGAGAGA C TGATGAGAGA C TGATGAGAG C TGATGAGAG C TGATGAGAG C TGATGAGAG C TGATGAGAG C ACCCTTGG C TGATGAGAG C ACCCTTGG C TGATGAGAG C TGATGAG C TGATGAG C TGATGAGAG C TGATGAGAG C TGATGAGAG C TGATGAGAG C TGATGAG C TGATG	ATCATCGTC ACTTCGACTGC TOGATGTGAC TOGATGTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTCAC TOGATGACTAC TOGATCACTCAC TOCACACACACACACACACACACACACACACACACACACA	420 480 540 600 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1620 1620
70 75	ATTGGGATCA TCAGGGAAGT TCAGGGAAGT GGAGTCTCGG AATGCGTGG AATGCGTCAC GATAACCTCT CACCTCTTG TGTGCCTCTC AGCTCAGGCI CTTCAGTTCC AGCAAGTACC CTCACGTTCC GATGGAAAAA CCTGTTCCTG GGTACGGCI TTAGTGGGAAAA CCCGTTCC TGAAGAGGA ACCCGTGCT TGAAGAGGA TCCCTGGA CGGCACCAG GCTGCTTTT	A TTGCATTGA' T ACAGATGTO T ACAGATGTO T ACAGATGTO T ACGCAAATG A GAGTGAGCA A GAGTGAGCA C ACAGCTGG A TCGTGGTT C TGTTGGACA A AGCCAAAGG G GCATCACCG G GGATCACCCG G GGATCACCC C ACGCGGGC A ATGCCAAGG G GCATCATCT C AGGGGGACA C C TCCCTTCC A CGGGCACAGC T AGCAGGCC T GGTTTTTTG T AGCAGGCC T TGTTTTTTTTT C ATTTTTTTTT C ATGCATGAT C TGCATGGACAAC C TCCCGTGT T AGCAGGCC T GTTTTTTTTTT C TAGCAGGCC T GTTTTTTTTT C TAGCAGCT C TGCAGGTGAT T AGCAGGCC T GTTTTTTTTT C TAGCAGCTC C TGCAGGTGAT T AGCAGGCC T GTTTTTTTTT C TAGCAGCCC C TCCAGTGT T AGCAGGCC T GTTTTTTTTT C TAGCAGCCC C TCCAGTGT T AGCAGGCC T GTTTTTTTT C TAGCAGCCC C TCCAGTGT T AGCAGGCC T TGTTTTTTT C TAGCAGCCC C TCCAGTGT T TAGCAGCCC T GTTTTTTT C TAGCAGCCC C TCCAGTGT T TAGCAGCCC T GTTTTTTT C TAGCAGCCC C TCCAGTGT T TAGCAGCCC T GTTTTTTT C TAGCAGCCC C TCCAGTGT T TAGCAGCCC T TGTTTTTT TGT TTTT TGT TTTT TGT TTT TGT TTT TTT TGT TTT TT TTT	TATTAGEACTY C CTCATACTT A COGGGAGGA T CACAGCTGC C GCTGGAGGG A GGTGACTGC A CCTGTGCA G AAACATGCA T CACGCCC G GCTGGAGCA T CACGCCT T CCCCCTTCA C CTCAGGAT G GTCCCTT T GCATCG G GGGGGGCC T TGGCATCG T GGACTGGA T GACCTGCA T GACCTGCA T TGGCATCG T TGGCATCG T TGGCATCGA T TTTTTGAGG AAAGAGCCA T TTTTTGAGC T CTCAGCTGCA T TTTTTGAGC T TTTTTGAGC T CCCCCTCAT T TTTTTGAGC T CACAGCTGCA T TTTTTGAGC T TACGATCGA T TTTTTGAGC T TTTTTGAGC T TGCATCGA T TTTTTGAGC T TTTTTGAGC T TTTTTGAGC T TGCATCGCAT T TTTTTGAGC T TTTTTGAGC T TGCATCGCAT T TTTTTGAGC T TTTTTGAGC T TGCATCGCAT T TTTTTGAGC T TTTTTGAGC T TTTTTGAGC T TTTTTGAGC T T TTTTTTGAGC T T TTTTTGAGC T T TTTTTTGACC T T TTTTTGAGC T T TTTTTTGAGC T T TTTTTTGACC T T TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	G GCCATTGGT:  T ANGTGTATO  G GATTACCGC  T TCGTGGAAG  C CACTGGGT  G TGCACAGCC  C TTGCTCTG  G GCTCTGTC  G TGCACAGCC  G TGCACAGCC  G TTCCCCAAG  A TCCCCATG  G GCCTCTGC  G TGCTGCC  G TGCTGCC  G TGCTGCC  C TCGCTGCC  C CTGGGGGC  C CTGGGGGC  C CTGGGGGC  C CACGAGAC  C CACGAGCAG  C CACGAGCAGA  C CCTTCCATC  C CCCTTCCATC  C CCTTCCATC  C CCTGGTGTGT  C CCCTTCCATC  C CCTGCTGCAC  C C C C C C C C C C C C C C C C C C	A AGTTTTTCC C TGGGCATCC G AGCTGATAGI T GTGTCCGGG A CCATGTGCT T TCCCAAGCT T CAGTATATG T CAGTATATG T CAGTATATG T CAGTATATG T ATCAGCCC A TGGACCA C TGATGACCA C TGATGACA C TGACTACT C AAGACAGC C TGATGACACA C TGAGAGAGA C TGATGACACA C TGATGACACA C TGATCACCC C TCTTGGC C TGATCACCC C TCTTGGC C TGATCACCC C TCTTGGC C TGATCACCC C TCTTTGC C TGATTCCC C TCTTTGC C TCTTTGC C TGTTTGC C TGTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTGC C TGTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTGC C TGTTGC C TGTTGC C TGTTTGC C TGTTGC C TGTTTGC C TGTTTC C TGTTT C TGTT C TGTTT C TGTT C TGT C TGTT C TGT C TGTT C	ATCATCGTC ACTTCGACTGC TCGATGTGAC TGGGTGTCAG TGGGGTGTCAG TGTCATCGAT TGAGGAGGAG AAGGGCCAGC TGTGATCATC TGTCATCATC TGCAGGCCAGC GCAGCCAGC TGGGGTCAC AGACCTCCC GCAGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CGCGGCCAGC CCACAGGGCCAGC CGCGGCCAGC CGCGGCCAGC CCACAGGGCC CGGGTGGCAGC CGGGTGCAGC CTGGGGTTAC CCACACCCGATC CCACACCCGATC CCCACCCGATC CCCACACCCCACC CCCACACCCCACC CCCACCCCACC CCCACCCACC CCCACCCCACC CCCACCCACC CCCACCCCACC CCCCACCC CCCACCCCACC CCCACCCCACC CCCCACC CCCCACCCCACC CCCCACCC CCCCACC CCCACCCCACC CCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCACCC CCCCACCCCACC CCCCCACCC CCCCACCCCACC CCCCACCCCACC CCCCACCCCACC CCCCCACCC CCCCACC CCCCCACCC CCCCCACC CCCCCACC CCCCACCC CCCCCACC CCCCCC	420 480 540 600 660 720 780 840 1020 1080 1140 1260 1320 1440 1500 1620 1680 1740 1800

	CCTCAGCTTC	CCCAGTAGCT	GGGACCACAG	GTGCCCCCCA	CCACACCCAA	CTAATTTTTG	1920
	TATITITAGT .	AGAGACAGGG	TTTCACCATG '	TTGGCCAGGC	TGCTCTCAAA	CCCCTGACCT	1980
	CAAATGATGT	GCCTGCTTCA	GCCTCCCACA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
5	CCTAGCCTCA	CGCTCCTTTC	TGATCTTCAC	TAAGAACAAA	AGAAGCAGCA	ACTTGCAAGG	2100 2160
,	ACATAACCAC	TEATTERCE	ATCTGGTTTT	CICICOGGG	ACCURACTOR	AAAAGACGCA	
						ACCAGAACCA	
	AACCCACCCT	TTCTACTTCC	AAGACTTATT	TTCACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
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			TACATTTGCT				60 120
20	CCCAATGAAG	AGCAGCAGAA	AGACGTCACA AGAACAGATC	AATATATOO	AAGACTGGTC	AGACTTTGCT	180
20	CTTTGGTGGG	AACAGAAGCA	TIGCTGGCTT	CTGAAAACCC	ACTGGACCCT	GGACAAATAT	240
	GGGGTCCAGG	CAGATGCAAA	GCTTCTCTTC	ACCCCTCAGC	ATAAAATGCT	GCGCCTTCGT	300
	CTGCCGAATT	TGAAGATGGT	GAGGTTGCGA	GTCAGCTTCT	CAGCTGTGGT	TTTTAAAGCT	360 420
25			CCTGAATATT			GGAACCCATA	480
23	ATTGAAGATA	TTCTAAACCT	GGAGAGTTCT	CCAACAGCTT	CAGGTTCATC	AGTAAGTCCT	540
	<b>GGTTTATACA</b>	GTAAAACCAT	GACCCCTATA	TATGACCCCA	TCAATGGAAC	ACCAGCATCA	600
			TGACAGCCCT				660
30			CCCAGAAGCA TGCAGGTTGG				720 780
50			GCTGCTCTTA				840
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	CTCTTAGAAG	AAATTGATTG	CACAGAGGAA	GAAATGTTGA	TCTTTGCAGC	TCTACAGTAC	960
35	CACATTAGCA	AACTGTCGTT	GTCTGCTGAA	ACACAGGATT	TIGCAGGCGA	GTCCGAGGTT AAAAGCGGAC	1020 1080
33						ATTATTTAGG	1140
	CCCAAGAAGT	TACTACCAAF	AGCTTTCAAA	CAATATTGGT	TTATCTTTAA	AGACACATCC	1200
	ATAGCATACT	TTAAAAATA	GGAACTTGAA	CAAGGAGAAC	CACTAGAAAA	ACTAAATCTT	1260
40						AATCAAGTTA	1320
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	TCCTACCAGC	CAGAGGTCCT	CAACATCCTT	TCATTTCTGA	GGATGAAAA	CAGGAACTCT	1500
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	GACATTCTGG	GAGTTTCAT	TAACAGGTTG	ATTAAAATTO	ATGCAGCCAG	CGGGATTCCA	
						AACCCGGCAG	1860
50	GTGGTCATCG	AGTTTGACC	AAACGTCTTT	ACTGCTTTCA	CCTGCCTGAC	TGCAGATTGC	1920 1980
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60						GTAGGAGGAA	
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						G AGTGTCAGTC A GCACCATAGC	
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						C GACCATAGAG C TGCTAGCCTG	
70						A TAAGGGCCCT	
	ACTACACTG	G CTTTTTTAG	G CTTAGAGAC	A GAAACTTTA	G CATTGGCCC	A GTAGTGGCTT	840
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	COGCOCGGGG AGCCAGCGGG GCTGAGCGGG GCCAGGGTCT GAACCCAGAT TTCCCAGACT AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCAG	120 180
	ACGTCCGCGG CCGCTGCCCT CCTCGCCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC	240
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5	TRANSPORT CARCTERIST ACTORDOCT GOTTCCCTGG GGCCACATCC ACAGTGGCTG	360
	CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCCTGGAA CCCTGGCCAT GACCAAGACC	420 480
	ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG	540
	TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT	600
10	GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTCAGC	660
	COCATOCITA CIATOCICIE AACTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC	720
	ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG	780 840
	CAGAAGGAGG CTATTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA	900
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	TTCCACTIGAA TIGATIGAAGIT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA	1020
	AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCCTTGGAGT TTTCTAACTG	1080
	TGAAAGGAAA TCCATCATCT TCAGTGGAAG ACCATATTGA ATATCATGGA CATCGAGGCT	1140 1200
20	CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG	1260
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	TATGCAATCG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG	1380
	AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT	1440
25	GCCGGAGCTA CCGTGTACGG TTCCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA CCATTGACAC CAATGTGAAC AGCACCATTC TGAACTTGGA GGATAATGTA CAGTCATGGA	1500 1560
23	AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT	1620
	TOTAL TOTAL TOTAL TOTAL TOTAL COLOR CONTROL CANADAGA CONTROL C	1680
	TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC	1740
20	TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC	1800 1860
30	ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT TTAAGGCAGC ACACTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC	1920
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35	TCACGGAAGA TGGGCCGGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCCTTGTCA	2160 2220
	AGTCTGGAAC CCTCCTCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCACAGAGG ACTCCTACCC GGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT	2280
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	GGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC GGCCGTTCCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCCCTGA	2520 2580
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	AGAACAGCTT GTTTGTTGGC GAGAGTGGCA ACGTGGGGAC GGAAATGATG GACAATAGGA	2820 2880
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5	ACTICTOACCE TETECECAAC TITITITIAAA AATTITAACC AGAAAATAAA GATAGTTAAA TECTAAGATA GAGATTAAGT CATGGTTTAA ATGAGGAACA ATCAGTAAAT CAGATTCTGT CCTCTTCTCT GCATACCAGG AATTTATAGT TAAGGATCCC TITGGTGTGA GGGTAGAAAA CCTCACCAAC TECACCAGTG AGGAAGAAGA CTGCGTGGAT TCATGGGGAG CCCTCACAGGC GCCACGCAGA CAGCCTCTGGG TGGGGTGCCC TTTAAGGACC GTTCTTTCCT TACTGGTCT GATAACAACA GCGAACCGTG CAGTGTGCAT TTTAAGACCT GGCCTGGAAT AAATACGTTT TGTCTTTCCC TC	2760 2820 2880 2940 3000 3060 3072
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20	AGAATGGT TOANTITH CTIGGTC ACCOUNTS AND AGACTCO ACCOUNTS AND ACTOCOTA ANTIGGTT TITCTTTGTA ANATGGGTT ATGAACAGTA CCTACTTCAA AATGTGTTTG TGAAGATTAA AAAAGTTAAC ATAAAGAGTT TAGAAGAGTG TCTGGCATAT TGTGCTCAAT AAGTGTTTAT TTATTTATTG CTGAATAAAC CAGTAATTA ATTAGTAT	480 540 598
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30	1 11 21 31 41 51	60 120
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70	CAAAGTCTCC CGATGCTGGG AGCAAAGCAG AGAGCTCCGA GAACAGCCGC ACTGAGATGG AAGGTCGGAG CAGTCTCCCT TCCACGTTTA TCCGAGCCCC GCCGACCTAT GTCAAGGTTG AAGTTCCTGG CACATTTGTG GGACCCTCGA CATTGTCCCC AGGGATGACC CCTTTGTTAG CAGCCCAGCC ACGCCAACA GCCAAGCAAC ATGGCTGAC ACGGTGTGG AAGAACTTCT	2520 2580 2640 2700
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10	THACTICTICE TOGGATCTIA TIGTATIGGA GGGTGACCAC CCTGGGGATG GGGTGTTGGC AGGGGTCAAA AAGCTTATIT CTTTTAATCT CTACTCAC GAACACATCT TCTGATGATT TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA AGTATATIGC CCAACTCTAT GTTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT	480 540 600 660 720 777
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		1020
	Windwardt Gerechere variantity erecettion graperiose erecettion	1080 1140
		1200
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	dallinetor resource to the second sec	

		3720
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50	Seg ID NO: 26	DNA Som	10000				
50	Nucleic Acid			equence			
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	1		1		 	 	60
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65	CAAGATAGG G	AAAACTTIC TACTTTTAT	GGAAGACTT	T TATGTGGTT	T TTACTCACT	C TTCATCTCAG	720
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70						G TGCAGCCTAC	1020
. •	TAAATCAGAA T	GAAAATAGA	AGTACAAGA	T TATAAACAA	A ATGCAATCA	A ACTITICITA	1080
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75						AAAAAAAA A	
, ,						A GAAATTATTT	1380
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80	Seq ID NO: 2	9 004 5-	mence				
00	Nucleic Acid			sequence			
		1	21	31	41	51	
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	TOUCHGOAGC T	GIGIIIGA	- CHOOTCATT	I WCCWIOCI		T CAACAGTATG	

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	GCTCCAAAGG						120
	TCCACCACAG :						180
	GGAGATAGTT (240
5	CATTATTCAC						300 360
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				CTCTCTATTA			1500
25				TAGTCTTCAC			1560
	TTACATTTAG	TATTTTCCCA	AT				1582
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				TICTICTIGG			60
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Seq ID NO: 33 DNA Sequence

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35	CCTTTTTCTT	TATTCTTTTT	GCTTTGAGA	AAGAGAATG1	GATTTAAGAG	TAATAATTTG	1920 1980
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50						C ATTGCATTTG T TGTTGAATTT	2760 2820
50						G ATCAATACAG	2880
		GCCCTGCTT					2907
	Sea ID NO:	34 DNA Se	mence				
55	Nucleic Ac	id Accessi	on #: NM_00	3979.2			
	Coding sec	quence: 254 11	1357 21	31	41	51	
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	GAACAGAGC	C TACTCTCA	AG AGGAAATC	AC TCAAGGTT	TT GAAGAGAC	AG GGGACACGCT	1200
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	AGCAGGGCCA	GCACGCCGTC	AGCGCCTACC	TGGCTGATGC	: CCGCAGGGCC	CTGGGGTCCG	1200
	CGGGCTGTAG	CCAACTCTTC	GCAGCGCTGA	CAGCCTATAR	GCAAGACGAC	GACCTCGACA	1260
	AGGTGCTGGC	TGTGTTGGCC	GCCCTGACCA	CTGCAAAGCC	AGAGGACTTC	CCCCTGCTGC	1320
	ACAGGTTCAG	CATGTTTGTC	CGTCCACACC	CACAAGCAGCG	CTTCTCACAG	ACGTGCACAG	1380
55	ACCTGACCGG	CCCCCCTAC	CCGGGCATGC	AGCCACCGG	ACCCCAGGAG	GAGAGGCTTG	1440
-	CCCTCCCTCC	TOTOCTTAC	CACAGGGCT	CCCAACCAGO	CCCCTCACGG	TCCGAGAAGA	1500
	000000000000000000000000000000000000000	CCBCACCAA	ATCTCCTCC	TOOTTAGACE	GAGGCCAGCA	GGGACTGTGG	1560
	CCGGGAAGAC	- CCAGAGGAA	AICICOICC	· receimence	ACCTCCCCAC	GGCCTGCAG	1620
	GGGCGGGCGG	TUAUGATGU	r GOICCOAGC	. AGICCICAG	CONCORCO	ACGGGAGCTC	1680
60	CATCIGAGIG	GGGTGAGCE	CATOGGAGA	2 ACA1000100		CACCOCACCAC	1740
oo	CGGGCGGGCC	CCTCTCAGC	GGCTGTGTG	r GCCAGGGCTC	- CECCECCO	GACGTGGTGC	1800
	CCTTCCAGTG	CCCTGCCTG	r GACTTCCAG	C GCTGCCAAG	CIGCIGGLA	CGGCACCTTC	1860
	AGGCCTCTAG	GATGTGCCC	A GCCTGCCAC	A CCGCCTCCAC	3 GAAGCAGAGC	GTCATGCAGG	
	TCTTCTGGCC	: AGAGCCCCA	G TGAGTGCCC	A CGGAGGCCC	C CAGCACACCO	AACGTGGCTT	1920
	GATCACCTGC	CTGTCCAGC	r ctggtgggc	C AAGAACCCA	C CCAACAGAA1	AGGCCAGCCC	1980
65	ATGCCAGCCC	GCTTGGCCC	G CTGCAGGCC	T CAGGCAGGC	G GGGCCCATGC	TTGGTCCCTG	2040
	CGGTGGGACC	GGATCTGGG	CTGCCTCTG.	A GAAGCCCTG	A GCTACCTTG	GGTCTGGGGT	5100
	GCGTTTCTGC	GAAAGTGCT	T CCCCAGAAC	T TCCCTGGCT	C CTGGCCTGTG	AGTGGTGCCA	2160
	CAGGGGCACC	CCAGCTGAG	CCCTCACCG	G GAAGGAGGA	G ACCCCCGTG	GCACGTGTCC	2220
	ACTTTTAATO	AGGGGACAG	GCTCTCTAL	T AAAGCTGCT	G GCAGTGCCC	A GGAAAAAAA	2280
70	AAAAAAA						2268
70	AAAAAA						
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		: 38 DNA Se					
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	TOCCCAGGO	GACCGGGGG	CAAAGGAGGT	G GCATGTCGG	T CAGGCACAG	C AGGGTCCTGT	60
	GTCCCCCC	G AGCCGCGCT	C TCCCTGCTC	C AGCAAGGAC	C ATGAGGGCG	C TGGAGGGGCC	120
	ACCOUNTED.	CTCCTCTCC	C TOGTOTTO	C CCTCCTCC	C CIGCIGCO	G TGCCGGCTGT	180
80	WOOCC101C	G GCAGAAACA	C CCACCTAC	C CECCCOCO	C GCAGAGACA	G GGGAGCGGCT	240
UU	ACGCGGGT	a aramanaca	c concerne		te consumerous	C CACACACOCC	
	GGTGTGCGC	C CAGIGCCCC	CAGGCACCI	1 IGIGUAGUG	~ ccoloccoc	C GAGACAGCCC	300
	CACGACGTG	T GGCCCGTGT	C CACCGCGCC	A CTACACGCA	G TTCTGGAAC	T ACCTGGAGCG	360
						G CTTGCCACGC	
	CACCCACAA	C CGTGCCTGC	C CCTGCCGC	C CGGCTTCTT	C GCGCACGCT	G GITICIGCTI	480

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	GGAGCACGCA TCGTGTCCAC CTGGTGCCGG CGTGATTGCC CCGGGCACCC CCAGCCAGAA	540
	CACGCAGTGC CAGCCGTGCC CCCCAGGCAC CTTCTCAGCC AGCAGCTCCA GCTCAGAGCA	600
	GTGCCAGCCC CACCGCAACT GCACGGCCCT GGGCCTGGCC CTCAATGTGC CAGGCTCTTC	660 720
5	CTCCCATGAC ACCCTGTGCA COGCTGCAC TGGCTTCCCC CTCAGCACCA GGGTACCAGG AGCTGAGGAG TGTGAGCGTG CCGTCATCGA CTTTGTGGCT TTCCAGGACA TCTCCATCAA	780
,	GAGGCTGCAG CGCTGCTGC AGGCCCTCGA GGCCCCGGAG GGCTGGGGTC CGACACCAAG	840
	GGCGGGCCGC GCGCCCTTGC AGCTGAAGCT GCGTCGGCGG CTCACGGAGC TCCTGGGGGC	900
	GCAGGACGGG GCCCTGCTGG TGCGGCTGCT GCAGGCGCTG CGCGTGGCCA GGATGCCCGG	960
	GCTGGAGCGG AGCGTCCGTG AGCGCTTCCT CCCTGTGCAC TGATCCTGGC CCCCTCTTAT	1020
10	TTATTCTACA TCCTTGGCAC CCCACTTGCA CTGAAAGAGG CTTTTTTTTA AATAGAAGAA	1080
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20	GGCATGGAGC CACCGGGACC CCAGGAGGAG AGGCTTGCCG TGCCTCCTGT GCTTACCCAC	180
	ACCCTTCCC AACCAGGCCC CTCACGGTCC GAGAAGACCG GGAAGACCCA GAGCAAGATC	240
	TOSTCOTTCC TTAGACAGAG GCCAGCAGGG ACTGTGGGGG CGGGCGGTGA GGATGCAGGT	300
	CCCAGCCAGT CCTCAGGACC TCCCCACGGG CCTGCAGCAT CTGAGTGGGG CCTCTAGGAT	360 420
25	GTGCCCAGCC TGCCACACCG CCTCCAGGAA GCAGAGCGTC ATGCAGGTCT TCTGGCCGGA GCCCCACAAG GACCATGAGG GCGCTGGAGG GGCCAGGCCT GTCGCTGCTG TGCCTGGTGT	480
23	TGGCGCTGCC TGCCCTGCTG CCGGTGCCGG CTGTACGCGG AGTGGCAGAA ACACCCACCT	540
	ACCCCTGGCG GGACGCAGAG ACAGGGGAGC GGCTGGTGTG CGCCCAGTGC CCCCCAGGCA	600
	CCTTTGTGCA GCGCCCGTGC CGCCGAGACA GCCCCACGAC GTGTGGCCCG TGTCCACCGC	660
	GCCACTACAC GCAGTTCTGG AACTACCTGG AGCGCTGCCG CTACTGCAAC GTCCTCTGCG	720
30	GGGAGCGTGA GGAGGAGGCA CGGGCTTGCC ACGCCACCCA CAACCGTGCC TGCCGCTGCC	780
	GCACCGGCTT CTTCGCGCAC GCTGGTTTCT GCTTGGAGCA CGCATCGTGT CCACCTGGTG	840
	CCGGCGTGAT TGCCCCGGGC ACCCCCAGCC AGAACACGCA GTGCCAGCCG TGCCCCCCAG	900 960
	GCACCTTCTC AGCCAGCAGC TCCAGCTCAG AGCAGTGCCA GCCCCACCGC AACTGCACGG CCCTGGGCCT GGCCCTCAAT GTGCCAGGCT CTTCCTCCCA TGACACCCTG TGCACCAGCT	1020
35	GCACTGGCTT CCCCCTCAGC ACCAGGGTAC CAGGAGCTGA GGAGTGTGAG CCTGCCGTCA	1080
33	TOGACTITGT GGCTTTCCAG GACATCTCCA TCAAGAGGCT GCAGCGGCTG CTGCAGGCCC	1140
	TCGAGGCCCC GGAGGGCTGG GGTCCGACAC CAAGGGCGGG CCGCGCGGCC TTGCAGCTGA	1200
	ACCTROCTOR GORGETCACG GAGCTCCTGG GGGCGCAGGA CGGGGGCGCTG CTGGTGCGGC	1260
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40	TCCTCCCTGT GCACTGATCC TGGCCCCCTC TTATTTATTC TACATCCTTG GCACCCCACT	1380
	TGCACTGAAA GAGGCTTTTT TTTAAATAGA AGAAATGAGG TTTCTTAAAA GCTTATTTTT	1440
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45	Nucleic Acid Accession #: NM_000593	
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45	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51 	_
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45 50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51	120
	Nucleic Acid Accession #: NM_000593 Coding sequence: 1657591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG TATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGGT TATCTAGTGA GCAGGCGGC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCG	120 180
	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51	120
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50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480
50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540
50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540
50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51 GEACGAGGG TGTGCGTGGT GGGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG AACTAGGCT TATCTAGTGA GCAGGAGGAC GCTTTCGATT TCGCGAGGG CCACTTTTCG AACTAGGCG TATCTAGTGA GCAGGAGGAC GCTTTCGATT TCCCAGAGGCCCCC TTCCCTCCC CAGCGCCAG ACCAGCCCTG TTCCGGACT TCCCGACGCCAG ACCAGCCCGG GACCGCCTC CCGCGCCTC TCCCCCC CAGCGCCAG ACCAGGCCG GACCGCGAC GCTGCCTC CCGCAGCTC CCGCGCCTC TCCCCCC TCCCCCC TCCCCCCC TCCCCCCC CAGCGCCCCC ACCCGGCCCC GACCGGCCCC CCGGACCT TCCCCCCC TCCCCCC TCCCCCCC TCCCCCCC TCCCCCC	120 180 240 300 360 420 480 540 600
50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540
50	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540 600 660
50	Nucleic Acid Accession #: NM_000593 Coding Bequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAATAG TCTGGGCAG CCACTTTTGG AAGTAGGGT TATCTAGTGA GCAGGGGGGC GCTTTCGATT TCGCTTTCCC TAAATGGCT GAGCTTCTCG CCAGGCGAGG ATCAGCCTGT TCCTGGGAGT TTCCGAAGGC CCCGCCCTGG TTCCTCCCC CAGCCGCAG TAGGGGAGGA CTCGGCGGTA CCCGAGCTT CAGGCCCAC CAGGCCCCAG AGAGTCCCAG ACCCGGCCG GACCGGGAGG CGTGCCCAC CAGGCCCCAC TACTGCTCC CCGCGGGTCC CCCTGCTCC CCGGACCGC GTGCCCCCC TACTGGTGC CACCGCGCTC CCCTGCTCC CCGGACCG GTGCCCCCC TCCTGGTGC CACCGCGTC CCCTGCTCC CCGGACCG GTGCCCCCC TCCTGGTGC CACCGCGTC CCCTGCTCC TCAGGCAAC GGTTCGCCCC CACCGCGGC CTCGGGGTCC TCAGGGCAAC GGTTGCCCCC AGGACGCGCACGCCTC CCGGGGTCC TCAGGGCAAC GGTTGCCCCC AAGACCGAGTCC CACGGCTCG CTGCTCCTT TGAAGCCAAT AGCTGCGGAA ACCCGCCCCGGGACGC TTCGAGGC TTCGAGGCTA AGCCTGGGC ATAGCACCAG CCAGGCTCG CTGCTGCTT TGAAGCCAAT AGCTGCGGAA ACCCGCGGGCCCC CGGGCCCCC CGGTCCCCCC GGTCCCCCC ATAGCACCAG CCAGGCCCC TTCCGAGGAC TAGCTCCACGC CTGGCCCCC ATAGCACCAGCCCC CCGGGACCCC TCCGGGGACCC CTTCGGTTC CAGGCCCCCC CCGCCCCCCCCCC CCCCCCCCC CCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540 660 720 780 840 960
50	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGGCGTGGAT GGGAAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGCAGCC GCTTTCGATT TCGCGAGGC CCACCCCTCG TTCCCTCCCC CAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTCG TTCCCTCCCC CAGCGCCAG TAGGGAGGA CTCGGCGAT CCCGAGGCTT CAGGCCCCAC GGGGCCGG AGAGTCCCAG ACCCGGCCGC GACCGGAACG GCTGCAGGT GCCAATGGCT AGCTCTAGGT TACTCGTACT TCTGCCGGC TGGGTGCTC CCGGAGCTT TCTCCACTGC TGGGGACAG TACTGCTACT TCTGGCCGAC TGGGTGCTC CCGGAGCTC CAGCGCCTC AAATGCCT AGCCCTAGGT CCGTGCTCC CACCGCCCTC CCACTGCTC TCCGCATGC CTGGGACAG ACCCGGGCTC CACCGCCTT CCACTGCT TCCGCATGC GGTGGCCCC AAATTCTCCC TGCTGGTGC CACCGCCCTC CACTGCTC TCAGGGCACG GCTGCCCCC AAATTCTCCC CCGTGCTCCT GCTGGGGGCTC TCGGGTGCT TGAAGCCATT AGCTGCGGAA ACCCAGGTGC CAGGGCTGC TGGCTGCTT TGAAGCCATT AGCTGCGGAA ACCCAGGTCC CAGGGCTGC TGGCTGGAGCC CTGCGCCCCC CTTCGTTGTC AGAGGCGAA ACCCAGGTCC CAGGGCTGC CTGGCTGCACC TTCAGGGGA CTGGGTCGGGAAAACCCAGGCCCC GCTGCCCCCC CTGGGCTGC CCGCAGCTCC CGCAGCCC CTGGGGAACC AACTCAGGC CTTCGTTGT AGTTAGCACGGA AGGCCGCCT TGGAAACCCT GTGGTGCTC TTCTAGGCGG CTTCGGGTTC CAGAGGCCCC GCCCTCTCCTC TGGAAACCCT GTGGTGCTC TTCTCCTCTT TGGGAGAG CCCCTCGGCTC AGGCCGCCT TGGAAACCCT GTGGTGCTC TTCTCCTCTT TGGGAGAG CCCCTCCGCCTT TCTTTAGGGG CCGCCTCACT CACTGGGTCT TTCCCTCTTT TGGGAGAGT CCCCTCCCTCTTT TGGGAGAGT CCCCTCCCTCTTT TGGGAGAGT CCCTTCACTC TTTTTAGGG CCGCCTCACT CACTGGATTC TACAAAATGG CTCAGCCGAT ACCTTCACTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50 55 60	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGGT TATCTAGTGA GCAGGGGGGC GCTTTCGATT TGCGTTTCCC TAAATGGCT GAGCTTCTGC CCAGGGAGG TGAGCCTGT TCCTGGGAGT TTCCGAAGGC CCACCCTGG TTCCTCCCC CAGCCGCAG TAGGGGAGGA CTCGGCGGTA CCGGAGCTT CAGGCCCAC GGGGCCCG AGAGTCCCAG ACCCGGCCG GACCGGGAGG CGTGCCCCAC GGGGCCCGG AGAGTCCCAG ACCCGGCCG GACCGGGACG CGTGCCCCC CAGGGCCCCC TACTGGTGC CACCGCGTC CCACTGCTCC CCGGACCT TCTCGCATG CTGGGGACAC TCTGGTGCC CACCGCGTC CCACTGCTC CGGGACCGC GGTGCCCCCC AAGACCA CCGCGCCC CCCCGCGTC TCCGGGGTCT TCAGGCAAC GGTTCGCTC AAGACCAATGCC TCCTGGTGC CACCGCGTC CCACTGCTC TCAGGCAAC GGTTGCCCCC AAGACCAAAAACCAGGTC CCAGGCCTC TCCGGGGACAC GGTTGCCCCC CACCGCTGC CCACGGCTCT TCCAAGGCAAC GGTTGCCCCC AAGACCAAAACCAG CCACGCCCC GGTCCCCCC CCTTCCTCGTT TGCAAGACCAT AGCTGCGGCA CCGGCCTCGGGAACACCT TCCGAGGACAC CACCGCCCC GGTCCCCCC GGTCCCCCGGAATGCCC CCGCGCCTC GGCACCAC CCCCCCCCC CCCCCCCCC CCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 840 900 960 1020 1080
50 55 60	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TETGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCT TATCTAGTGA GCAGGCAGCC GCTTTCGATT TCGCGTAGGC CCACTCCCC CCACGCGCAGG ACCACCTGT TCCTGCGACT TCCGGAGCT TCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGGCGTGGAT CGGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGGC GCTTTCGATT TCGCTGAGGC CCACGCCTGG TCCCCCC CAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTG TTCCCTCCC CAGCGCCAG ACCAGGCCGG GACCGGACG GCTGCAGGC CCCGCCCCCG TCCCCCC CAGCGCCCAG ACCAGGCCGG GACCGGACG GCTGCAGGC CCCGCCCCCG TCCCCCC CAGCGCCCAG ACCAGGGCGC CCCGGCCTC CCGGAGCTT CTCCCATGG TCCCCCCC CAGCGCCCC CCCGGGGTC CCCTGCCTC CCGGAGCCTC CTCCCATGC TCCCCCCC TCCTGCTCC CCCCGGGGTC CCACTGCTC CCGGAGCCTC AAATGCT ACCCTAGGT AACGCACGC CACCGGGCTC CACTGCTC TCCGGACCG GCTGCCCCC ATATTCTCCC TCCTGGTGCC CACGGGCTG CCACTGCTC TCAGGCACG GCTGCCCCC ATATTCTCCC CCCTGCCTGG CTGGGGGCC CCACTGCTC TCAGGCAAA GCCCAGGAAA ACCAGGTCC CAGGGCTG CTGGCTCCT TGAAGCCATT AGCTGCGGCA CTGGGCTGG ATAGCACCAG GCTACTGCAC TGGGGAAGC CACCTACCGC CTTCGTTGTC AGGGCCGGA ACGGCACTGCC CGCAGCACC CTGTGGCACA AACTCAGCGG CTTCCTGGTTC AGGAGCCACG AGGCCGCTC TGCAACCCT GTGCGTCGC TTCTAGGCTG CCTCGGGTTC CAGGACCCCC GCCCTCCCTC TGCAACCCT GTGCGTCGC TTCTAGGCTG CCTCGGGTTC CAGGACCCCC GCCCTCCCTC TGCAACCCT GTGCGTCCCC TTCTAGGCTG CCTCGGGTTC CAGGACCCCC GCCCTCCCTC TGCATCTCA TGCGTGGTCC TCTCCTCTTT TGGGAGGT CCCTCCGCGTTC AGGGCGGCTC TGCAACCCCT GTGCGTCCCC TTCTAGGCTG CCTCGGGTTC CAGGACCCCC GCCCTCCCTC TTCCTGGTC CTGGTGGTCC TCTCCTCTT TGGGGAGGT CCCATCCAT TCTTTACGGG CCGCCTCACT GACTGGATT TCCACACACCC ATGCCCAGCA TACCTCACT ACCGGAACTTAAC TCTCATGTCC ATTCTACCA TACCACAGCA ATCCACGAACACCC AGGGCGACTT ACCTTCATTCCACA ACGGGATCTA TAACAACACAC ATGGGCCACG TTCCAACGAA CCCACACGAACCACGT AACATCATGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1200
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCGT TATCTAGTGA GCAGGGCGGC GCTTTCGATT TCGCTTTCC CTAAATGGC GAGCTTCTGC CCAGGGAGG TGAGCCTGT TCTGGGACT TCCGGAGG CCACCTTTTCG AAGTAGGCGT CCAGGGAGG ATCAGCCTGT TCCTGGAGCT TCCGAGGC CCAGCCTGG TCCCTCCCC CAGCCGCAG ACCGGGCGG GCCTGCCTCC CCGGAGCTC CAGGCCCCAC GCGGGCCGC TACTGCTCC CCGGGGGTC GCCTGCTCC CCGGACGCT CCACGGCCCAC GCGGGCCAC TACTGCTTCT CTCGCGGAC TGGGTGCTC CCGGACGCT CAGGCCCCAC GCGGGCACA CCGTGCTCC CCGGGGTC CCACTGCTC CCGGACGCT TCTCGCATG CTGGGGACAA ACCCAGGTC CCACGGGTC CCACTGCTC CCGGACGCT GGGGCCCCAC GCGCCCCAC ACGCAGGCTC CCACGGGTC CCACTGCTC TCACGGCAAC GGTTGCCCCC AAGACCAAAA ACCCAGGTC CCACGGCTG CCACTGCTC TCACGGCAAC GGTTGCCCCC AGAGCCTACCCC CCTGCCCCC ATACTCCCCCGG ACTGCTCT TCCCAGAGC TGATCTCATG GGGGCCCC GGTCCCCGA ATAGCACAAG CCTACTCCAC TGGGGACAA AACTCGGGA CTTGCTTCACC CGCACTGCC GCACAGCCC CTGTGGCAAA AACTCGGGA CTTCCTGGTC CGGGACGCC CTCTGGTGC CCCGGGGTC CCAGGCCCC GGTCCCCGG ACGCCTCTCGCT GTCCTCGTC CTGGTGTCC TCACGGCACA CCCCGCGTC GGCCCCCGGCTC GCCCTCCCCC GCCCCCCC CACCGCCCC CCTCCCCCCC AGGCCCCC GCGCCCCCC CGCTCCCCCC CCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Acid Accession #: NM_000593 Coding sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGGGGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CAGGCTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGCAGCG GCTTTCGATT TCGCTGAGAGC CCACGCCCTG TCCCCCCC CAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCCGCCCTG TTCCCTCCC CAGCGCCAG ACCGGCCGG GACCGGAGAC GCGTCGAGGC CCCGCCCTG TTCCCTCCC CAGCGCCAG ACCGGCCGG GACCGGAACG GCGCCTCC CCGGACCTCC CCGGGGCCGG AGAGTCCCAG ACCGGCCCG GACCGGAACG GCGCCTCC CCGGACCTT TCTCGCATG CTGGGACAG TACTGCTACT TCTGCCGGC CGCTGCCTC CCGGAGCTC CCACGGCCCCA ATATTCTCCC TGCTGGTC CACGGGCTG CACTGCTC TCCGGACGC GTGGCCCCA ATATTCTCCC TGCTGGTGC CACGGGCTG CCACTGCTC TCAGGGCAG GCTGCCCCC ATATTCTCCC TGCTGGTGC CACGGGCTG CCACTGCTC TCAGGGCACG GTTGGCCCC ATATTCTCCC CCCTGCCGG ACTTGCCTTG TTCCGAGAGC TGAGCCATT AGCTGCGGAA ACCAGGTGC CAGGGCTG CTGGGTGCT TGAAGCCATT AGCTGCGGAA ACCAGGTGC CAGGGCTG CTGGGTGCT TGAAGCCATT AGCTGCGGAA ACCAGGTGC CAGGGCTG CTGGGTACC TGAGGCAAA AACTCAGGAG CCTCTGGGTG CCCTGCCCGC GCAGCAGCC CTGTGGCACA AACTCAGGG CCTCTGGGTC AGGGCGCTC TGCAAACCCT GTGGTGCAC AACTCAGCG CTTCGTGTTC AGTTATCCAG AGGCCGCTC TGCAAACCCT GTGGTGCC TTCTAGGCTG CTCGGGGTC CAGGAGCCCC GCCTCTCCCT TTCCTGGTC CTGGTGGTC TCTCCTCTT TGGGAGAG CCCTCCGGGTA ACGCAATTAAC TCTCATGTCA TGGGGAACT AACTCAGAG CTTCGGGAAACTCACT GTTTTTAGGG CCGCCTCACT GACTGGATT TACAAAATGG CTCAGCGAA TACTCCAT TCTTTAGGG CCGCCTCACT GACTGGATT TACAAAATGG CTCAGCCAA TACCCAAGCA TTCCACTCCAT GGGCTTCTC TGCGCCAGGA ACGGGTTTT TCCAACAGAC ATGCCAAGGA TACATCCAT GGGCTTCTC TGCGCCAGGAA ACGGAGTTTT TCCAACAGAA CCAGCAAGTT TACCAACACC ATGGCCCAAG TACACACCT TACACACACC ATGCCCAAGAACACC TCCACCAGAA ACCCAAGACA CCAGACAGT TACACACACC ATGGCCAAGTT TCCAACACAC ATGCCAAGGAA CCAGAAGTTTT TCCAACAGAA CCAGCAAGTTTT TCCAACAGAA CCAGCAAGTTTT TCCAACAGAA CCAGCAAGTTTT TCCAACAGAA CCAGCAAGGCAAG	120 180 240 300 360 420 480 540 660 720 780 960 900 910 1080 1140 1200 1260
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCGT AACTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCGT TATCTAGTGA GCAGGGCGGC GCTTTCGATT TCGGTTTCCC CTAAATGGC GAGCTTCTCG CCAGGGAGG ATCAGCCTGT TCCTGGAGCT TCCGAGGC CCAGCCTGG TCCCTCCCC CAGCCGCAG ACCGGGCGG GACGGGGACG GCTGCCCAG GACGCCCCAG GACGGGGCCCAG GACGGGGGCCAG GACGGGGACG GCTGCCCCAG GACGGGGCCCAG GACGGGGGCCCAG GACGGGGGCCCAG GACGGGGTC CCACGGGGTC CCACGGGTC CCACGGGTCC CCAGGGGTCC CCAGGGGTCC CCACGGGTC CCACTGCTCC CCGGAACGC GTGCCCCCAC AGGCCCCAC ATATTCTCCC TCCTGGTGCC CACGGGGTC CCACTGCTC CCAGGACGA GGTGCCCCCA ATATTCTCCC CCGTGCTCTC CACGGGGTC CCACTGCTC TCAGGGCAAC GGTGGCCCCA AGCCCCCAC ACGGCCCCAC CCCCTGCTCC CCCGGACGCC CCTTGCCTCC CCGGGGCCCCAC ACTGCCTCTC CCCTGCTCC CCAGGGCCAAC GGTTGCCCCC CACGGGCCCCAC CCCGGGGCCCC CCGGTCCCCCC CCGTGCCCCC CCGGCCCCCAC ACTGCCTCTC TCCGAGGACAA ACCCTACCCC CTTCGTTGTC AGGTTAGCACACAC GCTACTGCAC TGGGGAACAA AACTCGGGAG CTTCTGGGT CCCGGGGGCCCC GGGCCCCCAC GCCCCCCCAC GCCCCCCCAC GCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1250 1320 1340
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540 600 660 720 1080 1020 1140 1200 1250 1380 1440 1500
50 55 60 65 70	Nucleic Acid Accession #: NM 000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGCT ACCAAATAG TCTGGGCAGG CACTTTTGG AAGTAGGGT TATCTAGTGA GCAGGGGGGC GCTTTCGATT TCGCTTTCC CAGGCCGCG GAGATTCTCAG AAGTAGGCGT TATCTAGTGA GCAGGGGGGGC GCTTTCGATT TCGCTAGGC CAGGGCAGG TAGGGGAGG CTCTGGGGGAT TCCGGGAGG CCAGCGCAG ACCGGGCCG GACCGGGGTC CCGGGGGTC CAGGCGCCC GACCGGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CCGCGGGTC CACCGCGCC CACCGCGCTC CACCGCGTC CCCGGGGCTC CACCGCGCTC CACCGCCTC CACCGCGTC CCACGGCCCC CACCGCGTC CACCGCGTC CACCGCGTC CACCGCGTC CACCGCGTC CACCGCGTC CACCGCCTC CACCGCGTC CACCGCCTC CACCGCGTC CACCGCCTC CACCGCGCTC CACCGCGTC CACCGCTC CACCGCGTC CACCGCTC CACCGCTCC CACCGCTC CACCGCCTC CACCGCCAC CACCCCCC CACCACCAC CACCCCCC CACCACACAC CACCAC	120 180 240 300 420 480 540 660 660 720 780 840 1020 1080 1140 1260 1320 1440 1560
50 55 60 65	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCG AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTG AAGTAGGCGT TATCTAGTGA GCAGGCGGCC GCTTTCGATT TCGGTTTCCC CTAAATGGC GAGCTTCTCG CCAGGGAGG ATCAGCCTGT TCCTGGGACT TCCGAGGCCCCG GAGCTCCCC CAGGCGAGG ATCAGCCTGT TCCTGGGACT TCCGAGGCT CAGGCCCCAG GACCGCGCG GACCGGCGCCG GACCGGCGCCG GACCGGCGCCG GACCGGCCCC CAGGGGTCC CCGGGGGTC CCAGGGGTC CCAGGGGTC CCACGGGGTC CACGGGGTC CACGGGTCC CACGGGGTC CACGGGGTC CACGGGGTC CACTGCTCC CACGGGCTC CACCGCCCC CACCGGCCCC CACCGGCCCC CACCGGCCCC CACCGGCCCC CACCGGCCCC CACCGCCCCC CACCGGCCCC CACCGGCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCCC CACCGCCCC CACCGCCCCC CACCGCCCC CACCGCCCC CACCGCCCCC CACCGCCCCC CACCCCCCCC	120 180 240 300 360 420 480 600 660 720 720 780 840 1020 1080 1140 1250 1320 1350 1440 1500 1620
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 420 480 540 600 660 720 1020 1020 1140 1200 1320 1380 1440 1560 1560 1680
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGGG TGTGCGTGGT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAATAG TCTGGGCAG CCACTTTTG AAGTAGGCGT TATCTAGTGA GCAGGCGCGC GCTTTCGATT TCGCTTTCCC TAAATGGC GAGCTTCTCG CAGGCGCAG ACCGGCCGG GCTGCTCCCC TCCGCGAGGT TCCGGAGGG CCACCTGGTC CAGGCGCAG ACCGGCCGG GACCGGGCTC TCCGGAGGT TCCGGAGGC CCAGCGCCAG ACCGGCCCG GACCGGGCGCAG GCCGACCGG GCCAATGGCT CAGGCCCCAG ACCGGCCCG GACCGGGCCCC CCGGAGCTC CAGGCCCCAC CAGGCCCCAC CAGGCCCCC CACGCGCTC CCCGGGGTCC CCGGGGCTC CACCGCCTC CCCGGGGCTC CACCGCCTC CACCGCGTC CCACTGCTC CCGGACCG GTGCCCCCC CACCGCTC CACCGCGTC CACCCCTCACCCCTC CACCCCTCACCCCTC CACCCCTCACCCCTC CACCCCTCACCCCTC CACCCCTCACCCTC CACCCCTCACCCCTC CACCCCTCACCCTC CACCCCTCACCCTC CACCCCTCACCCCTC CACCCCTCACCCTC CACCCTCACCCTC CACCCCTCACCCTC CACCCCTCACCCTC CACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACCCTCACC	120 180 240 300 360 420 480 540 660 660 720 780 840 1020 1080 1140 1250 1320 1440 1550 1620 1660 1740
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCAGG CCACTTTTGG AAGTAGGCGT TATCTAGTGA GCAGGGCGCC GCTTTCGATT TCGCTTTCCC CTAAATGGC GAGCTTCTCG CCAGGGAGG ATCAGCCTGT TCCTGGGACT TCCGAGGCCCCG GAGCTCTCCCC CCAGGCAGG ATCAGCCTGT TCCTGGGACT TCCGAGGCCCCG GAGCCTCCCC CAGGCCCAG ACCGGGCCG GACCGGGACG GCGCCCAGC CCAGGGCCCCC CAGGGGGCCC GCGGGGTCC CCGGGGCTC CCAGGGCTC CCGGGGCTC TCCTGGTCC CACGGGGTC CCACTGCTC CCGGACGCT TCTCGCATG CTGGGGACAG TACTGCTACT TCTCGCCGAC TGGGTGCTC CCAGGGCCCC GAGCCCCCC CACGGGCTC CCACGGGGTC CACCGGGTC CCACTGCTC TCCAGGCCAAC GGTGCCCCCC CCCCCCCGGGGTC CACCGGGTCC CCACTGCTC CAGGGCCAC GGTGCCCCC AGCCCCCC TCCTGCTGG CCACGGGGTC CCACTGCTC TCAGGGCAAC GGTTGCCCCC AGAGCCAC ACCAAGGTC CACGGGGTC CACCTGCTC TCAGGGCAAC GGTTGCCCCC AGAGCCAA ACCAAGGTC CACGGGGCC TGGCTGCTT TCAAGGCAAA ACCAAGGTC CCACGGGCCC TGGCTGCTC TCAAGGCAAC GGTTGCCCCC AGAGCCCCC GGGCCTCCGG GCTACTGCCT TCCGAGGAC ACCCTACCGC CTTCGTTGTC AGAGCCAAA ACCAAGGTC CCACGGGCCC TGGGGGACCA AACTCCGGGG CCTCTGGGT CCGGGGCCCC GGCACTGCC GCACAGGCC CTGGGGACAA AACTCCGGGG CCTCTGGGT CCCGGGGTC AGGCCGCC TGGAAACCCT GTGCGTCCC TCCACGCCC CTTCGTTGTC AGTTATCCAC AGGCGACTCC TGGAAACCCT GTGCGTCCCC TCCACGCGC CCTCGGGTC CAGGGCGCCC GCCTCTCGCT GTTCCTTGGTC CTGGTGGTC TCTCAGCCGAT ACCTTCACTC TCTTTAACGG CCGCCTCACT GACTGGGTC TCCACCTCAC TCCGCGGAAC ACCTTCCAT TCCTTGAGC CCCCCCACGA ACCGACAGC CTTCCACTCA ACCTTCACTC CAGACAAACCC GCCCCCACA ACCACACAA CACCACACAA ACCTTCACTC GGACTTCCT GCCCCAGGA ACCACACACA CACACAACAC ACCTTCACTC CCCGCACTAC GAGCACCC CTCACCTCA TCCCCCTAC AGCACAGCA ACCTTCCACTC GGCCTCACCT GCCCCAGGA ACCACACCAC TCCCCCTAC AGCACAGCA ACCTTCCACTC TCCTGGGAAC ACCACTACCTC CCCCTACCCTA GCCCACACACACA ACCTCCCTACCTT GAGCCACACAC ACCTACCCTA GCCCCTACCCTA	120 180 240 300 360 420 480 600 660 720 780 840 1020 1080 1140 1200 1350 1440 1500 1562 1680 1740
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51	120 180 240 300 360 360 420 480 540 600 660 720 1080 1020 1140 1200 1140 1320 1380 1440 1560 1680 1740 1880
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGGCACCAGG GCTGCTCCG AGATTCTCAG ATCTGATTTC CAGGCTTGCT ACCAAAATAG TCTGGCAGG CCACTTTTCG AAGTAGGCT TATCTAGTGA GCAGGCGGC GCTTTCGATT TGGCTTTCCC CTAAATGGCT GAGCTTCTCG CAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCGGAGGT GCCAATGGCT GAGCTCCCC CAGCGCCAG TAGGGAGGAG CTCGGCGGTA CCCGAGCTT CAGGCCCCAG CAGGCGCCAG ACCAGGCCGG GACCGGGAC GCTGCCCCC CGGGGCCCG GCCGCCCCC CGGGGCTC CAGCGCCCAG CACCGGCCCG GACCGGGAC GCGTCCCCC CGGGGCCCG CCCGGGCCCC CAGGCGCCCC CAGCGGCCCC CACCGGGTC CCCGGGGTC CCCGGGGCCC CGGGGCCCG CAGCGCCCCC CAGGCCCCAC CGGGGCCCC TACTGCTACT TCTCGCCGAC TGGGTGCCCC CGGGGCCCG GTGGCCCCG ATATTCTCCC CAGCCAGCCC CACCGGCCC CACCGGCCCC CACGGCCCC CACGGCCCC CACCGGCCCC CACCGCCCC CACCGCGCCC CACCGCCCC CACCACCAC CACCACCAC AACCCCACCAC CACCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1080 1140 1260 1320 1380 1500 1620 1680 1740 1860 1980
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCACG GCTGCTCCCC AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCACGG CCACTTTTGG AAGTAGGCT TATCTAGTGA GCAGGCAGCC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCAGCCCCAG GAGCCTCTCCC CAGCGCCAG ACCGGGCCG GACCGGGACG GCTCCGAGC CAGCGCCCA TAGGGGACG CCTGCCTCC CCGGAGCTT CTCGCCAGC AGAGTCCCAG ACCGGGCCG GACCGGGACG GCGCCCCCC CGGGGCCCG TACTCCTCC CCCGGGGTC CCCTGCCTCC CCGGAGCTT TCTCGCAGAC TCCTGGTCC CACCGGGTC CCACTGCTC CCCGGACCTT TCTCGCAGC GTGGGCCAG ACAGGTCC CACCGGCTC CACCGCGCTC TCCGCGACCTC TCTCGCAGC GTGGGCCCG CCTGCTCTG GCTGGGGCC TCGCGGTCT TCAGGCAACA GGTTGGCTCA GAGCGCAAC ACCAAGGTC CACGGGCTG CCACTGCTC TCCGGAACCC GTGGCCCCG ATATTCTCCC TCTGGTGCC CACGGGCTG CCACTGCTC TCAGGCAACG GTTGGCCTC AGGCCAAC ACCAAGGTC CACGGGCTG CCACTGCTC TCAGGCAACG GTTGGCTCA GAGCCGAAC ACCAAGGTC CACGGGCTC TCGGGGACG TCAAGGCAAC GGTTGGCTC AAGCCAACA ACCAAGGTCC CACGGGCTC TGGGGAAGC TCAAGGCAAC GGTTGGCTC AAGCCAACA ACCAAGGTCC CACGGGCTC TGGGGAAGC TCAAGGCAAC GGTTGCTTCA GAGCCAACA CCCACCAGG CCTTCCGT TTCCAGAACCC TTGGGTACC CTTGGGTTC CAGGCAACA CCGCACTTCCC CGCAGCACC TGGGGAACT AACCTCAACCA CTTGGGTTC CTTCGGTTTC AGTTATCCAG GCCCTCAGCT TGGAAACCCT TGCGTGGCC TTCCATCTCC CTTCGGTTTC AGTTATCAG GCCCTCAGCT TGGAAACCCT TGCGTGGTC TCTCCCTCT TCGGGAAGT CCCTTCCAT TCTTTACGG CCCCCCACT GACTGGATTC TACAAGAACA AACTCAGCACA TTGCACACACA AACTCACACA AACACACA AACACACA AACCACACA TAGCCAACAC AGGGCGGTT TCAACCACACA AACCACACA AACCACACA AACCACACA AACCACACACA AACCACACA AACCACACA AACCACACA AACCACACA AACCACACA AACCACACACACACACACACACACACACACACACACACAC	120 180 240 300 360 420 480 540 600 660 720 1080 1020 1140 1200 1140 1320 1380 1440 1560 1680 1740 1880 1920 1980
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCGT TACTGATTTC CACGCTTGGT ACCAAAATAG TCTGGGCAGG CCACTTTTCG AAGTAGGCGT TACTGAGGCAGG CCACTTTTCG CAAGCTTCTCG CCAGGGAGG ACCAGGT ACCAAAATAG TCTGGGCAGG CCACCTTTTCG AAGTAGGCGT TACTGAGGAG ACCAGGAGG ACCAGGCGCAG ACCAGGCGCAG ACCAGGCGCAG ACCAGGCAGG	120 180 240 300 360 420 480 600 660 720 780 840 1020 1080 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1860 1980 2040
50 55 60 65 70	Nucleic Acid Accession #: NM_000593 Coding Sequence: 1652591 1 11 21 31 41 51 GGCACGAGGG TGTGCGTGAT GGAGAAAATT GGCACCAGG GCTGCTCCCC AGATTCTCAG ATCTGATTTC CACGCTTGCT ACCAAAATAG TCTGGGCACG GCTGCTCCCC AGATTCTCAG ATCTGATTC CACGCTTGCT ACCAAAATAG TCTGGGCACGG CCACTTTTGG AAGTAGGCT TATCTAGTGA GCAGGCAGCC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCC CCAGCGCAGG ATCAGCCTGT TCCTGGGACT TCCCGAGGC CCAGCCCCAG GAGCCTCTCCC CAGCGCCAG ACCGGGCCG GACCGGGACG GCTCCGAGC CAGCGCCCA TAGGGGACG CCTGCCTCC CCGGAGCTT CTCGCCAGC AGAGTCCCAG ACCGGGCCG GACCGGGACG GCGCCCCCC CGGGGCCCG TACTCCTCC CCCGGGGTC CCCTGCCTCC CCGGAGCTT TCTCGCAGAC TCCTGGTCC CACCGGGTC CCACTGCTC CCCGGACCTT TCTCGCAGC GTGGGCCAG ACAGGTCC CACCGGCTC CACCGCGCTC TCCGCGACCTC TCTCGCAGC GTGGGCCCG CCTGCTCTG GCTGGGGCC TCGCGGTCT TCAGGCAACA GGTTGGCTCA GAGCGCAAC ACCAAGGTC CACGGGCTG CCACTGCTC TCCGGAACCC GTGGCCCCG ATATTCTCCC TCTGGTGCC CACGGGCTG CCACTGCTC TCAGGCAACG GTTGGCCTC AGGCCAAC ACCAAGGTC CACGGGCTG CCACTGCTC TCAGGCAACG GTTGGCTCA GAGCCGAAC ACCAAGGTC CACGGGCTC TCGGGGACG TCAAGGCAAC GGTTGGCTC AAGCCAACA ACCAAGGTCC CACGGGCTC TGGGGAAGC TCAAGGCAAC GGTTGGCTC AAGCCAACA ACCAAGGTCC CACGGGCTC TGGGGAAGC TCAAGGCAAC GGTTGCTTCA GAGCCAACA CCCACCAGG CCTTCCGT TTCCAGAACCC TTGGGTACC CTTGGGTTC CAGGCAACA CCGCACTTCCC CGCAGCACC TGGGGAACT AACCTCAACCA CTTGGGTTC CTTCGGTTTC AGTTATCCAG GCCCTCAGCT TGGAAACCCT TGCGTGGCC TTCCATCTCC CTTCGGTTTC AGTTATCAG GCCCTCAGCT TGGAAACCCT TGCGTGGTC TCTCCCTCT TCGGGAAGT CCCTTCCAT TCTTTACGG CCCCCCACT GACTGGATTC TACAAGAACA AACTCAGCACA TTGCACACACA AACTCACACA AACACACA AACACACA AACCACACA TAGCCAACAC AGGGCGGTT TCAACCACACA AACCACACA AACCACACA AACCACACA AACCACACACA AACCACACA AACCACACA AACCACACA AACCACACA AACCACACA AACCACACACACACACACACACACACACACACACACACAC	120 180 240 300 360 420 480 600 660 720 780 840 1020 1080 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1860 1980 2040

		2220
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_	100MIGNIGG CACCAGIGGG CIOOMIGGG INCIDENTIAL CACCAGIGGG	2400
5		2460 .
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	CTCCAGAATG AAAGCCTTCT CAGACCTGCG CACTCCATCT CCCTCCCTTT TCTTCTCTCT	2640
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	20.000.000.000.000.000.000.000.000.000.	
	CACCACTGCC ACTCGGGAGG GCACCAGGGC TGCTGGCTAG GGAGGGACAG GGCAGGAGG	360
	CACCACTGCC ACTCGGGAGG GCACCAGGGC TGCTGGCTAG GGAGGGACAG GGCAGGGAGG CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT	
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT	360
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG	360 420
55	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGGA GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGGGAAA CCCAAGGAGA AGGAGCAGG GGATGAGCAG AGCCTCCTGGGGCCCCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGGACT GGGCCGGGCC	360 420 480
55	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGGA GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGGGAAA CCCAAGGAGA AGGAGCAGG GGATGAGCAG AGCCTCCTGGGGCCCCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGGACT GGGCCGGGCC	360 420 480 540
55	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGGA GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGGGAAA CCCAAGGAGA AGGAGCCAGG GGATGAGCAA AGCCTCCTGG GGCTGTTGC CCCTGGAGCA GCCCCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGGACT GGGCCGGGCC	360 420 480 540 600
55	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCGAG ACCTGCCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCCGGGCC TGTGGCCCAG GCCCCACG ACTGGCGAAA ACCTGTGGG CACTGGCCCT ACTCACCTGC CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCGC TGCCCCAGGC CCAGTGGCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCGC TGCCCCAGGC CCAGTGGCGG	360 420 480 540 600 660
55	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGAG GATTGTGTGC AAAATCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCGAGA ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGGACT GGGCCGGCC TGTGGCCCAG GCCCCACGG ACTGGCCAGA ACCCTGTGGG CACTGGCCCT ACTCACCTGG CTGGCTGCCT TCCTGTACCA GGGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCGC TGCCCCAGCG CCAGTGGGGG GCTTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCCG GCATTCGGCA CTCAGCGATG	360 420 480 540 600 660 720
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC ANANTCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCAGGA ACCGGCACC TGCATGGACT GGGCCGGCC TGTGGCCCAG GCCCCCAGGA ACCGGCAGCA CACTGGCCCT ACTCACCTTGC TGGCTGCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCGC TGCCCCAGGC CCATGGCGGG GCTTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCGG GATTGGGA CTCAGGGATG CCGACATCTT CCACCTGGCC ANTCTGACA GGCTGCCCCC CAAGAACCCG GATGGCCAC CTCCGCCTGG CTGCGCTAC CAGAGCCTG ACATGGTAGA CATCGTCAAC CGCACTGGCC	360 420 480 540 600 660 720 780
55 60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC ANANTCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCAGGA ACCGGCACC TGCATGGACT GGGCCGGCC TGTGGCCCAG GCCCCCAGGA ACCGGCAGCA CACTGGCCCT ACTCACCTTGC TGGCTGCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCGC TGCCCCAGGC CCATGGCGGG GCTTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCGG GATTGGGA CTCAGGGATG CCGACATCTT CCACCTGGCC ANTCTGACA GGCTGCCCCC CAAGAACCCG GATGGCCAC CTCCGCCTGG CTGCGCTAC CAGAGCCTG ACATGGTAGA CATCGTCAAC CGCACTGGCC	360 420 480 540 600 660 720 780 840
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTGC AMARTCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGGACT GGGCCGGCC TGTGGCCCAG GCCCCCACGG ACTGCGCAGA ACCCTGTGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCC TGGCCCAGG CCATGGGCG GCTTCCCGGC TGTCACCCTC TGCATATACA ACCGCTTCCG GCATTGGCA CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCC CAAGACCGG CATCAGGGATG CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCC CAAGACCCG GATGGGCAC GTGCGGCTGG CCTGCCCTAC CCAGAGCCTG ACATGTAGA CATCCTCAAC GGACTGGCC ACCACCTGCC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTCC CCGCCAGGCA	360 420 480 540 600 660 720 780 840 900
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC ANATCANAT TTGCTGAGGA GATGCGANA CCCAAGGAGA AGAGGCAGG GGATGAGAG AGCTCCTGGGGCTGTTGC CCCTGGAGCA CCCCCGAGA ACCTGGCCAC CTTTGCCAGC ACCAGCACCC TGCATGACCT ACTCACCTGG CTGGCTGCAT TCCTGTACCA GGGGGTGGC CTGCCCGGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCGC TGCCCCAGG CTTGCGGAG ACCTTGGGGATG CTGCACCTCC TGCAATATCA ACCGCTTCCG CTGCCCCAGC CCAGTGGCGG CTCCCGGGC TGTCACCCTC TGCAATATCA ACCGCTTCCG CAAGAGCCG GATGGGCAC CTGCGGCATGCC CCAGAGCCTG CCGACATGCTC CCAGAGCCTG ACATGTAGA CATCCTCAAC GCGACTGGCC ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GATCACTGC TCCCCCAGCA ACTTCTGTG GATCACTGC CCGACATGCTC ACCAGCTCGA GATGCTCAACGCG GATCACTGC CTCCACGGCA ACTTCTGTG GATCACTGC CTCCACGGCA ACTTCTGTG GATCACTGC CTCCACAGGC GACCCGGCAACACTCTCTTATACT CCCCCAGCACACCACTCGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC ACTTCTGTG GGCACTCACTGC CTCCAACGGC GACCCGGGAACACTGC ACTTCTATACT CCCCCAGCACACCACTGGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC CTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCAACGGC GACCCGGGAACACTGC ACTCCACACGC CTCCAACGGC GACCCGCGAACACTGC ACTCCAACGGC GACCCGCGAACACTGCAACACACACACACACACACACACA	360 420 480 540 600 660 720 780 840 900 960
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCTCCTCG GGGTGTTGC CCCTGGAGCA GCCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGCCT ACTCACCTCG CTGGCTCACT CCCTGACA ACCAGCACCC CACTGGCCCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTGAC CTGGTGGCAA TGGACCCGC TGCCCCAGCC CCAGTGGCGG GCTTCCCGGC TGCACCATCT CCACTGGCC ATCTGACAG GCTTGCCCC CAAAGACCGG ACTGGCCCA ACCAGCTCGC CAACAGCCTG CCAGCATGTT AGAGCCTGA ACTTCAGTGG GATCATGC TCCGCCAGCACTCT CACAAGCCTG ACATGGTAGA CATCCTCAAC GGCACTGGCC AACTGCTCG CGACATGCTT AAGAGCTGCA ACTTCAGTGG GATCATCGC TCCGCCAGCACCCC CGACATGCTC ACCAGCTGC GACCATGGTAAACCCG GACCCCGGAACCCCC CGACATGCTC CCAGAGCCTG ACTTCAGTGG GATCATCGC TCCGCCAGCAACCTCCCCC CAACCAGCTCC CAACAGCTGGC GACCATGGTCAACC CTCCAACCG GACCCCGGAACCCCC CAACCACTCC CACACTGGTAACC CTCCAACCCG GACCCCGGAACCCCCC CAACCACCCCC CAACCACCCCC CAACCACTCC CGCCAGCAACCCCC CAACCACTCCC CAACAGCCTGAACCCC CAACACCCCGC GACCATGCTC ACCACCTGCC CAACCACCCCGCAACCCCCCC CAACCACCCCCC CGACATCATC CGCCAACCCCCCCCCC	360 420 480 540 600 660 720 780 840 900 960 1020 1080
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCGAG ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCCGGCC TGTGGCCCAG GCCCCCACG ACTGGGCAGA ACCCTGTGGG CACTGGCCCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGG GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCC TGCCCCAGC CCAGTGGCGG GCTTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCCG GATTCGGCA CTCAGCGATG CGGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCC CAAGAGCCGG GATGGGCAC GTGCGGCTGG CCTGCCCTAC CCAGAGCCTG ACATGCTAGA CATCCTCAAC GGCATCGCC ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC GCTCCCTCC CAGCCGGGCA GGGGGCATGG CCAGCGCGGG ACCTCCTCCC CAGCCGGGCA CGGGGCATGG CCAGCGCGCGA ACTGCTCCC CAGCCGGGCA CGGGGCATGG CCAGGGCCT GGAGATCAT CTGGACATCC ACCAGGAGGA GTACCTGCCC ATCTGGAGGG GAACAAAATGA GACGTGGTT GAGCCAGCTA	360 420 480 540 660 720 780 840 900 960 1020 1080 1140
	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC ANATCANAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGGCAG GGATGGAGA ACCACGGAGA ACCTGGCCAC CTTTGCCAG ACCAGCACC GGGCTGTGC CCCCTGGAGCA GCCCCCAGGA ACCTGGCCAG ACCAGGACCA ACCTGGCCCA ACCACGACACA ACCTGGCCCACAGA ACCTGGCCAGA ACCTGGCCAGA ACCAGGACCA ACCAGGACCA CACCAGGACCA ACCAGGACACA ACCAGGACACA ACCAGGACACA ACCAGGACACA ACCAGGACACA ACCAGCACACACA	360 420 480 540 600 650 720 780 840 900 960 1020 1080 1140 1200
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCTCCTCG GGGTGTTGC CCCTGGAGCA GCCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGCCT ACTCACCTCG CTGGCTCACT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGGC CTGGCCCAGG ACCGCTGGC CTGGCCCGGG GCTACCTGGC CTGGCCCAGG TGCACCAGG CCCAGGACATCT CCACCTGGC CTGGACATCA ACCGCTCAG GCTGCCCC CAAGAGCCTG CCGACATCTT CCACCTGGCC AATCTGACAG GCTGCCCC CAAAGACCGG GATGGCACC CCACAGCTCT GGACATCTT CACCTGGCC AATCTGACAG GCTGCCCCC CAAAGACCGG GATGGCACC ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCATCC TCCGCCAGCA ACTTCTCTGT GGTCTATACT CGCTATGGA ACTTCTCAGTGG GACCACCGCA ACCAGCTGC CACCAGGCTG CGGGCATGG GAGCATGCT CGCCCAGACATCT CGCCCAGGA ACTCCTCAAC GGACCACCGCA ACCAGCTGC CACCACCTGC GGGGCATGG GAGCAAATGA GACCTCGTT GAGGCAGTAC TCCGCCAGGA GTACACCACCC CAGAGGGGG GACCAAATGA GACCTCGTT GAGGCAGTAC TCCGCCCAGG TTCCCCCAGG CTTCCACAGC CACCAGCTG CCCCTACAT CCACCAGCTG GGTCCCCCC CACCAGCACACCACCACCACCACCT CCACCAGCTG GAGCACCACCTC GAGGATCATC CACCACCACCT GAGGCACCACCT GAGGCACCACCACCT CCACCACCACCT GAGGCTGACC TACCTCCCCCCC CACCACCACCT GAGGCTGACC TACCTCCCCCCC CACCACCACCT GAGGCTGACC TACCTCCCCCCCCCTACAT CCACCACCT GGGGTCCCCCCCCCC	360 420 480 540 600 660 720 780 840 900 960 1020 1180 1200 1260
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTG GGGCTGTTGC CCCTGGAGCA GCCCCCCGAG ACCTGCCCCC CTTTGCCAGC ACCAGCACCC TGCATGGCCT ACTCACCTG CTGGCTGCT TCCTTACCA GGCGGCTGGC CTGGCCCGGG GCTACCTGAC CCGGCCTCAC TGGGGGCAA TGGACCCCC TGCCCCAGCC CCAGTGGCGG GCTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCGG GATTCGGCA CTCAGCGAG CCGGCATACTT CCACCTGGCC AATCTGACAG GGCTGCCCC CAAGAGCCGG GATGGGCAG ACCAGCTCGC CGACATGCTT AAGAGCCTGA ACTTCAGTGG GCATCACTGC ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC GCTCCCTGCC CAGCCGGGCA GGGGGCATGG CCAGTGGCCT GGACTCATC ACCAGCTGGC CAGCCGGGCA CGGGGCATGG CCAGTGGCCT GGAGTCATG CTGGCACTCC ACCAGGAGGA GTACCTGCCC ATCTGGAGGG GAACAAAATGA GACGTCGTT GAGCCAGCTA TTCGGGTGCA GATCCACACC CAGGAGGAGC CGCCTACAT CACCAGCTG GGGTTCGGGC TGCCCCGGG CTTCCAGACC TTTGTGTCCT GCCAGGAACA GCGCCTGACT CACCGGGG AGCCCTGGGC CACCTGGGCC CAGGAGGAGC CGCCCTACAT CACCAGCTG TACCTGCCC AGCCCTGGGC CACCTGGACC CTTTCTGTGTCT GCCAGGAACA GCGCCTGACC TACCTGCCC AGCCCTGGGC CACCTGCCC CAGGAGGAGC CGCCTACAT CACCAGCTG TACCTGCCC AGCCCTGGGC CACCTGGCC CGCAGGAGGT ACCTCAGGGA CCTCAGCCT CACCGGGCAGCC CCAGGAGAGT ACCTCAGGGC CCTGACCT CACCAGCTG CAGCGCGGCAGCC CCCCTGACCT CACCAGCTG CAGCCCCCCCCCC	360 420 480 540 600 650 720 780 840 900 960 1020 1140 1200 1260 1320
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGACA AGCAGCACG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA CCCCCCGAG ACCTGCCCC CTTTGCAGC ACCAGCACCC TGCATGACCT ACCACGCACC TGCATGACCT ACCACGCACC TGCATGACCT ACCACGCACC TGCGCCCAG ACTGGCCCA ACCAGGACCC CACTGGCCCT ACCACGCACC CTGGTGCCAA TGGACCCCG TGCCCCAGC CCAGTGCCCG CTTCCCGGC TGCCCCAGC CTGCTCCGGC TGCCCCAGC CTAGGCCAGC CTCAGGCATTC CCACACTCT CCACCTGGCC AATCTGACAG GGCTGCCCC CAAAGACCG GATGGCACC GTGCGCATC CCACACTCT CCACCTGGCC AATCTGACAG GCTGCCCCC CAAAGACCG GATCACTGC ACCACTCGC CAACACTCT AGAGCTGCA ACTTCAGTAG CATCCTCAAC CGCACTGGC AACTCCTTGTGG GCATCACTGC TCCGCCAGCA ACTTCTGTGG GCATCACTGC TCCGCCAGCA ACTTCTGTGG GCATCACTGC TCCGCCAGCA GCCTCAGCAC ACCTCCTTCAAC CGCACTGCC CAGCAGAGAGA ACTTCATGTG GCATCACTGC TCCGCCAGCA GCCCTGCGCA ACTCCCAGCA GACCACTCC CAGCCAGGAGA ACACTACTTC TCGGCAGCAC TCCGCCGGAACTC AGCACAGCAGC GACCCCACACAC CTCCAAGACC GACCCGCGAACTC AGCACAGCAGCA CCCCCTACAT CACCAGCTG GGGTTCCCCAGCA CCCCTCACAC CAGCAGGAGC CCCCTTCAAC CACCAGCTG GGGTTCCCCAGCA ACCTCCAGCAC CACCAGCAGAACAA CACCCTGGCAC TACCTGCCC AACCCCCCCCCC	360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGGAGGCAG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA GCCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGCCT ACCACCTCG CTGGCTCCAG GCCCCCAGGA ACTGGCCAGA ACCAGGCACC CTGCATGGCCA CTGGCCCAGG ACCAGGACACC CTGGCCCAGG ACCAGCACCC CAGCACACCT ACCACCTCG CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG GCTTCCCGGC TGCCCCAGGACACCT CCACCAGGCACCC AATCGACACG ACCAGCTCGC CAACACCTCT CCACCAGGCATGC AATCGACAG GCTGCCCC CAAAGACCGG GATGGGCAC CCAGCACACCT CAACACTCGC CGACAGCCTT AAGAGCTGCA ACTTCAGTGG GCATCACAC CGCACTGGCC AACCACTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACAC CGCCCGGA ACCACTCGC CGACAGGCTT CGCCCAGGA ACTTCTCATGC GCACTGGCC CACCAGGCAG GACCACACCAC	360 420 480 540 600 660 720 780 840 900 1020 1080 1140 1260 1320 1340
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC ANATCAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGGAGGAGG GATGGAGA ACCATGGACA AGGAGCAGG GATGGAGA ACCATGGACA TGGACACAC TGGACACAC CTGGACACAC ACCATGGACA ACCATGAGACAC CTGGACACAC ACCAGCACAC ACCAGCACACAC ACCAGCACACACA	360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1320 1380 1480
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGACA AGCAGCACG GGATGAGCAG ACCTCCTGGGGCTGTTGC CCCTGGAGCA CCCCCCGAGA ACCTGCCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCTCCTGC CCCCCCGGC TGCCCCAGG ACTGGCCCAC ACCAGCACCC CACTGGACCT ACCACCTCAC CTGGCTCACT TCCTGTACCA GGGGCTGCC CTGGCCCAGG CCTCCCAGG ACTCCCGGC CCAGTGACCC CTGGTGCCAA TGGACCCCG TGCCCCAGC CCAGTGGCCG CTTCCCGGC TGCCCCAGG ACTCCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC AATACCTGC CAGCACTCT CCACCTGGCC AATACTGACAG GGGTGCCCC CAAAGACCG GATGGCACC GAGCACTCT CACCTGGCC AATACTGCA ACTCCTCAGG GATCACTGC TCCGCCAGCA ACTTCTGTGG GCATCACTGC TCCGCCAGGA ACTTCTGTG GCATCACTC TCCGCCAGGA ACTTCTGTG GCATCACTGC TCCGCCAGGA ACTTCTGTG GCATCACTG TCCGCCAGGA ACTTCTGTG GCATCACTG TCCGCCAGGA ACTTCTGTG GCATCACTG TCCGCCAGGA ACTTCTGTG GCATCACTG TCCGCCAGGA ACTTCCAGG GACCAGCTT AGCACACTC CAGCAGGAGG GACCAAAATAA GACCTGTTT GAGCCAGGTA TCCGCCAGGA GCCCTTACAT CACCAGGCTG GGGTTCCCCAGGAACA ACTCCCAGGC GACCTGCAC TACCTGCAGA ACTCCCAGGC GACCTGCAC TACCTGCCC CAGCAGAGAGA ACCTCAGGCT GGGCTTCCCAGGA ACCTCCAGGC GACCTGACC TACCTGCCC CAGCAGAGACA ACTCCCAGGCT GAGCACACT TCCGCCCACA AATACTCCC TCCGCCTACAC TCCACCACA GCCTCACCT TCCGCCCCC GCCACACAATAAAAAAAAAA	360 420 480 540 600 650 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA CCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGCCT ACCACCTCG CTGGCTCAGC ACCCCCAGG ACTGGCCAGA ACCTGGCCCG CACTGGCCCACG ACCGCACGA ACCAGCACCC CTGGCCCAGG ACCGCCAGG ACCGCTGAC CTGGCCCAGG CCTACCTGGC CTGGCCCAGG ACCGCTGAC CTGGCCCAGG CCTACCAGG CCCCAGGCACTCT CCACCTGGCC CTGGCTGACA TGGACCCCC CAAAGACCGG CTCAGGGACTGC CAGCACTCTT CCACCTGGCC AATCTGACAG GCCTGCCCC CAAAGACCGG CTCAGGCACACCC CAACAGCCTC GGACATCCT AAGAGCCTG ACCAGCTGGC CAACAGCTCG CACCAGCTGCC CAACAGCCTG GACCACTGGC CAACAGCCTG GACCACTGCC CAACAGCCTG CCTGCCCCC AATCTGAGA CATCCTCAAC CGCACTGGCC ACCAGCTGCC CACCAGGCAC CCCCCCAGCA CCTCCAGCC GACCACTGCC CACCAGGAGAACA CTCCAGGAGAGA GACCACACCC CAGCAGCACAC CAGGAGGAGA ACCCCCACCCC CAACACCACCTG CGCCCCAACACCACCAGCTG CACCAGCAGCACACCC CAGGAGGAGA CACCACCAGCTG CACCAGCAGCACACCCC CACCAGCAGAGACACACCACCACCAGCACACCCCCCCC	360 420 540 660 720 780 900 900 1020 1140 1260 1320 1380 1440 1500 1620
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC ANATCAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGACAG GATGCGACA ACCACTGACCA CTCTGCCAGC GGGCTGTGC CCCTGGACCA CCCCCCGAG ACCTGCCAC ACCAGCACCC TGCATGACCAC CTGGCTCACT TCCTGACCCT TCCTGACCAC TCCTGGTGCCT TCCTGACCCC TGCCCCAGC ACCGCCCAGC ACCCCCAGC CCAGTGCCCAGC CTTGGCCAGC CCAGTGGCCCA CTCGGCCACAC ACCCTGGCCAC TGCCCCAGC CTCAGCCAGC CTCAGCGCACACACCC TGCCCCAGC CTCAGCCAGC CTCAGCGCACACACACCC TGCCCCAGC CTCAGCCAGC CTCAGCGATTCCGC CTCAGCCACACCCC CTGCCCCAGC CTCAGCCACACCCC CTCAGCCACCC CTCAGCCACCCC CTCAGCCACCCC CAAGAGCCCAGC GATGGCCCC CAAGAGCCCAGCACCCC CAAGACCCAG GATCCGCCAACACCCC CTCACACCCC CAACACCCCC CAACACCCCG GATGGCCCC CAACACCCCC CAACACCCC CACCAC	360 420 540 660 720 780 840 900 1020 1180 1200 1260 1320 1380 1440 1500 1560 1680
60 65 70	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGACA AGCAGCACG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA CCCCCAGGA ACCTGCCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCTCCTCG CCCCCAGGA ACCTGGCCAC ACCAGCACCC CACTGGACCT ACCACGCAC CTGGCCCAC TGCCCCAGG ACTGCCCAGG ACCTGGCCAG ACCTGGCCAGG ACCTGGCCAG ACCTGGCCAGG ACCTGGCCAGG ACCTGGCCAGG ACCTGGCCAGG ACCTGGCCAGG ACCTGGCCAGG ACCTGGCCAGG ACCTCCAGGC CCAGGACCT ACCACGCAGC CTGCCCAGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCCGGC TGCCCCAGG ACTCGGCAGC ACCTCCAGGCAGC ACCTCCAGGCAGC ACCTCCAGGCAGC ACCTCCAGGCAGC ACCTCCAGGCAGC ACCTCCAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	360 420 540 660 720 780 900 900 1020 1120 1220 1320 1320 1340 1500 1560 1620 1620
60	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GATCGAAAA CCCAAGGAGA AGAGGCAGG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA CCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCTGCTC ACCACCTCA CTGGCTGCT TCCTGTACAA GGCGCTGCC CTGGCCCGG CCTACCTGGC CTGGCCCAGC ACCACCGCACG ACCGCCAGGA ACCATGGCCG CCTACCTGGC CTGGCTGCCC CTGGCTGCCA TGGACCACC TGCCCCAGG ACCACCTGGCC CAGTGGCCG GCTACCAGGA CTCACCTGGC CTGGCTGCCC CTGGCTGCCC CAGCACTCTT CCACCTGGCC AATCTGACAG GCCTGCCCC CAAAGACCGG CCACAGCATCT CACCACGCCC CAACCACTCGC CGACATGCTT AAAACCGG ACCACGTGGC CAACAGCCTG GCACACTGCT AAAGACCTGG CCACAGCTCG CGACATGCTT AAAGACCTGA ACTTCTCTGT GGTCTATACT CGCTATGGA ACTTCAGTGG GCATCACTCC CACCAGGAGCAC CACCACTGCC CAACCACTCC CACCAGGAGA GTACCTGCC CACCAGGAGA CTTCCAGGG GACCACCGGA ACTTCTCAGTG GCATCACTC CACCAGGAGA GTACCTGCCC CACCAGAGCCT GAGAAATAA GACGCTTTT GAGCCAGGA GCCCCCGGA ACCACCTGC CACCAGCAG CACCACCTC CACCAGCTG CCCCCCACACACCACCTG CGCCCACACACCC CACCAGCAGAGAAAAAAAAAA	360 420 540 660 720 840 960 1020 1140 1220 1320 1320 1440 1500 1560 1620 1680 1740
60 65 70	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGAGGA GATGCGAGA ACCAGGACAC GGGCTGTTGC CCCTGGAGCA CCCCCCGAGA ACCTGGCCAC CTTTGCCAGA ACCTGGCCAC GGGCTGACC TGCACGACAC TGCGCCAGC TGCCCCAGGA ACCTGGCCAG ACCAGGACAC CTGGCCCAGGA ACCTGGCCAGA ACCTGCCCAGACACCAC CGACAGACACA ACCTGGCAAAAACAA ACCGCTTCAGACAC GACACTGGCC CAAGAGCCAG GATCACTGCA ACCTGCCAGACACACACACACACACACACACACACACACA	360 420 540 660 720 780 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1560 1680 1740 1860
60 65 70	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMARTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGACA AGCAGCACG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA GCCCCCAGG ACTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGGACT GGGCTCCTCAC GGGCTCCTCACCA GGGGCTCACC CTGGTGCCAC CTGGCCCCACG ACTGGCCACA ACCAGCACCC CCAGGACCC CACTGGCCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GGGGCTGCC CCAGGACCC CCAGGACCT CCACCTGGCC TGCCCCAGG ACTCCCAGC CCAGGACCC CCAGGACCT CCACCTGGCC AATCCACCAG GCTCCCAGC CTCAGGCATC CCACCAGCACCC TGCCCCAGC CTCAGGCATC CCACACTCT CCACCTGGCC AATCCACCAG GCTGCCCCC CAAGACCCG GTGCGCCC CAAGACCCG GACGCCCC CAAGACCCG GACGCCCC CAAGACCCG GACGCCCC CAAGACCCG GACGCCCC CAAGACCCG GACACCCC CCAGCACCC CCAGCACCC AACACCACCTCGC CGACACCCT AACACCACCTCGC CGACACCCT AACACCACCTCGC CGACACCCT AACACCACCTCGC CGACACCCC AACACCACCTCGC CGACACACCC CAACACCACCAC CAACACCACCAC CAACACCAC	360 420 540 660 720 780 900 960 1020 11260 1220 1380 1440 1500 1560 1620 1740 1800 1800 1920
60 65 70	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCGGATGA GATTGTGTC AMATCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGCAGCAGG GGATGAGCAG AGCTCCTCG GGGCTGTTGC CCCTGGAGCA CCCCCAGGA ACCTGGCCAC CTTTGCAGC ACCAGCACCC TGCATGAGCA GGCCCCACGG ACTGGCCAC ACCAGCACCC CTGCTGCCCC CTGGTGCCA TGGACCCCG GCCCCCAGG ACTGGCCAGA ACCAGTGGCGG CCTACCTGGC CTGGCTGCCC CTGGTGCCA TGGACCCCC GCCCCCAGG ACTGCCCAGG ACCAGGACCC CAGGCACTCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGG GCTACCCGG GCTCCCAGG CCCCCAGG ACTCCCAGG CCCCCAGG ACCACTGCCCC CAGGCATCCT TGCACATCA ACCACTTCG GCACTTCCCCC CAGCCTGCCC CAACCACTCC CCACAGCCCC CACAGCCCC CAACCACTCGC CGACATCCT AAACCAGAGCCT AACCAGCTCG CGACATCCT AAAGACCCG GACCACTGGC CAACCACTCGC CGACATCCT AAAGACCTGA ACTTCTCAGTG GCATTCACC CACACACTCG CGACATGCT AAAGACCCG GACCACTGCC CAACCACTCG CGACATGCT AAAGACCTGG CACCAGGAGA GACCACAGCCC CAACAAGCCCG GACCACAGCCC CAACAAGCCCG GACCACAGCCC CAACAAGCCCG GACCACAGCCC CAACAAGCCCC CAACAAGCCCG GACCACAGCCC CAACAAGCCCG GACCACACCC CAACAAGCCCG CACACACCCC CAACAACCCC CAACAACCCC CAACAA	360 420 540 660 720 840 900 1020 1140 1200 1320 1380 1500 1560 1620 1680 1740 1860 1980
60 65 70 75	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMATCAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGAGGAGGA GATGCCAG GATGCGACA CCCCAGGA ACTGGCCAC CTTTGCCAGA ACCAGGACCC GGGCTGTGC CCCTGGAGCA GCCCCCAGGA ACCTGGCCAG ACCAGGACCC CACTGGCCT ACCACCTGC CTGGCTGCAT TCCTGACACC CTGGCCCAGG ACTGGCCAGA ACCAGGACCC CACTGGCCT ACCACCGGC CTGGCCCAGG ACCCCCAGGA ACCAGGACCC CACTGGCCT ACCACCGGC CTGCCCCAGG ACCCCCAGGA ACCCTGGCCG CTACCCTGGC CTGCCCCAGG ACCCCCAGGA ACCCTGGCC CAGGACCCC CAGGACCCC CCAGGACCC CCAGGACCCC CTGCCCCAGG CTCCCCGGC TGCCCCAGG CTCCCCGGC TGCCCCAGG CTCCCCGGC TGCCCCAGG CTCCCGGC TGCCCCAGG CTCAGGGATG CCGGCATCTTC CACACCTC TGCAATATCA ACCGCTTCCG GCATTCGGC CTCAGGGATG CTGCCGCACTCTC CCAGAGCCTG ACATCGTAGA CATCCCTCAAC CGCACTTCGC CAGCACTCGC CAGAGACCTG ACATCGTAGA ACTCCTCAAC CTCCAACGGC GACCCGCGGA ACTTCCTGG GATCACTGC TCCCCCAGGC AGCACCAGGA GACCCACCAGA ACTTCCAGCAG GACCCAGGGA CCCCTACAT CTCACCCC CAGCACACCACAC	360 420 540 660 720 780 840 900 1020 1120 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1920 1920
60 65 70	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMANTCAAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGCAGCAGCAC GGGCTGTTGC CCCTGGAGCA GCCCCCAGGA ACTGGCCAC CTTTGCAGC ACCAGCACCC CACTGGACCT ACCACCCCC CTGGCTGCCT TCCTGTACCA GCGCCCTGGC CTGGCCCGGC CACTGGCCCT ACCACCTCC CTGGTGCCA TGGACCCGC TGCCCCAGG ACCTCCAGGC CCAGGACCC CACTGGCCCC CAGGACCCC CTGGCTGCCA TGGACCCGC TGCCCCAGG ACCTCCAGGC CCAGGACCC CAGGACCCC CTGGCGCCAC TGGCGCCAGG ACCTCCAGGC CCAGGACCCC CCAGGACCCC CTGGCGCCAC TGGCGCCCGC CCAGGACCCC CCAGGACCCC TGCCCCAGC CCAGGACCCC CAGGACCCG ACTCCAGGC CCAGGACCCC AAATACCACCCG GCCCCCCCC CAAGACCCG GACGCCCCAGG ACTCCCAGC CCAGCACCCC CAGCACCCG ACCACCACCC CAGCACCCG ACCACCACCC CAACACCCG GACCACCCC AAATACCACCACCCC CGCACAGCCC AACCACCTGC CGCACAGCCC AACTCCACAC CGCACACCCC CACAGACCCG GACCACCCC ACCAGCACCG GACCACCCC AACACCCCCC CACAGACCCG GACCACCCAC	360 420 540 660 720 780 900 960 1020 1260 1220 1380 1440 1500 1620 1620 1740 1800 1980 2040 2100
60 65 70 75	CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATGA GATTGTGTC AMATCAAT TTGCTGAGGA GATGCGAAA CCCAAGGAGA AGGAGGCAG GATGCGCA ACCAGGACAC GCGCCTGTGCCAGC GGGCTGTGC CCCTGGAGCA GCCCCCAGG ACTGGCCAC ACCAGCACCC TGCATGACC TGGGTGCCT TGCTACCTG CGGGCTCTCT CTGGTGCCT TGCTACCTG CGGCCTCACC TGCCCCAGC ACCGCCAGG ACCGCCAGG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAG ACCTGGCCAGC CCAGGGCCTCAC CTGGCTGCCT TGCTACACCT TGCTACCCT TGCTACACCT TGCTACCCT TGCTACCCC CGCCCCAGG ACTCGGCA ACCTGGCC ACCAGGCCT ACCTGGCC ACCAGGCCC TGCCCCAGC CCAGTGGCCAG ACTCGGCAAAACCC GGGGCTCCC CAAGACCCG GATGGGCAC ACCAGCTCGC CAAAACCCG GATCGGCAAACACC CTACGCAAAACAACCCTTCAGCAAACACCAACACCCC CGACAGCTCG CCAAAACACCG GATCGGCAAACAACACCCCC CGACAGCCT ACAAGACCGA GACTCACTCAC CACCAGCTCGC CAACAACACCACCCC CGACAACACAAC	360 420 540 660 720 840 900 1020 1140 1200 1140 1320 1380 1440 1500 1560 1680 1740 1860 1980 2040 2160
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50	Coding sequil GCATCCCGA GAGCTGCGC GGCGGGGGT CGGCCTGTCT GGTGCTTGG GGCAGCGA TCCCTGCCAG GGAAGGGGG CAGAGCGAGG	ience: 641. 11 GTGCACCGCT CAGGGCTTCG GTCGGCCCCC GTCGGGCCCC GTCGGGCCCC GTCTGGGCCCC CCGCGCTTCC GTTTCGGGTC GTTTCGGGTC GTTTCGGTTC GTTTCGGGTC CCCCCCGCAC CCCCCCCCCC	.2299 21	31	CCCAACCCAC CACCAGGGT CACCTGGGCT CGCCTCGTG GAGTCAGTTT GTGGCGCGT GCTTGGCTG GCTCGCTTCT ATCCTGGGTG TGACCGCCGG ATGCGGGGGCG CTGCTTTCT	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CCTCGAGCGC TAGAGCG TAGAGCTCCC GGGGTGCCCC TGACTCGTCG TCTTGGAAC	120 180 240 300 360 420 480 540
50 55	Coding sequil GECATCCCGA GAGCTGCGCC GGGCGGGGT CGGCTGTGT GGTGCTTGGCAC GGAGCGGGC CGGAGCGGGC CGGAGCGAGCGAG	ience: 641. 11 GTGCACCGCT CAGGGCTTGC AGGGCCCCCT GTGGGGCCCC AGGGCTTGC AGGGCTTGC AGGGCTTGC GTTTGGGGT CTTGCAGGAT CGCTGGCAG CGCGCTTCT TTGGAGGTG CAGCTTTCT TTGGAGGTG AGCTTTGGG	.2299 21	31 C CCCGCCTTGC C CCCGCAACAG C CCCCAACCG C CCCCAACCG C CAAAGGGACG G GATCACGGG A TGAGGGACA A TGAGGGGGGAC A TGAGGGGGGGAC A TGAGGGGGGGGAC A TGAGGGGGGGGAC A TGAGGGGGGGAC A TGAGGGGGGGAC A TGAGGGGGGGGAC A TGAGGGGGGGGGG	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CGCCCTCGGGG GGTTGGCTGCTTCT ATCCTGGGTG ATCCTGGGGGGG ATGCGGGGGG ATGCGGGGGG ATGCGGGGGG ATGCGGGGGGG ATGCGCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCGC TAGAGCTCCCC TGACTCCCCC TGACTCGTCCCC TGACTCGTCCCC TGACTCGTCGCCCC TGACTCGTCGCCCC	120 180 240 300 360 420 480 540 600 660
50	Coding sequil GCCATCCCGA GAGCTGCGC GGCGGGGGT CGGCCTGTCT GGTCCTTGCCA TCCCTGCCAC GGAAGGGAGC CAGAGCGAGC CAGAGCGAGC CAGAGCGAGC	ience: 641. 11 GTGCACCGCT CAGGGCTTCG GTCGGCCCCC GTCGGGCCCC GTCGGGCCCC GTTTCGGGTCC GTTTCGGGTC GTTTCGGGTC GTTTCGGGTC GTTTCGGGTC GCCCCGGA GCTCCCC GAGCTTTC TTGGAGGTG GACCTCTTC GACCTCTTC GACCTCTTC GACCCCGGAC GACCACCCCC GACCACCCCCC GACCACCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCC GACCACCCCC GACCACCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCCC GACCACCCCC GACCACCCC GACCACCCC GACCACCCC GACCACCCCC GACCACCCC GACCACCCC GACCACCCC GACCACCCC GACCACCC GACCACCCC GACCACCCC GACCACCC GACCACCCC GACCACCC GACCACCC GACCACCC GACCACCC GACCACCC GACCACCC GACCACCC GACCACCC GACCACC GACCACCC GACCACC GACCACCC GACCACC GACCACC GACCACCC GACCACC	.2299 21	31	CCCAACCCAC CACCGAGCGT CACCTGGGCT CACCTGGGCT CGCCCTCGTG GGTGGGTGCT ATCCTGGTTC ATCCTGGTC ATCCTGGTC ATCCTGGTC ATCCGCGCGC CTGCTTCT ACCCCTAAG CACCCTAAG CAGCGGAGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CGCTACGACACACC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTCGTCG TCTTCGAAGC TTCTGGAACC CTTCCGAACC CTTCCGAACAC CTTCCGAACG CCAAAAAGTG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Coding sequil Coding sequil	ience: 641. 11 GTGACCGCT CAGGGCTTCG AGGCCCCCCT GTCGGGCCCCC AAGGCGCTCCC AAGGCGCCCCC CCGCGCTTCG AAGGCGCCCC CCGCGCTTCG ATTCAGGAT CCTCGCCAGAC CCAGTCTTCC TTGAGGAT GACTCTCC GACGACCCCC GACGACCCCC GACGACCCCC GACGACCCCC	.2299 21	31 CCCCCCCTTGC CCCCCCCGCTTGCC CCCCCCGCGGGGGGGG	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGACATC CTTCGAAGCG TAGAGCTCCC TGGTCGCCC TGGTGCCCC TGGTGAGCGC CTTGGGAGG CTTGGGAGG CTTGGGAGG CTTGGGAGG TGGAGCGGAT TGGTGTATTG	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	Coding sequil GECATCCCGA GAGCTCCCGC GGCGGCGGT CGGCCGCTTGCT GGTCCTTGCCAC GGAGCGGGC CGGAGCGAG CCGGACCTAG TCCTGCACCA GCAGCGAGG CGGACCTAG CGGAGCGAG CGGACCTAG CGGACCTAG CCGGACCTAG CCGGACCTAG CCGGACCTAG CCGGACCTAG CCGGACCTAG CAGAGCAGA CCGGACCTAG CAGAGCAGA CACGACACA CACGACAC CACGAC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	ience: 641. 11 GTGCACCGCT CAGGCTTCC AGGCCTCCC GTCGGGCCCC AGGCCCCCC GTTGGGCCCC CCGCGCTTCC GTTTCAGGAC CCTTGCAGGA CCCCCCGCGCTTC TTGCAGGAC CCAGCCTTC CCACCCACC CCGCCACC CCGCCACC CCGCCCACC CCCCCCCC	.2299 21	31 C CCCGCCTTGC C CCCGCACAGG C CGCCACCCG C CCCCACCCG C CAAGGGGGC C CAAGGGGGG A TGGCTTCAACTGG A TGGCTGCTG A TGGCTTCAACTGG C CCCACCCG G CATCACGGG C CACCCACCC A TGCTTCAACTGGGGC C CCCCACCCG C CCCCACCCG C CAAGGGGACC C CAAGGGGACC C CAAGGGGACC C TGATTCAACTGCTG C TGATTCAACTGCTG C CACTTCCAACTGCTG C CACTTCCAACTGCTG C CACTTCAACTGCTG C CACTTCAACTGCTG C CACTTCCAACTGCTG C CACTTCCAACTGCTG C CACTTCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CGCCCTCGGGG GGTTGGCTGGCT ATCCTGGGTG TGACCGCGG ATGCGGGGGG ATGCGGGGGG TGACCGCGGG ATGCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGACTCCCC TGACTCGT CTTCGGAAGCG CGGGTGCCCC TGACTCGTCG TGACTCGTCG TGACTGGTAAC CTTCGGAAGGG CCAAAAAGTG AGTAGCGGAT TGGGTGTATTG CGCTCCACGCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900
50 55	Coding sequil GCATCCCGA GAGCTGCGC GGCGGGGGT CGGCTGTCT GGTGCTGGCAGCCA TCCCTGCCAC GGAAGGGAGG CAGAGGAGG CAGAGGAGG CAGAGGAGG CAGAGGAAG TGACTGGTCTG CAAGAGGAAG TGACTGGTCTG CAAGAGGAAG TGACTGGAC CGCGTTGGT CTCCAGCAAT CACGACCT	ience: 641. 11 GTGCACCGCT CAGGGCTTCG GTCGGCCCCC GTCGGGCCCC GTCGGCCCCC GTTCGGCCCC GTTTCGGGTCC GTTTCGGGTC GTTTCGGGTC GTTTCGGTT GTTTCGGGTC GTTTCGCGT GTTTCGCGT GTTTCGCGT GGCCACC CGCGCAC CCACCTGTCG GACGACCCC CGGGCCATC CCACCCACT ATCCCCACT ATCCCCACT ATCCCCACT 11 ATCCCCACT ATCCCCCCCCCCCCCCC ATCCCCCCCCCCCCCCCCCCCC	.2299 21	31	CCCAACCCAC CACCGGCGC CACCGGCGC CACCGGCGC CGCCCTCGGC GGTGGGTG GGTGGGGGG TGACCGCGGC ATCCGGGGG CTGCTTCT ACCCCTAGG TATCTGGATC CAGCGGGGG CAGCGGAGGCC CACCGAGGGCC CACCGAGGGCC CACCGAGGCC CACCGAGGCC CACCGAGGCC CACCGAGGCC CACCGAAC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCGGG GGGGAACATC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTGGTCG TCTTGGAAGC TCTGGGAAC TCTGGAAGC TCTGGGAAC TCTGGAAAAAGT GCGAAAAAGT GTGAGCGGAT TGGTGTATTG GGGAAATCAT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50 55	Coding sequil Coding sequil	ience: 641. 11 GTGACCGCT CAGGGCTCCCT GTCGGGCCCC AAGGCGCTCCC AAGGCGCCCCCT GTTGCAGGAC CCGCGCTTCC AAGCCGCCC CTTCCAGGAC CCGCTCCC ACGCCCCCC GTTTCCAGCAC CCACTCTCC CACCCACT ATCCCCACT ATCCCCACT ATCCCCACT ATCCCCACT ACCCCCACT ACCCCACT ACCCACT ACCCCACT ACCCACT ACCCCACT ACCCCCACT ACCCCCCCACT ACCCCACT ACCCCCCCACT ACCCCCCCC	.2299 21	31	CCCAACCCAC CACCAGGCT CACCTGGGCT CACCTGGGCT CGCCCTCGTG GGTTGGCTGC GCTCGCTTC ATCCTGGTT TGACCGCGG ATGCGCGCG ATGCGCGCG ATGCGCGCG ATGCGCGCG ATGCGGCGCG ATGCGGCGCG ATGCGGCGCG ATCTGATC ACCCCTAAG TACTGAAT TGCACACTG AGGAGGCC AGGAGGCC AGGAGGCC AGGAGGCC AGGAGGCC AGGAGGCC AGGACTACTGATC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGGTGCCC TGGTGCCC TGGTGCCC TGGTGAGCG CTTCGGAGCG CTTCGGAGCG CTTGGGAGCG CTTGGGAGCG CTGAGAGCGAGC TGGTGATTGG TGGTGATTG TGGGAAATCAT AATTGCCCAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900
50 55 60	Coding sequil GECATCCCGA GAGCTCCCGC GGCGGCGGT CGGCTGTCT GGTGCTTGGC GGCAGCGGG TCCTGCCAC GGAGCGGGC CGGACGTAG TCCTGCAC GGAGCGAG TCCTGCTAG CGGACGTAG CGGACGTAG CGGACGTAG CGGACGTAG CGCGGTTGGT CAAGAGGAAG GCGGACTAG GCCGTTGGT CAAGAGAAA CACGAAC ATTAGTGGAC ATTAGTGGAC ATTAGTGGAA	ience: 641. 11 GTGCACCGCT CAGGCTTCG CAGGCTCGC AGGCCCCCT GTGGGCCCC AGGCGCTCC GTTTCAGGAT CGTTTCAGGAT CGCTCGCCAG CGCCGCTTCT TTGGAGGTG CACCTCTCC CAGCCACC CACCCCC ATCCCCACC ATCCCCACC ATCCCCACT ATCCCCAGT GACTTCAGGA GACTTCAGGA GACTTCAGCA TTGCCCAGT TTGCCCAGT TTGCCCATTCAGT TTGCCCATTCAGT TTGCCCATTCAGT TTGCCCAGT TTGCCCATTTCAGC TTGCCCAATT TTGCCCATTTCAGC TTGCCCAATT TTGC	.2299 21	31 C CCGGCTTGC C CCGGCACAGG C CGCTACAGG C CCCCACCCG C AAAGGGACG G GATCACGGG A TGCTTCAAC G CACCCAGG C ACGCTCCAG C AGGGGACCG A TGCTTCAAC G CACCCACCA A TGCTTCAAC A AGGTCTGAA	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CGCCCTCGGGCT GAGTCAGTTT GTGGGGGGGT ATCCTGGGTGCT ATCCTGGGTGCT ATCCTGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCGGG GGGGAACATC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTGGTCG TCTTGGAAGC TCTGGGAAC TCTGGAAGC TCTGGGAAC TCTGGAAAAAGT GCGAAAAAGT GTGAGCGGAT TGGTGTATTG GGGAAATCAT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080
50 55 60	Coding sequil GECATCCCGA GAGCTGCGCC GGCGGCGGTTGCT GGTGCTTGGCACCCA GGAAGGGGGC CAGAGGGAGG CCGGACGTAG GCAGCGAA GCAGCGAA GCAGCGAA GCAGCGACA GCAGCGACA GCAGCACAA CCAGCACAA CAGAGCAAT GCTCAGAAC CAGACCTAG CTCAGACC ATTAGTGAA GGTGAAATGC TGACATCCCC CTGCCTCCAGCCC	ience: 641. 11 GTGCACCGCT CAGGCCTTCC AGGCCCCCT GTCGGGCCCC ACAGCCTCCC AAGGCGCCCC GTTTCCAGGA CCCTCTCC ATTCCAGGA CCCTCTCC ATTCCAGGA CCAGTCTTC GACTCTCC ATCCCCAGT ATCCCCAGT ATCCCCAGT ATCCCCAGT ATCCCCAGT CAGCCCCC CCTCTGCAGA CAGGCACC CCCCTTTGCAGCAT CCGCGGAC CCGCTCTCC CCCCTCTTGC CCCCCTTTC CCCCCTTC CCCCTTC CCCCCTTC CCCCCTTC CCCCCTTC CCCCCTTC CCCCCTTC CCCCCTTC CCCCTTC CCCCCTTC CCCCCTTC CCCCTTC CCCTTC CCCCTTC CCCCTTC CCCCTTC CCCTTC CCCCTTC CCCTTC CCCCTTC CCCCTTC CCCCTTC CCCCTTC CCCTTC CCCTTC CCCTTC CCCTTC CCCCTTC CCCTTC CCCT	.2299 21	31	CCCAACCCAC CACCAAGCCT CACCTGGGCT CACCTGGGCT CACCTGGGCT CGCCTCGTG GGTTGGCTGC GGTCGGTG ATCCTGGTT TGACCGCGG ATGCGGCGC ATGCGGCGCG ATGCGGCGCG ATGCGGCGCG ATGCGGCGCG ATGCTGTTCC ACCCTTAAG TATCTGAATC CAGCGGAGG TGCACCTGCAC CAGCTCATCC CGGTCCCGG CACCTGTCACC CACCTGCACC CACCTGTCACC CACCTCC CACCTCC CACCTCC CACCTC CACCT CACCTC CACCT CACCTC C	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGGG TAGAGCTCCC TGACTCGT CTTCGAAGGG CTGACTCGGT CTTCGAAGGG CTGACTCGGT CTTCGAAGGG CTGACTCGT CTTCGGAAGG CTGACCGGACG CCAAAAAGTG GGTAACCGAT AGTTGTATTG GGTCCACGCT GGGAAATCAT AATTGCCCAA ATTCGCGAGGG TGAACAGGGA TGTGCCCTGT	120 180 240 300 360 420 480 540 600 660 720 840 900 1020 1020 1140 1200 1260 1320
50 55 60	Coding sequil GGCATCCCGA GGCGGCGGT GGCGGCGGGT GGTGCTTGGC GGCGGGGGGGC TCGGCAGCGGG TCGGCAGCGGG CGGACGTAG TCCTGCCAC GGAAGGGAGG CGGACGTAG TGCTCAGGACCA TGCTCAGGACC ATTAGTGGAT CGCGACTTGGT CAGGACC ATTAGTGGAT TGCTCAGGACC ATTAGTGGAT TGCTCAGGACC TGCTCCAG	ience: 641. 11 GTGCACCGCT CAGGCTTCGC ACAGCCTCCG ACAGCCCCCG ACAGCCCCCG ACAGCCCCCG ACAGCCCCG ACAGCCCCG ACAGCCCCG ACAGCCCCG CCGCGCTTCC GTTTCGGGTT CTTGCAGGAT GCCCCGGAA CCAGCTCTCC GACCACCC ACACCCCC ACCCCACCC ATCCCCACCC ATCCCCACCC ATCCCCACCC ATCCCCACCC ATCCCCACCC ATCCCCACCC CCCCTCTTCG CACCCCACC ATCAGCCACC CCCCTCTTCG ATCACCCACC ATCACCCACC ATCACCCACC ATCACCCACC	.2299 21	31	CCCAACCCAC CACCGAGCGT CACCTGGCT CACCTGGCT CGCCCTCGTG GAGTCAGTTT GTGGCGGCGT TGACCGCCGG ATCCTGGTTC ATCCTGGTG TGACCGCCGG TGACCTAGT CACCCTAAGC CACCTAAGC CACCTAAGC CACCTAAGC CACCTAAGC CACCTAAGC CACCTAAGC CACCTAAGC CACCTAGC CACCTGGCGC CACCTGGCGC CACCTGGCGCG CACCTGGGC CACCTGGGGC CACCTGGGG CACCTGGGGG CACCTGGGGG CACCTGGGGG CACCTGGGGGG CACCGGGGTG CACCCGGGGGG CACCCGGGGGG CACCCGGGGGG CACCCGGGGGG CACCCGGGGGGG CACCCGGGGGGG CACCCGGGGGGG CACCCGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGACTCCCC TGACTCCCC TGACTCGGCCCC TGACTCGGACGC CCTTCGGACGC CCTTCGGACGC CCTTCGGACGC TGACTCGTCCC TGACTCGCCCC GGGGAAAAAGTG AGTTATTG AATTGCCACGCT TGGGACGC TGACCACGCT AATTGCGGCGCG TGAACAGGGA ATTGCCCCTGT AATTGCCCAGGGT AATTGCCCAGGGGAAGTGCCCTGT AGCTCAGAGGGAAGGGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 91020 1020 1220 1260 1320
50 55 60 65	Coding sequil GGCATCCCGA GGCGGGGGGGGGGGGGGGGGGGGGGGG	ience: 641. 11 GTGCACCGCT CAGGGCTTCG GTCGGCCCC GTCGGGCCCC GTCGGCCCC GTCTGGGCCCC GTTCGGCCCC GTTCGGCCCC GTTCGGCCCC GTTCGGCTCC GTTCGCGCAC CCACCCGCAC CCACCCCC ACACCCCCC ATCCCCACC ATCCCCACC CCACCCCCC CCACCCCCC CCCCCCCC	2299 21	31	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAGGCT CACCTGGGT GAGTCAGTTT GTGGCGCGT GCTCGCTTCT ATCCTGGTTC CTGACCGCGCC ATGCGCTCCT ATCCTGATC CACCAGGAGCC CACCTCAACC CACCTCAACC CACCTCATC CACCAGGAGCC CACCTCATC CACCAGGGCC CACCTCATC CACCAGGGCC CACCTCATC CACCAGGGCC CACCTCATC CACCAGGGCC CACCTCATC CACCAGGGCC CACCTCATC CACCAGGGCC CACCTCACC CACCAGGGCC CACCAGGCC CACCAGC CACCAGGCC CACCAGGCC CACCAGC CACCAGC CACCAGC CACCAGC CACCACAC CACCACAC CACCACAC CACCACAC CACCAC	GATGGTCTGG TTCGGTCGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTGGTAAC CTTCGGACGC TCTGGACGC TCTGGACGCG TCTGGACGCG TCTTCGAACGGT TGGTGTATTG GGCAAAAAGT TGGTGTATTG TGGGGGGG TGGACACGGT AAATTGCCCAA TTCGGGGGG TGAACAGGGA TTGGGGCGC TGAACAGGGA TTGGGCCCTGT AATTGCCCAGGT TGGGCCCTGT AGCTCAGGGA TGTGCCCTGT AGCTCAGGGA TGTGCCCTGT AGCTCAGGGA TGGCCCTGT AGCTCAGAGG AGAAGGCTCC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1020 1260 1320 1340
50 55 60	Coding sequil GECATCCCGA GAGCTGCGCC GGGCGGGTTGTC GGGCTTGGC GGCGCTTGGCAC GGAAGGGGG CGGAAGGGAGG CGGAACTAGG CGGACTTAGC CAGAGCAAG GCGGTTGTC CAAGAGCAAG GCGGTTGGC ATTAGTGGAC ATTAGTGGAT GGTGAAATGC TGACTCCAGCAC ATTAGTGGAT GGTGAAATGC TGACTCCAG GATCGATATCG GGGTTTGACATCCCC GATCGATTAGT GGGAAATGC CTGCGTCCAG GATCGATTAGT GGGATTGAC GGGCTTTGAC GGGCTTTGAC GGGCTTTGAC GCGCTTGACAC GCGCCTGGAC GCGCTGGAC GCGCTTGAC GCGCTGGAC GCGCTGGAC GCGCTGGAC GCGCTGGAC GCGCTTGAC GCCCTGGAC GCCCTGAC GCCCTGGAC GCCCTGAC GCCCCTGGAC GCCCCTGGAC GCCCCTGGAC GCCCCTGGAC GCCCCTGGAC GCCCCTGAC GCCCTGAC GCCCCTGAC GCCCCTGCAC GCCCCTGCCCTCC GCCCCTGCCC GCCCTGCCCC GCCCTGCCCC GCCCTCCCT	ience: 641. 11 GTGCACCGCT CAGGGCTTCC AGGCCCCCT GTCGGGCCCC AGGCCGCTTCC AGGCCCCCC GTTGCAGGA CCTTGCAGGA CGCTCGCCAG CGCCTTCC CGCCGCTTC TTGGAGGTGC CGCCCCCC CGCCCTCT TTGGAGGTGC CAGCCCC CCACCCACT ATCCCAGCA TTGCCAACT ATCCCAGT CAGCCCCC CGGCCATC CAGCCCCC CGCCCACT TTGCGCAAT TTGCGCAAT TTGCGCATC TTGCGCATC CAGGGCACC CCACCGCT CCCCCGCGCTC CCCCCGGCCC CCCCCCTCTTC CCCACCGGGCCC CCCCCCGCTCT CCCCACCGGGCCCC CCCCCCGGGCCCC CCCCCCCCCC	2299 21	31 CCCGCCTTGC CCCGCAACAG CCCGCAACAG CCCCACCAG CCCGCACCAG CCCCACCCA	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCCACACCCAC CACCCACACCCAC CACCCACACCCAC CACCCACACCCACACCCC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGGCS TAGAGGTCCCC TGACTCGTCGC TGACTCGTCG CTTCGAAGGC CTAGAGGCCCC TGACTCGTCG TCTGGAAGGC CTTCGGACGC CCAAAAAGTG GCTCACACGCT CGGGAAATCAT AATTCCCAA ATTCGGGGCGC TGACCCCGT GAACAGGCT AGTCAACAGGG TGAACAGGCC TGAACAGGCC TGAACAGCCCT AGCTCAAGAGC TGAACAGCTCG AGAAGGCTCG TCTTCCTGAT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1020 1200 1200 1320 1380 1440
50 55 60 65	Coding sequil GGCATCCCGA GGCGGCGGGT GGCGGCGGGT GGTGCTTGGC GGCGGGGGGGG	ience: 641. 11 GTGCACCGCT CAGGCTTCG GAGGCCCCCT GTCGGGCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCC CCGCCTTCC TTTGCGGTT CTTGCAGGAT CCACCCACC ACACCCCC ACCCCACCC CCACCCAC	.2299 21	31	CCCAACCCAC CACCGAGCGT CACCGAGCGT CACCTGGGCT CACCTGGGCT CACCTGGCTC CACCTGGCTC CACCTGGCTC ATCCTGGCTC ATCCTGGTGT ATCCTGGGTC ATCCTGGGGG ATCCTGATC ATCCTGGGGG ATCCTTAATC CAGCGGGAG ATCCTGATC CACCTCAGG CACTGTGTTC CACCTGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGACTCCCC TGACTCCCC TGACTCGTCCC TGACTCGGACGC CCTAGGGAAAAGTG GCTCCACGCT GGGGAAATCAT AATTGCCCAA A TTCGGGGCGC TGACCAGGCT TGACAGGGA A TTCGGGAGGC TGAACAGGGA TTCGGAGGCCC TGACTAGGGCCC TGACTAGGGCCCC TGACTAGGGCCCC TGACTAGGGCCCC TCTTCGGAGGC TGAACAGGGA TTCGGGGTGCCTTT TGGTCCCTGT TGGACAGGGC TGTTCCTGGAT TCTCGGGTGGC TCTTCGTGAT	120 180 240 300 360 420 480 600 600 720 780 840 1020 1080 1140 1260 1320 1440 1560
50 55 60 65	Coding sequil GGCATCCCGA GGCGGGGGG GGCGGGGGGGGGGGGGG	ence: 641. 11 GTGCACCGCT CAGGGCTTCG GTCGGCCCC GTCGGGCCCC GTCGGGCCCC GTCTGGGCCCC GTTCGGGCCCC GTTCGGCCCC GTTCGGCTCC GTTTCGGTTC GTTTCGGTTC GTTTCGGTTC GTTCGCCAC GCCCCCCC GGGCCATC CCACCCACT ATCCCCACT ATCCCCACT CCACCCAC	.2299 21	31	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCCACACCCAC CACCAC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGGCS TAGAGGTCCCC TGACTCGTCGC TGACTCGTCG CTTCGAAGGC CTAGAGGCCCC TGACTCGTCG TCTGGAAGGC CTTCGGACGC CCAAAAAGTG GCTCACACGCT CGGGAAATCAT AATTCCCAA ATTCGGGGCGC TGACCCCGT GAACAGGCT AGTCAACAGGG TGAACAGGCC TGAACAGGCC TGAACAGCCCT AGCTCAAGAGC TGAACAGCTCG AGAAGGCTCG TCTTCCTGAT	120 180 240 300 360 420 480 600 660 720 720 720 900 900 910 1020 1080 1140 1220 1320 1350 1440 1500 1650
50 55 60 65 70	Coding sequil GGCATCCCGA GGCGGCGGT GGCGGCGGGC GGCGGGGGGGGGG	ience: 641. 11 GTGCACCGCT CAGGCTTCC AGGCCCCCT GTCGGGCCCC AGGCCCCCC AGGCCCCCC AGGCCCCCC AGGCCCCCC AGGCCCCCC AGGCCCCCC CCGCCTTCC TTGCAGGAT CCTGCCAGA CCAGCTCTC ATCCCCACCAC ATCCCCACCAC ATCCCCACCACC CCCCCACCAC CCCCCCACCAC TTGCGCAAC CCCCCCACCAC TTGCGCAAC CCCCCCACCAC TTGCGCAAC CCCCCCACCAC TTGCGCAAC CCCCCACCAC TTGCGCAAC CCCCCACCAC TTGCGCAAC TTGCTTTCG TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTTC TTGAGCTC TTGAGCCT TTGAGCTC TTGAGCTC TTGAGCCT TTGAGCT TTGATTTAAA	2299 21	31	CCCAACCCAC CACCGAGCGG CACCGAGCGG CACCGAGCGG CACCTGGGCG CACCTGGCGG CACCTGGCGG ACCCTGGCGG ACCCTGGCGG ACCCTGGCGG ACCCTAGGG ACCCCTAAGG ACCCCTAAGG ACCCCTAAGG CACCCTAAGG CACCCTAAGG CACCTGGAGG CACCTGGGGGGGG CACCGGGGGGGGGG	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGACTCGT CTTCGAAGCG TGACTCGTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTACG TGAGCGGAT TGGGACGGC TGACTGGACGGC TGACTGGACGC TGACTGGACGC TGACTGGACGC TGACTGGACGC TGACCAGGT AATTGCCCAAG TTCGGGACGC TGAACAGGGA TTCGGGTCGC TGACTGGACGC TGAACAGGGA TTCGGGTCGC TGTCCCTGTATG TCTGGGTGG TCTTCTGGATG ATCGGGTGG AGATCACAAG TTCGGGTGG TCTTCTGGATG ATCGATGGAAA TGATGACAAA TGATGATACAA	120 180 240 300 360 420 480 600 660 720 780 840 1020 1020 1140 1260 1320 1440 1550 1620 1620 1620
50 55 60 65	Coding sequil GEATCCCGA GAGCTGCGC GGCGGCTGTCT GGTGCTTGGC GGCATCCCA GGAGCGGGC CGGCAGCCA GGAGCGGGC CAGAGCGAGG CAGAGCGAGG CAGAGCGAGG CAGAGCGAGG CAGAGCGAGG CAGAGCGAGG CACAGAGCAGA GCACTTAGC GCACTTAGC CAGAGCGAGC CAGAGCGAGG CTCAGGACC TAGAGTGGAC GGCGTTGGT GCTCAGGACC TGCACTCCAG GACATAGGACC CGACAAAGCTT CGCACAAACCTG CGCACAAACCGCA TGCCAAACACTG GCAAAACCGCA CGCAAAACCGCA CGCAAAACCGCA CGCAAAACCGCA CGCAAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAAACACTG CCCAAAACACTTACCCAAACACTTC CCCAAAACACTTACAACACTACACCCC CCACAAACACTTACCCAAACACTTACCCAAAACACTTACAAAACACTTACAAAACACTATAAAACATATAAAAAA	ience: 641. 11 GTGACCGCT GTGACCGCT AGGCCCCCCT AGGCCCCCCC AGGCCTCCC AAGGCGCCCCC AAGGCGCCCCC AAGGCGCCCCC AAGGCGCCCC CCGCGCTTCC ACGCCCCCC ACGCCCCCC ACGCCCCCC ACGCCCCCC ACCCCACT ATCCCCAGT ATCCCCAGT CAGCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCC	.2299 21	31 CCCGCCTTGC CCCGCCTGCC CCCGCCGCGGGGCCCCG CGCAGCCGGG CCCCCACCCG CCCGCACCCC CAAAGGGGACC CCGCAACCC CAAAGGGGACC CTGAACCGG GATCAGGGG ATGAGTTCAA A GGCTTCCAC CG CACCCTACC AAAGGGACC AAAGGGACC CTGAACGGGGACC CTGAACGGGACC CTGAACGGGACC CTGAACGGGACC CTGAACGCGAACCCCTACC CCCTACCGCACCCCTACC CCCTACCGACACC CCCCTACCGACACC CCCCTACCGACACC CCCCTACCGACACC CCCCTACCGACACC CCCCTACCGACACCC CCCCACACCCCACC CCCCCACCC CCCCCCCC	CCCAACCCAC CACCGAGCT CACCGAGCT CACCGAGCT CACCGAGCT CACCTGGGC CACCGAGT CACCTGGGC CACCGAGT CACCCTCAC CACCCGAGC CACCCTAC CACCCCACA CACCCCACA CACCCCACA CACCCCACA CACCCCACA CACCCCACA CACCCCACA CACCCACAC CACCAC	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC TGATGGCCC TGACTCGTAG CTTCGGAGG CCTAAAAGTG GGGAAAATTA TGGGGAGA TTGGGAGG TTGGGAGG TTGGGAACT TGGTAATCAG TTCGGGGGG TGGAAAATCAT AATTGCCAA TTCGGGGGC TGTCACGGT TGTGCCCTGT AGTCACAGGT TGTGCCCTGT AGTCACAGGA TTCGGGGGCC CTGATGGAAAA TTGTGGGAAA ATGTTGAGAAA AATGTTGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAAA AATGTTGAGAGAGA	120 180 240 300 360 420 480 540 660 720 780 840 900 950 1080 1140 1200 1320 1320 1440 1500 1680 1740 1680 1740
50 55 60 65 70	Coding sequil Gecatocoga Gecatocoga Gecatocoga Gecatocoga Gecatocoga Gecatocoga Gecatocoga Gecatocoga Tocotocoga Gecatocoga G	ience: 641. 11 GTGCACCGCT CAGGGCTTCC AGGGCCCCCT GTCGGGCCCC AGGCGCTCCC AGGCGCTCCC AGGCGCTCC AGGCGCTCC AGGCGCTCC AGGCGCTCC AGGCGCTTC ATTCAGGAT ATTCAGGAT CAGCCCCC CACCCACT ATCCCAGT ATTCCCAGT ATTCCCAGT CAGCCACT CCCACCCACT ATTACCAG TTGCGCAACT CAGGCACCC CCCACCAGAG TTGCGCAACT CCCACCGAGG TTGCGCAACT CCCACCGAGG TTGCGCACC CCCACCGAGG TTGCGCACC CCCACCGAGG TTGCGCACC TTGCGCCC TTGCGCCACC TTGCGCCC TTGCGCCC TTGCGCCC TTGCGCCC TTGCGCCC TTGCGCCC CCCCACGGAG TTCCCCCCCCCC	.2299 21	31	CCCAACCCAC CACCGAGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGCTGC CACCTGCT ATCCTGGTT ATCCTGGTT ATCCTGGTT ATCCTGGTT ATCCTGAT ATCCTAATC ACCCCTAAGC ACGGGGGGG CACTGTATC CAGCTCATC CAGCTCATC CAGCTCATC CACCTCATC CACCTGTGAGG ACGGGGGGG ACTGGAGGG ACTGCAGGG ACTGGAGGG ACTGGAGG ACTGGAGGG ACTGGAGG ACTGGAGGG ACTGGAGG ACTGGAG ACTGGAGG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGAG ACTGGA	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGGG TAGAGGTGCCC TGACTCGTCG CTTCGAAGGG CTGACCCC TGACTCGTAC CTTCGAAGGG TGAGCGGAT AGTGAGCGGAT AGTGAGCGGAT AGTTCGAAGGG TGACCCGT TGGGAACACGGA ATTCGGGGCGC TGAACAGGGA ATTCGGGGCGC TGAACAGGGAA ATTCGGGGCGC TGAACAGGGAA TTCGGGGCGC TGAACAGGGAA ATTCGGGTGG CAGAGAGCTCCC CTGATGGAAA ATTGATGAACAG ATGAATACAA ATGATTGAACA	120 180 240 300 360 420 480 600 660 720 1020 1020 1140 1200 1320 1380 1440 1550 1650 1660 1740 1860
50 55 60 65 70	Coding sequil GGCATCCCGA GGCGGCGGT GGCGGCGGGC GGCGGGGGGC GGCGGGGGGGG	ience: 641. 11 GTGCACCGCT CAGGCTTCGC ACAGCCTCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCC CCACCCAC	.2299 21	31	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCCAGGCT CACCTGGGCT CACCTGGGCT GAGTCAGTTT GTGGCGCGGT GCTTGCTGCT CACCCGGCTCCT ATCCTGGTTC ATCCTGGTTC ATCCTGGTTC ATCCTGGTTC ATCCTGGTC ATCCTGCTC ATCCTGGTC ATCCTGATC ACACCTCAACC CACCTCAACC CACCTCAACC CACCTCAACC CACCTCATC CACCTCACG CACCTCATC CACCTCACG CACCTCATC CACCTCACG CACCTCACC CACCTCACG CACCTCACC	GATGGTCTGG TTCGGTCGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTGGCC TGACTGGTAAC CTTCGGACAGC TGGTGTATTG GGCAAAAGTO GTGAGCGGATATTG AATTGCCGA TTGGGGGGG TGACAGGGT AATTGCGGGGG TGACAGGGA TTGGGGGGG TGACAGGGA TTCTCGGGTGG TGTGCCCTGT TCTTCTGGT AATTGCCCAG TTCTCTGAT AATTGCCCAG TTCTCTGAT AATTGCCCAG TGACAGGGA TTGGGGTGG CTCTCTCGTGAT TCTTGGGGGGG GAGATCGTCCC CTGATTGAAAA AATGTTGAGAG ATGAATACAA AATGTTGAGAG ATGGAAAATACAA ATGCGGAAAATACAA ATGGGGAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGGGAAAATACAA ATGCGAACAGAG	120 180 240 300 360 420 480 600 660 720 780 840 900 950 1020 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800 1800
50 55 60 65 70 75	Coding sequil GEATCCCGA GAGCTGCGC GGCGGCTGTCT GGCACCCG GGCACCGGC GGCACCGGC GGCACCGGC CGGAGCGGC CGGAGCGGC CGGAGCGGC CGGAGCGGC CAGAGGGAGC CAGAGGGAGC CTCAGCACT GCTCAGCACT GCTCAGCACT GCTCAGCACT GCTCAGCACT GCTCAGACC CGGCTCAGG GCATAGGGCC CGGCTCAGG GCATAGGCC CGGCTCAGG GCACAAGCC CGACAAGC CGACAACCC GGCACAACCC GGCACAACCC GCACAACCC GCACAACCC GCACAACCC CCACACACC GCACAACCC CCACACCC CCACACACC CCACACCC CCACACCC CCACACCC CCACACCC CCACACCC CCACACCC CCACACC CCACACCC CCACACC CCACAC CCA	ience: 641. 11 GTGACCGCT CAGGCTTGC AGGCCCCCT GTGGGCCCC AGGCCTTCC AAGCCGCCCC AAGCCGCCCC AAGCCGCCCC AAGCCGCCCC AAGCCGCCC CGCCCTCC ATCCAGGAC CCACTCTTC CACCACT ATCCCAGT TTGGAGCACC CCACCACT ATCCCAGT TTGCCAAT CAGGCACC CCCCTCTTG CATTAACCG TTGAGCACC CCCCCCCCC CCCCCCCCC CCCCCCCC CCCCCC	.2299 21	31 CCCGGCTTGC CCCGCCTTGCC CCCGCCTGCCCCGC CCGCCGCGGGGTCCCG CCCCCCACCGG CCCCCCACCGG CCCCCCACCGG CCCCCCACCGG ATGGCTCCAC ATGGCGGGGCCCCACCCG CAAAGGGGACC CTGAAGTGCAG A TGACTGCAG A TGACTGCAG T CACCTTCCAC GC ACCCCTACC A AGGGGACCG T CCTGACAGC T CCTGACAGC CCCTACCTTCACAGC CCCTACCGC A AGGGGACCT T CCTCGACAGC CCCTACCGC A AGGGCACCT CCCTTCACAGC CCCTACGC A AGGGCACCT CCCTTCACAGC CCCTACGC A AGGCACCT CCCTTCACAGC CCCTACGC A AGGCACCT A ATTAGATAT A ATTAGATAT CCCTTCACAGC CCCTGCGAGGC CCCGGAGGCACCT CCCTCCTCCTCCC CCCTCCCCCC CCCCCCCCC	CCCAACCCAC CACCGAGCT CACCTGGGCT CACCTGGGCT CACCTGGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTTGCTGCT CACCCTTCGCT CACCCTTCGCT CACCCTTAGCT CACCCTAAGC CACCCTAAGC CACCCTAAGC CACCTAAGC CACCTAGC CACCTAGC CACCTAGC CACCTGAGC CACCTGAGC CACCTGAGC CACCTGGAGC CACCTGGAGGG CACTGGAGC CACCTGGAGGG CACTGGAGG CACTGGAGGG CACTGGAGG CACCCCAAGGG CACCCAAAC CACCCAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAC CACCCAAAC CACCCAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAC C	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CGCGAGACATC CTTCGAAGCG TAGAGCTCCC TTGGAAGCG TGGATCCC TTGGAAGCG TGGAGCGAC CTTCGACGC CTTCGACGC CTTCGACGC CTTCGACGC CTTCGACGCG CTCACACAGCT TGGTTATTG GGAAATCAT AATTCCCAA ATTCCCCAG TTCGGGGGCC CTCACGCT TCTCGGGGCC CTCACGCT CTCACGACAC CTCACACAC CTCACACAC CTCACACAC CTCACTCA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1020 1140 1260 1320 1320 1350 1440 1500 1680 1740 1860 1860 1920
50 55 60 65 70	Coding sequil GGCATCCCGA GGCGGCGGT GGCGGCGGGC GGCGGGGGGC GGCGGGGGGGG	ience: 641. 11 GTGCACCGCT CAGGCTTCGC AGGCCCCCC AGGCCCCCC AGGCCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCC ACAGCCCC ACAGCCCC ACAGCCC ACAGCCCC ACAGCCC ACAGCCC ACAGCCC ACAGCCC ACAGCCC ACAGCCC ACAGCCC ACAGCCC CCACCCAC	.2299 21	31	CCCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCAACCCAC CACCCAGGCT CACCTGGGCT CACCTGGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGCTTCT CACCCCCC CATCGCTCCT CACCCCACAC CACCTGACC CACCTCCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTC CACCT CACCTC CACCTC CACCTC CACCTC CACCTC CACCT	GATGGTCTGG TTCGGTCGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGCG TAGAGCTCCC GGGGTGCCCC TGACTGGTAAC CTTCGGACGG TCTGGAAAGTG GTGAGGCGAT TGGTTATTG GGCAAAATCAT AATTGCCGAA ATTCGGGGGG TGACAGGGG TGACAGGGG TGACAGGGG TGACAGGGG TGACAGGGG TGACAGGGAAT TCTGGGGGGG CTGATGGAAA ATTGCGGGGGG CTGATGGAAA ATTGCGGGCGC CTGATGGAAA ATGTTGAGAG AATTGCAGAGG CTGAGAGATACAA AATGTTGAGAG CTGAGAGAGG CTGAGAGAGG CTGAAGGAGG CTGAAGGAGAG CTGAAGAGAG CTGAAGAGAG CTAAAGTTGACAC CTGGCGCCCC CTGGCGCCCC	120 180 240 300 360 420 480 600 660 720 780 840 1020 1080 1140 1200 1320 1320 1440 1500 1620 1620 1680 1740 1800 1980 2040 2100
50 55 60 65 70 75	Coding sequil GEATCCGA GAGCTGCGC GGCGGCTGTCT GGCAGCCG GGCAGCGGGC GGCAGCGGGC GGCAGCGGGC GGCAGCGGGC GGAAGGGGGG CGGAAGGGGGG CGGACGTAG GCAGCGGAG GCAGCGGAG GCAGCGGAG GCAGCGGAG GCAGCGGAG GCAGAGGGAGA GCGGGTTGGC GGAAAGGCGG GGAAAGGCT GGCAGACC GGACAAGGCTCAG GCGGTTGGA GCGCTCGAG GCACAAGGCT GGAGAACTT GCCAACAG GCATTGGAC GCACATAGCACC GCACAAGGCT CGCACACAG GCATTGGAC GCACACC GCATTGGAC GCATTGGAC GCACACC GCATTGGAC CCACCAGAAGTCC CCACCAGCAGAC CCACCAGAAGTCC CCACCAGGAC CCACCAGCAGAC CCACCAGCAGCAC CAGCAGCAC CAG	ience: 641. 11 GTGACCGCT CAGGCTTCC AGGCCCCCT GTCGGGCCCC AGGCCTCCC AAGCCGCCCC AAGCCGCCCC ACGCCTTCC AAGCCGCCCC GTTTCCAGGAC CCCCCCGGAC CCACCACT ATCCCAGGAC CCACCACT ATCCCAGGAC CCTCTGTG CTTTCCAGGAC CCCCCTGTTC CCCCCGGAC CCCCCCCCC CCCCCCCC CCCCCCCC CCCCCCCC	.2299 21	31 CCCGCCTTGC CCCGCCTGCC CCCGCCACGCG CCCCCCCGC CCCCCCCGC CCCCCCACCCG CCCCCCACCCG CCCCCCACCCG CAAGGGGACC CTGAGTGCAC CTGAGTGCAC CTGAGTGCAC CTGAGTGCAC CTGAGTGCAC CTGAGTGCAC CTGAGTGCAC ATGGCTCACCGC CAAGGGGACC CAACTTCACC CACCTTCCAC CACCTTCCAC CACCTTCACC CACCTTCACCC CACCTTCACCC CACCTCCCC CACCTTCACCCC CACCTCCCCC CACCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCAACCCAC CACCCAACCCAC CACCCAACCCAC CACCCAGGCT CACCTGGGCT CACCTGGGCT CGCCTCGTG GGTTGGCTGC CGCTTCTGCTGC CGCTGCTTCT ATCCTGGTTC TGACGCGGCT ATGCGGCGC ATGCGGCGCC ATGCGGCGCC ATGCGGGGGGC ATGCGGGGGGC ACGCTAAG CACCCTAAG CACCTAAG CACCTAAG CACCTAAG CACCTAAG CACCTAAG CACCCAAC CACCTGGGGGG CACTGGAGG CAATGGAC CACCCAAAC CACCAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC CACCCAAAC C	GATGGTCTGG TTCGGTCGCC CGCTCCGAGT CTCCTCCCGC CGCTCTGGTCCT CTTCGAAGCG TTAGAGCTCCC TTTCGAAGCG TGAGCGCCC TGACTCGTCCC TGACTCGTCCC TTGCGACGC CCTAAAAAGTA TTCGGACGC TGACACGCT AATTCCCAA TTCGGGCGCC TGACTCGTCACC TTTCGGACGC TGACACGCT TGGTAATCAC TGTCACACGCT TGGTGATATCCCAA TTCGGGGCGC TCTTCGTGAT TTTCGGGGCGC CTGATGGAAA TTCTGGGGTGG TCTTCGTGAT TCTGGGTGG TCTTCGTGAT TCTGGGTGG TCTTCGTGAT TCTGGGTGG TCTTCGTGAT TCTGGGTGG TCTTCGTGAT TCTGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTTCGACAGAGG TTAAGTTGAGG TTAAGTTGAGG TTAAGTTGAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1680 1740 1860 1740 1860 1920 1860 1920 2040 2160
50 55 60 65 70 75	Coding sequil GECATCCGA GAGCTGCGC GGGCGGGGG GGGCGGGGG GGGCGGGG GGGCGGGGG TCGGCAGCGGG CGGAGCGGG CGGAGCGGG CGGAGCGGG CGGAGCGGG CGGAGCGGG CGGAGCGAG GCGGGCGTTGGT CAAGAGGAG GCGCGTTGGT CCAGGAC ATTAGTGGA CGGGACTAG GGGAATTGG CGGACTAG GGGAATTGG CGGCCTGGAC CGGCCCGGAC CGGCCCTGGAC CGCCCTGGAC CGCCCTGGAC CGCCTGGAC CGCCTGAAC CGCCTGGAC CCACTGGAC CCACTGCAC CCACTCGAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTAC CCACTCCAC CCACCAC CCACTCCAC CCACCAC CCACTCCAC CCACTAC CCACTCCAC CCACTCCAC CCACTCCAC CCACTCCAC CCACTCCAC CCACTCCAC C	ience: 641. 11 GTGCACCGCT CAGGCTTCC AGGCCCCCT GTCGGGCCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCTCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACAGCCCCC ACCCCACT ACCCCCACT ACCCCCCCACT ACCCCCACT ACCCCCACT ACCCCCCCC	2299 21	31	CCCAACCCAC CACCGAGCT CACCGAGCT CACCGAGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT CACCTGGCT ATCCTGGCT ATCCTGGTT TGACCGCGC ATGCGCT ATCCTGGTT TGACCGCGC ATGCGTGTT CACCCTAAGC TATCTGATT CAGGGGAG TATCTGATT CAGGGGAGG CACTGTAGC CACTGTAGC CACCTGCAGG GACCCTAC AGGTCCCGG GACCCTAC AGGTCCCGG CACCTGCAGG GACCCTAC AGGTCCCGG CACCTGCAGG GACCCTAC AGGTCCCGG CACCTTGCCC CACCGGGAGG GACCCTACGG GACCCTACGG CACCCTACGG CACCCTACGG CACCCTACGG CACCCTACGG CACCCTACGG CACCCTACG CACCCTACGG CACCCTACT CACCCTACGG CACCCTACT CACCCTACGG CACCCTACT CACCCTACGG CACCCTACT CACCCT CACCT CACCCT	GATGGTCTGG TTCGGTCGGC CGCTCCGAGT CTCCTCCCGG CCCTATCGGC GGGGAACATC CTTCGAAGGG TAGAGCTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTCCC TGACTCGTCC TGACTCGTACGC CCTAGAGCGC CCAAAAAGTG AGTGACCGGT AATTGCCAA TTCGGGCCCC TGACTCGTAC ATTGGGTGGC CAGAAAGTGA TTCGGGCCGC TCTCGGACGC CAGAAAACTGA ATTGCCAA TTCGGGTGG AGTCACCTT AGTTGACAGGG AGATCATCC CTGATGGAAA CTGGGGTGG CAGAAAAGTG TCCACACT TCTGGGTTGG CTGACAGAGG CTGAGACAGAG CTGAGAAAATAT CTCGACAGAG CTGAGAAAATAT CTCGACAGAG CTGAGAAAATAT CTCGACAGAG CTGAGAAAATAT CTCGACAGAG CTGAGAAAATAT CTCGACAGAG CTGACACAGAG CTAAAAGTTGAG CTAAAACTTGAC CTGGCCCCC AAACTGGTTC GTGATGCCAC	120 180 240 300 360 420 480 600 660 720 780 840 1020 1080 1140 1260 1320 1440 1500 1680 1740 1880 1920 1980 2100 2100 2100 2220
50 55 60 65 70 75	Coding sequil GGCATCCGGA GAGCTGGGC GGCGGGTTGTCT GGTGCTTGGC GGCAGCGGC GGCAGCGGG GGCAGCGGG GGCAGCGGG CGGAGCGGG CGGAGCGAG GGAGCGAGG CAGAGCGAG GCAGTTGGC CAGAGCAGAG	ience: 641. 11 GTGACCGCT GTGACCGCT CAGGGCTTCC AGGCCCCCCT AGGCCCCCCC AGGCCTCCC AGGCCTCCC AGGCCGCCC CCGCCGCAC CCGCCCCCC AGGCCGCCC CCGCCCCC AGGCCGCCC CCGCCCCC AGGCCGCC CCGCCCCC AGCCCCCC AGCCCCCC AGCCCCCC ATCCTCGCA ATCCCCAGT TGGACGCCC CCCCCCCC TTGGACGCCC CCCCCCCC TTGGACCCC CCCCCCCC TTGGAGCCCC CCCCCCCC TTGGAGCCCC CCCCCCCC TTGGAGCCCC CCCCCCCCC TTGGACCCC CCCCCCCCC TTGGCCCCC CCCCCCCCC CCCCCCCC	.2299 21	31 CCCGGCTTGC CCCGGCACGG CCCCGGGGGGGGGGGGGG	CCCAACCCAC CACCGAGCT CACCGAGCT CACCGAGCT CACCTGGGCT CGCCCTCGT GGGGGGGGGG	GATGGTCTGG TTCGGTCGCC CGCTCCGAGT CTCCTCCCGC CGCTCTGGTCCT CTTCGAAGCG TTAGAGCTCCC TTTCGAAGCG TGAGCGCCC TGACTCGTCCC TGACTCGTCCC TTGCGACGC CCTAAAAAGTA TTCGGACGC TGACACGCT AATTCCCAA TTCGGGCGCC TGACTCGTCACC TTTCGGACGC TGACACGCT TGGTAATCAT AATTCCCAAA TTCGGGGCGC TCTTCGTGAT TTTCGGGGCGC CTGATGAAAA TTCTGGGTGG CTGATGAAA TTCTGGGTGG CTGATGAAA TTCTGGGGTGC CTGATGAAA TTCTCGACAGG TCTTCCTGAT TCCGACAGAG TCTCGACAGAG TTCCGACAGAG TTAAAGTTGAG TTAAAGTTGAG TTAAAGTTGAG TTAAAGTTGAG TTAAAGTTGAC CCTGGCCCCC AAACTGGTCC AAACTGGCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1080 1140 1220 1380 1560 1560 1670 1880 1740 1890 1980 2000 2010 2160 2160 2160 2160 2220

	CCCTGGACCA GAACAGACTG GAAACTGGGC AGCAAGCAGC CTGGAACCAC CTCAGACATC CTGGACTGGG AGGTGGAGGC AGAGCCCCCC AGGACAGGAG CAACTGTCTC AGGGAGGACA	2400 2460
	GAGGAAAACA TCACAAGCCA ATGGGGCTCA AAGACAAATC CCACATGTTC TCAAGGCCGT	2520
5	TAAGTTCCAG TCCTGGCCAG TCATTCCCTG ATTGGTATCT GGAGACAGAA ACCTAATGGG AAGTGTTTAT TGTTCCTTTT CCTACAAAGG AAGCAGTCTC TGGAGGCCAG AAAGAAAAGC	2580 2640
,	CTTCTTTTC ACTAGGCCAG GACTACATTG AGAGATGAAG AATGGAGGTT GTTTCCAAAA	2700
	GAAATAAAGA GAAACTTAGA AGTTGAAAAA AAAAAAAAAA	2741
	Seg ID NO: 53 DNA Sequence	
10	Nucleic Acid Accession #: Eos sequence	
	Coding sequence: 4001959	
	1 11 21 31 41 51	
	GCCATCCCGA GTGCACCGCT CCCGCCCCGC CCCGCCTTGC CCCAACCCAC GATGGTCTGG	60
15	GAGCTGCGCC CAGGGCTTGG CGCTGGCGGC CCCGCAACAG CACCGAGCGT TTCGGTCGGC	120 180
	GGGCGGCGGT AGCGCCCCCT CTCAGAGCCC CGCTCACTCC CACCTGGGCT CGCTCCGAGT CGGCCTGTCT GTCGGGCCCG CCCTCCCCGC TCACTCCCTC CGCCCTTCTC TTCGAAGCGG	240
	GAAGGGCGCC TTGCAGGATC CTGCCGCCCC TCCAACCGGA TCCTGGGTCT AGAGCTCCCC	300
20	AGAGCGAGGC GCTCGCCAGG ACTCCTGCCC CGCCAACCCT GACCGCCGGG GGGTGCCCCC	360
20	GGGACGTAGC GCCGCGGAGA GGAAGCGGCA AAGGGGACCA TGCGGCGCCT GACTCGTCGG CTGGTTCTGC CAGTCTTCGG GGTGCTCTGG ATCACGGTGC TGCTGTTCTT CTGGGTAACC	420 480
	AAGAGGAAGT TGGAGGTGCC GACGGGACCT GAAGTGCAGA CCCCTAAGCC TTCGGACGCt	540
	GACTGGGACG ACCTGTGGGA CCAGTTTGAT GAGCGGCGGT ATCTGAATGC CAAAAAGTGG	600
25	CGCGTTGGTG ACGACCCCTA TAAGCTGTAT GCTTTCAACC AGCGGGAGAG TGAGCGGATC TCCAGCAATC GGGCCATCCC GGACACTCGC CATCTGAGTG TATTAAACCG CACCCCTACG	660 720
23	CATCTGATCC GGGAAATCAT ATTAGTGGAT GACTTCAGCA ATGACCCTGA TGACTGTAAA	780
	CACCTUATUR ROTTOUTURE GETGRARATGU TTGCGCARTA ATGRACGGCA AGGTCTGGTC	840
	CGGTCCCGGA TTCGGGGCGC TGACATCGCC CAGGGCACCA CTCTGACTTT CCTCGACAGC	900 960
30	CACTGTGAGG TGAACAGGGA CTGGCTCCAG CCTCTGTTGC ACAGGGTCAA AGAGGACTAC ACGCGGGTGG TGTGCCCTGT GATCGATATC ATTAACCTGG ACACCTTCAC CTACATCGAG	1020
	TCTGCCTCGG AGCTCAGAGG GGGGTTTGAC TGGAGCCTCC ACTTCCAGTG GGAGCAGCTC	1080
	TCCCCAGAGC AGAAGGCTCG GCGCCTGGAC CCCACGGAGC CCATCAGGAC TCCTATCATA	1140 1200
	GCTGGAGGGC TCTTCGTGAT CGACAAAGCT TGGTTTGATT ACCTGGGGAA ATATGATATG	1260
35	CGCAGCCTAG AGATCGTCCC CTGCAGCCGA GTGGGGCACG TCTTCCGGAA GAAGCACCCC	1320
	TACGTTTTCC CTGATGGAAA TGCCAACACG TATATAAAGA ACACCAAGCG GACAGCTGAA	1380 1440
	GTGTGGATGG ATGAATACAA GCGATACTAT TACGCTGCCC GGCCATTCGC CCTGGAGAGG CCCTTCGGGA ATGTTGAGAG CAGATTGGAC CTGAGGAAGA ATCTGCGCTG CCAGAGCTTC	1500
	AAGTGGTACC TGGAGAATAT CTACCCTGAA CTCAGCATCC CCAAGGAGTC CTCCATCCAG	1560
40	AAGGGCAATA TCCGACAGAG ACAGAAGTGC CTGGAATCTC AAAGGCAGAA CAACCAAGAA	1620
	ACCCCAAACC TAAAGTTGAG CCCCTGTGCC AAGGTCAAAG GCGAAGATGC AAAGTCCCAG GTATGGGCCT TCACATACAC CCAGCAGATC CTCCAGGAGG AGCTGTGCCT GTCAGTCATC	1680 1740
	ACCTTGTTCC CTGGCGCCCC AGTGGTTCTT GTCCTTTGCA AGAATGGAGA TGACCGACAG	1800
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	ACTIGIAAAT A	ATTIALTII I	ANGGGAIGG	CTATTICCAA	TATCTTAGG 1	TATTCAGTA	3600
5	TTCAGGTTTG T	CHICKLIA A	TTTAAACTA	AAATGTGTTT	ICTGAAGAAA	AAATAATAG	3660
-	TTTACACAAA T	TTACAATCA 1	ragaataage .	ATTITAAGCT (GGCGACTAGT (STTCTATAGA	3720
	TTACABACCA A	CAAAACTTT (TATGAAGAT	AAATGACCTT '	TTGCCTGAAG A	AGTACAGATA	3780
	AAATCAAAGA 1	GTGTGCAAG (TAGTTTTTG	gaagaagtga '	TGCTTCTCTT (CTTTAAAGAG	3840
	ACAGTCACCA A	ATACTTGGT :	TAACTCGAC	TATTGACTTG (GGCATTGAGA (GAGATGATAT	3900
10	ATACATCTTT C	GAAAGTGAA (STCAATGTTC	AAGAGGTGAT .	AGAAGCTTTA (CTTTTTAGTG	3960
	ATCAGAAATA T	TTAGTGCAT	CTTTTCAGAC	AGGAAGAATT	TTATCATCAA	GTATTCCCTT	4020
	ATAAAACCAA C	TAACACTTC '	TTATCAGTA	ACTITIAGAA	CTTAAAAGAA	AGCAAAAAGT	4080 4140
	AAATGGAATT	TAGGCAATT '	TATGAATCCT	AGTAGATTIT	ACARTATGIA	ATTIMICTIC	4200
15	TTTACAGTAT A	ATAAACACTA	AGTTTTGTGT	TAAAIGIGAI	TTATTTCACC	CACCCAATC	4260
13	CCAGCATTTT (CACAAATTCC	AGAATTAGCC	ANGARIIGI TCICCIACTC	ACCACTTOCA	ATCACCCTG	4320
	ACCAACATGG 1	PCARACCTCT	TCTCTACTA	AAATACAAAA	TTAGCCGGGC	ATGGTGGCAC	4380
	ATGCCTATAA	TCTCAGCTAC	TCAGGAGGCT	GAGGCAGGAG	GATCGCTTGA	ACCCGGGAGG	4440
	CAGAGGTTGC	AGTGAGCCAA	GATTGCGCCA	CTGCACTCCA	GCCTGGGCAA	CAGAGTGAGA	4500
20	CTCTCTCTCA 2	AAAAAAAA	AAAASSAAAA	GAAAAGAAAA	AGGTTTATTT	GAATAATTGG	4560
	AACTCACTTT	TOATTACKE	ATTTTTCAGC	AGTAGGGAAT	TTCTCCAATT	ACATTCATGT	4620
	TGAATGAATT '	ATATTTATT	TATAGCTTAC	CCTTCCAAAA	TAAAAGTGTT	TTTTTAATGT	4680
	TGTTTTGTTT '	TGTTTTGTTT	TTTTCCTTTT	TTGAGACGGA	GTTTCACTCT	TGTTGCCCAG	4740
0.0	ACTGGAGTGC	AGTGGCACAA	TCTCAGCTCA	TIGCAACCTC	TGCCTCCTGG	GTTCAAGTGA	4800
25	TTCTGCTGCC	TCAGCCTCCT	GAGTGGTTGG	GATTACAGGC	ATCCACCACC	ACCCCCAGCT	4860 4920
	AATTTTTTTG	TATTITCAGT	AGAGATGGGG	GTTTCACCAT	ACCCCTCCCA	CTGATCTCAA	4980
	ACTCCTGACC	TCAGGTGATC	BACTTTTTTT	TODATABACA	ATATCCGAAA	TTACAGGCAT GACAATTAGT	5040
	TTCTTCACAT	CTATTTTCAA	ARGITITOTA	AGAGCTAGTG	TITCTATTCA	TTTTCACAAT	5100
30	TTABABACAG	CTCTTAACAT	TECTGAAGTT	GGGAGAACTT	TCCATCTCTT	CTTAATAACA	5160
50	GTGCAAGATT	TTGTAAATTC	TITITIGIGI	TTAATGTTTA	ATAAAACGAG	TATTAAGCTT	5220
	AAATTACTGA	AGTACCTGGG	AGAAGTAATG	ATGTGTACTT	TCAAAAAAAT	GGAAAATGCT	5280
	TTTATTTAT	TTTCTATAAT	TTGTTAACAT	GATATGTAAA	ATTAAACTTC	GGAGCACAAT	5340
	GAAATGCCGA	TTATTTTTAC	CTTGTTTGGG	CTTAAAGTAG	GTATTTAAGG	TTTATGTGTT	5400
35	CAAAATGCCT	TGGTAAATTG	GATGACCTCT	AACTTTACTG	TCCATATGGA	GTTTGTCATT	5460
	CTTTATGGAT	AAGAGAACTT	AAGGAAAAGT	TACTGTTTTT	CTTCAGTCTT	TTTATATCTA	5520
	TCTGATTTAA	AATCTGTTAC	TTTATTAAAA	GGCTTCAACA	ACAGGTTGTT	AGGATGTAGT	5580 5640
	CTTACATCCA	GGTTCACATA	ATAACCCCAT	TIGAATCCAA	ATTTGTGTAT	AIIIICIIAI	5687
40	GCCAGCAGTA	TTIGTATCCA	ATTTTAACTT	AGGTTTGTTT	ICIIONG		2001
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45	 	 TTTTTTTAAA	TCACAACACC	 : TCTGAATATG	 TTTAATGACA	 GAGCAATTAG	60
45	 TTTTTTTTTT AAACAAAAGT	 TTTTTTTAAA TTAATTTTAT	TCACAACACC ACATCATAGA	 : TCTGAATATG ATTACTATTT	 TTTAATGACA AGAAACAAAT	GAGCAATTAG AGGACATGTT	120
45	 TTTTTTTTT AAACAAAAGT AGAAGTAAGA	 TTTTTTTAAA TTAATTTTAT AAAAATAAAA	TCACAACACO ACATCATAGA CACTTTGTTO	 TCTGAATATG ATTACTATTT AAGTTATATA	TTTAATGACA AGAAACAAAT CCTATTTGGA	GAGCAATTAG AGGACATGTT TTTTTTAAA	120 180
45	TTTTTTTTT AAACAAAAGT AGAAGTAAGA AGCATTACCC	 TTTTTTTAAA TTAATTTTAT AAAAATAAAA AATAGGCTAT	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGC	 C TCTGAATATG A ATTACTATTT C AAGTTATATA C CAACACATAA	TTTAATGACA AGAAACAAAT CCTATTTGGA TGCCAGGTTG	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG	120 180 240
	TTTTTTTTT AAACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG	 TTTTTTTAAA TTAATTTTAT AAAAATAAAA AATAGGCTAT AATGTGACAT	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGC GACTGTCTAA	 TCTGAATATG ATTACTATTT AAGTTATATA CAACACATAA TGGGTATAAA	; TTTAATGACA ; AGAAACAAAT ; CCTATTTGGA ; TGCCAGGITG ; GCTCCCTTTT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA	120 180 240 300
45 50	TTTTTTTTT AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG	TTTTTTTAAA TTAATTTTAT AAAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGC GACTGTCTAA	 TCTGAATATG ATTACTATTT AAGTTATATA CAACACATAA TGGGTATAAA TGGCAAATGT	; TTTAATGACA AGAAACAAAT ACCTATTTGGA ATGCCAGGTTG AGCTCCCTTTT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA	120 180 240 300 360
	TTTTTTTTT AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA	 TITTTTTAAA TTAATTTTAT AAAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGC GACTGTCTAA GTAGTGGTAC	 CTCTGAATATG ATTACTATTT AAGTTATATA CCAACACATAA TGGGTATAAA TGGCAAATGT GTGGTGTAAA	; TTTAATGACA AGAAACAAAT ACCTATTTGGA ATGCCAGGTTG AGCTCCCTTTT GCTAAACGCC ATTCCTATAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT	120 180 240 300 360 420
	TTTTTTTTTT AAACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAA	TTTTTTAAA TTAATTTAT AAAATAAAA AATAGGCTAT AATGTGACATA GATCTAGATA TGGTTTAATT AAGTGGCTGA	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGC GACTGTCTAA GTAGTGGTAC GTATAATTTT	TCTGAATATG ATTACTATTT AAGTTATATATA CAACACATAAA TGGGTATAAA TGGGAAATGT TGTGTGTAAAA	TTTAATGACA AGAAACAAAT ACCTATTTGGA TGCCAGGTTG GGTCCCTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT CAATTATTCT AGCCCTTGGT	120 180 240 300 360 420 480
	TTTTTTTTT AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTACA	TTTTTTAAA TTAATTTATA AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGATA AATTTAATTC	TCACAACACC ACATCATAGA CACTTTGTTC AGAACGATGG GACTGTCTAA GTAGTGGTAC GTATAATTTT CCAGATTTGG CCATATGCT	CACACACATA CACACATA CACACATA CACACATA CACCACATA CACCACATA CACCACACATA CACACACA	; TITANTGACA AGAAACAAAT AGCAGGTTG AGCTCCCTTTT GGTAAACGCC ATTCCTATAT ATGCTTGTCA	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAATCCTCCTTCGT TTTAATCATT	120 180 240 300 360 420
50	TITITITITI AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTAG TACATTAGAA	TTTTTTTAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATT AATTGGATA AATTTAATTC	TCACAACACC ACATCATACAC ACATCTATACA CACTTTGTTC AGAACGATGC GACTGTCTAA GTAGTGGTAC GTATAATTTT CCAGATTTGG CCATATGCT TTTTGAAAC	CACAGAGATATO CACACATAA CACACATAA CACACATAA CACCACATAAA CACCACATAAA CACCAAGAGAC CACAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGACAC CAAGAC CAAGACAC CAACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACA	I TTTAATGACA AGAACAAAT CCTATTTGGA TGCCAGGTTG GCTCACTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA	120 180 240 300 360 420 480 540
	TTTTTTTTT AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTACA TACATTAGGAA AAATTATTAGA	TTTTTTTAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATT AATTGGATA AATTTAATTC	TCACAACACC ACATCATACAC ACATCTATACA CACTTTGTTC AGAACGATGC GACTGTCTAA GTAGTGGTAC GTATAATTTT CCAGATTTGG CCATATGCT TTTTGAAAC	CACAGAGATATO CACACATAA CACACATAA CACACATAA CACCACATAAA CACCACATAAA CACCAAGAGAC CACAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGACAC CAAGAC CAAGACAC CAACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACA	I TTTAATGACA AGAACAAAT CCTATTTGGA TGCCAGGTTG GCTCACTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAATCCTCTCT AGCCCTTGGT	120 180 240 300 360 420 480 540 600
50	TITITITITI AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTAG TACATTAGAA	TTTTTTTAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATT AATTGGATA AATTTAATTC	TCACAACACC ACATCATACAC ACATCTATACA CACTTTGTTC AGAACGATGC GACTGTCTAA GTAGTGGTAC GTATAATTTT CCAGATTTGG CCATATGCT TTTTGAAAC	CACAGAGATATO CACACATAA CACACATAA CACACATAA CACCACATAAA CACCACATAAA CACCAAGAGAC CACAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGAGAC CAAGACAC CAAGAC CAAGACAC CAACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACAC CAAGACA	I TTTAATGACA AGAACAAAT CCTATTTGGA TGCCAGGTTG GCTCACTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA	120 180 240 300 360 420 480 540 600 660
50	TTTTTTTTT ARACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTACA TACATTAGTA AAATTATTAC GTACACA Seq ID NO:	I TITTITAAA TAAAATAAAA AATAAGCTAT AATGTGACT GATCTAGATA TAGTGGCTGA AATTTAATTC ACATGGAATTT	TCACAACACC TCACAACACC ACATCATAGA CACTTTGTTC AGAACCATGC GACTGTCTA GTAGTGTAATTTC CCAGATTTGC CCATATCCT TTTTGAAACC TTTTATTTG	TTCTGAATATG AATTACTATTT AAGTTATATA CAACACATAA TGGGTATAAA CTGGGAATG CCAAGGACC GAAATAGTA A CCAAGGACC GAAATAGTA T ATAATATGT AGTAACGGG	I TTTAATGACA AGAACAAAT CCTATTTGGA TGCCAGGTTG GCTCACTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA	120 180 240 300 360 420 480 540 600 660
50	TTTTTTTTT ARACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTACA TACATTAGTA AAATTATTAC GTACACA Seq ID NO:	I TITITITAAN TAANATAANA AATAGGCTAT AATGTGACAT GGTTTAATT AAGTGGCTGA AATTTAATTC ACATGGGATTTTAATTC ACATGGGATTTTAATTC ACATGGGATTTTTTTTTT	TCACAACACC TCACAACACC ACATCATAGA CACTTTGTTC AGAACCATGC GACTGTCTA GTAGTGTAATTTC CCAGATTTGC CCATATCCT TTTTGAAACC TTTTATTTG	TTCTGAATATG AATTACTATTT AAGTTATATAT CAACACATAA TGGGTATAAA TGGGTATAAA CTGGGTATAAA CCAAGAGACC GAAATAGTA ATAAATATGTT AGTAACGGG	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATTCCTATAT ATGCTATTGTA ATGCTGTCAT ATGCTGTCAT ATGCTGTCAT ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGCATGG GAAGTGAAAA AATGAATAATTCA TAGCACTTGGT TTTAATCATT ATGAACACTA TTATTTTGCT	120 180 240 300 360 420 480 540 600 660
50	TTTTTTTTT ARACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAAA TTAAATAAAC TTATGCTACA TACATTAGTA AAATTATTAC GTACACA Seq ID NO:	I TITTITAAA TAAAATAAAA AATAAGCTAT AATGTGACT GATCTAGATA TAGTGGCTGA AATTTAATTC ACATGGAATTT	TCACAACACC TCACAACACC ACATCATAGA CACTTTGTTC AGAACCATGC GACTGTCTA GTAGTGTAATTTC CCAGATTTGC CCATATCCT TTTTGAAACC TTTTATTTG	TTCTGAATATG AATTACTATTT AAGTTATATA CAACACATAA TGGGTATAAA CTGGGAATG CCAAGGACC GAAATAGTA A CCAAGGACC GAAATAGTA T ATAATATGT AGTAACGGG	I TTTAATGACA AGAACAAAT CCTATTTGGA TGCCAGGTTG GCTCACTTTT GCTAAACGCC ATTCCTATAT ATAGTTTGTC ATGCTGTCAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA	120 180 240 300 360 420 480 540 600 660
50	TITITITIT ARACARAGT AGRAGTAAGA AGCATTACCC AGRATGGGAG ARTTACTTG GCACATTAAA TTAARATAAAC TTATGCTACA TACATTAGCTACA TACATTAGCTACATTAGCTACA TACATTAGCTACATTAGCTACA TACATTAGCTACATTAGCTACATAGCTAGC	I TITITITAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATTC ACATGGGATT TGTGGAATTI 61 DNA Secid Accessic	TCACAACACC TCACAACACC ACATCATAGA CACTTTGTTC ACAACCATCG GATGTCTAA GTAGATTTG CCAGATTTG CCAGATTTG TTTTGAAACT TTTTATTG quence on #: Eos s 21 1	TOTGAATATG AATTACTATTT AAGTTATATA CAACACATAA TGGGAATGA TGGGAATGT GTGGTGTAAA CCAAGAGACC GAAATAGTA TATAATATGTI AGTAACGGG equence 31	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GGTAAACGCC ATTCCTATAT ATGCTATATAT ATGCTATAT ATGCTATAT ATGCTATATAT ATGCTATATAT ATGCTATATAT	GAGCAATTAG AGGACATGTT TTTTTTTAAA TTTTTTTAAA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA TTATTTTGCT	120 180 240 300 360 420 480 540 600 667
50	TTTTTTTTT ARACARAGT AGRAGTANGA AGCATTACCC AGRATGGGAG ARTTACTTTG GCACATTANA TTANACTACA TACATTAGAA ANATTATTAC GTACACA Seq ID NO: Nucleic Ac 1 GACCTANGAA	I TITITITAAA TTAATTITAT AAAATAAAA AATAGGCTAT AATGGCTAT AGGCTAT AGGCTATAATTAATTC ACATGGATTAATTC ACATGGATTTAATTC 61 DNA Secid ACCESSIC 11	TCACAACACC TCACAACACCACACACACACACACACACA	TATTGAATATG A ATTACTATTT AAGTTATATAT C CAACACATAA T TGGCAAATGT G TGGCTATAAA C CCAAGAGACAC G GAAATAGTAT ATAATATGTT AGTAACGGG equence 31 G TATGAGAAT	TITTAATGACA AGAAACAAAT CCTATTTGGA CCCCAGGTTG GCTCAAACGCC ATTCCTATAT AGCTACCTATAT ATGCAATTAT ATGCAATTAT AGTATGCAATTAT AGTATGCAATT	GAGCAATTAG AGGACATGTT TTTTTTTAAA CAAGCATGG GAAGTGAAAA AATGAATAATTCT TTTAATCATT AGCCCTTGGT TTTAATCATT TATTATTGCT	120 180 240 300 360 420 480 540 660 667
50	TITITITIT ARACARAGT AGAAGTAAGA AGCATTACAC AGAATGGGAG AATTACTITAG GCACATTAAA TITATACTACAA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA COTTTAAGTA	TITITITAAA TTAATTITAT AAAATAAAA AATAGGCTAT AATGTGACAT GATCTAGATA TGGTTTAATT AAGTGGATA TGGTTAATT ACATGGAATT 61 DNA Sec id Accessic 11 CTTATCAAAA TTGTAGAAA	TCACAACACC ACATCATAGA ACATCATAGA CACTTGTTA ACAACCATGG GACTGTCTAA GTATAGTTTA CCAGATTTGC TTTTTAAATCT TTTTTAATTG Quence n #: Eos & 21	TOTTGAATATG AATTACTATT AAGTTATATA CAACACATAA TGGGAATG GTGGGGAATG ACCAAGAGACC GAAATAGTAT AATAAATGTA AATAAAATGTA AATAAAATGTA AATAAAATGTA CAAGTAACAGGAATA T CAAGTCTCT CCAAGTCTCT	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATGCTGTTTGTA ATGCTGTCAT ATGCAATTAT ATGCAATTAT ATGCAATTAT 41 A GATCAATTAT ATGCAATTAT TITTCCACTT	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGAAAA AATGAATAATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TIATITIGCT	120 180 240 300 360 420 480 540 660 667
50 55 60	ITTTTTTTT ARACARAGT AGRAGTANGA AGCATTACCA AGRATGGGAG ARTTACTTTG GCACATTANA TTANATARAC TTATGCTACA TACATTAGTA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac I GACCTANGAA CCTTTANGTA CCTTTANGTA	TITITITAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATGGACAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATTC ACATGGGATT 61 DNA Sec id Accessic 11 CTTATCAAAC TTTGAGAAAT TTTAGAAAC TTTGAGAATAT GGGGATTTC	TCACAACACC TCACAACACC ACATTAGTA ACAACCATGC GACTGTCTA GTAGTCTA GTAGTCTA GTAGTTTG CCAGATTTG CCAGATTTG TTTTGAAACT TTTTATTG Quence on #: Eos # 21 GAACTCAGCA TCATTACTA ACATTACTA ACATTACTA	TOTGAATATG A ATTACTATT A AGTTATATA C CAACACATAA TGGGTATAAA C TGGCAAATGT G TGGTGTAAA C CCAAGAGACC G GAAATAGTA T ATAATATGTI AGTAACGGG equence 31 G TATGAGAAT. T CAATACCTT C CAATACCTT T CAATACCTT	TITTAATGACA AGAAACAAAT CCTATTTGGA CCTACTTTGGA GCTCCCTTTT GGTAAACGCC AATTCCTATAT ATGCAATTAT AGTATCAATAT AGTATCAATAT AGTATCAATAT 41 AGATCAATACT TTTCCACTT TAAAAAATGTT AAAAAATGTT	GAGCAATTAG AGGACATGTT TTTTTTTAAA AATGAATAAT ATGAACACTT TTTAATCAT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAGGGTTT A TAGAGAGGTTT A TAGAGAGGGTTT A TAGAGGAGTTT A TAGAGGAGGGAACAAGCAGT	120 180 240 300 360 420 480 540 660 667
50	TITTITITI ARACARAGT AGAGTARGA AGCATTACCC AGAATGGGAG AATTACTITIG GCACATTAAA TTAAATAAAC TTATGCTACA AAATTATTACG GTACACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTTTAAGTC AATCAGACTI CCATCTGAAT	I TITITITAAA TTAATTTTAT AAAATAAAA AATAGGCTAT AATATTAAT AATAGGCTAT AGTCTAGATT AAGTGGCTGA AATTTAATT AAGTGGCTGA AATTTAATT ACACAGGATT 61 DNA Sec id Accessic 11	TCACAACACC ACATCATAGE ACATCATAGE ACACCATTGTTC ACAACGATGC ACACCATTGTTC ACACCATCATC ACACCATCATC CCAGATTGC TTTTAATAC TTTTAATAC TTTTATTG Quence Discourse 1 1 2 1 2 3 ACACCAGGC TCATTACTC CAGTTAACTA CAGTTAACTA AATGTCAAGA AATG	TTCTGAATATG AATTACTATTT AAGTTATATA CAACATAAA TGGGTATAAA CTGGCAATGT GTGGTGTAAA ACAAAAAATAGTAT AAATAAAAAAAAAA	TITTAATGACA AGAAACAAAT ACCTATTIGGA GCTCCCTITI GCTAAACGCC ATTCCTATAT ATAGTTIGTA AGAATTAT AGTATGAATTAT AGTATGAATTAT AGTATGAATTAT AGTATGAATTAT AGTATGAATTAT TITCCACTI TAAAAAATGTT TAAAAAAATGTT TAAAAAAAAATGTT TAAAAAAAA	GAGCAATTAG AGGACATGTT TTTTTTTANA CAAGGCATGG GAAGTGANA AATGAATAAT CAATTATTCT AGCCCTTGGT TTTAATCATT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAGGGGTTT A TAGAGAGGG GAACAAGCAGG GAACAAGCAGG TTAAACAGCACTA TTATTTGCT 71 72 73 74 75 75 75 75 75 75 75 75 75 75 75 75 75	120 180 240 300 360 420 480 540 660 667
50 55 60	TITITITIT ARACARAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTITG GCACATTAAA TITATGTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac 1' GACCTAAGAA CCTTTAAGTA AATCAGACTI CCATCTGAAT TTGCAGTTG	TITITITAAA TTAATTTATA AAAATAAAA AATAGGCTAT AATTGACAT GATCTAGATA TGGTTAAATT TGGTTAAATT TGTGAAATT 61 DNA Sec id Accessic 11 CTTATCAAAA TGTTATCAAA TGTTATCAAA TGGGATATC AATTATACCA TATATACCA TATATACA TATATACCA TATATACA TATATACCA TATATACCA TATATACA TATATACCA TATATACA TAT	TCACAACACCAC ACATCATAGA CACTTGTTA AGAACGATGC GACTGTCTAA GTATAGATTA CCAGATTTGC TTTTTAAAATTT CCAGATTTGC TTTTTAATTGC TTTTTAATTGC TTTTTAATTGC TTTTTAATTGC TTTTTAATTGC TCATTACTC AGATCAGCA TCATTACTC AGATTAACTC AGATTAACT AGATTC AGATTAACTC AGATTAACT AGATTAACTC AGATTAACTC AGATTAACTC AGATTAACTC AGATTAACTC AGATTAACT AGATTAACTC AGATTAACTC AGATTAACT AG	TCTGAATATG A ATTACTATT A AGTTATATA C AGCAATATA C TGGGAATG G TGTGGTGTAAA A CCAAGGACC G GAATAGTA A ATTACTATA A ATTACTATA C TGGCAATG G TATACAGGA equence 31 G TATGAGAAT T CCAGTCTT C CAATACCTT C CAATACCTT C CATTAGCA T CAGTTAGCA T CAGTTAGCA T CAGTTAGCA	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATACCTATAT ATACCATATA ATACCATATA ATACCATATA ATACCATATA ATACCATATA ATACCATATA TATACCATTAT A GATCAATAAC TTTTCCACTT TAAAAAATGTT CAAGAGAGAGAA	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGAAAA AATGAATAATCT CAATTATTCT ATGAACACTA TTATTTTGCT 51 I A TAGAGGGTTT A TAGAGGGTTT A TAGAGAGAGG G AACAAGCAGT TATAAAGGTCC TAAAAGGTCC TAAAAGGTCC TAAAAGGAAAAAA	120 180 240 300 360 420 480 660 667
50 55 60	TITITITIT ARACARAGT AGRAGTAAGA AGCATTACCA GACATTACA GACATTACA TATACTTAG TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac I GACCTAAGAA CCTTTAGGTA CCTTTAGGT AATCAGACTI CCATCTGAAT TIGCAGTTG TIGCAGGTACT	TITITITAAA TTAATITTAT AAAATAAAA AATAGGCTAT GATCTAGATA TGGTTTAATT AAGTGGCTGA AATTTAATT ACTGGGATT 61 DNA Sec id Accessic 11 CTTATCAAAC TTTGTAGAAAC TTTGTAGAAAC TTTGAGATATC TGGGGATTTC TAGGGGTG TGGGATTTC TTTGTAGAAC TTTGAGAAC TTGGGATTTC TAGGACTA	TCACAACACC TCACAACACC ACATTTGTTC ACAACCATC GATAGTCTAA GTAGTCTAC GTAGTCTAC GTAGTCTAC CCAGATTTG CCAGATTTG CCATATTGT TTTTGAAACT TTTTATTTG Quence on #: Eos # 21 GAACTCAGCA TCATTACTA AAATTACTA AAATTCAAGG GTATTCTAGG GTATTCAAGG GTATTCTAGG GTATAGT GCATAAATAT	CACTACCT CACTACT CACTACCT CACTACC CACTACCT CACTA	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GGTAAACGCC AGTTCCTATAT AGCAATTAT AGTATCCTATAT AGTATCCAATTAT AGTATCAATTAT AGTATCAATTAT AGATCAATTAT TAAAAAATGT TAAAAAATGT TAAAAAATGT CAGGAGGAGAGT TTGAAATAACT TGAAATAACT TGAAATAACT	GAGCAATTAG AGGACATGTT TTTTTTTAAA AATGAATAATT ATGAACACTT TTTAATCATT ATGAACACTT TTAATTTTGCT 51 A TAGAGGGTTT A TAGAGGGTTT A TAGAGAGGT T TAAAGGTGT T TAAAGGTGT T TAAAGGTCCT C AAGGAAAAA A TTGATTCCT	120 180 240 300 360 420 540 660 667
50 55 60 65	TITITITIT ARACARAGT AGAGTARGA AGCATTACCC AGAATGGGAG AATTACTITIG GCACATTAGA TTAAGTACAC TAAGTAGAA AAATTATTACG Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTITAAGTC AATCAGACTI TGCAGTGT TGAGGACAA	I TITITITAAA TTAATTTATA TAAATAAAA AATAGGCTAT AATATTAATA AATAGGCTAT AATTTAATT AAGTGGCTGA AATTTAATT AAGTGGCTGA AATTTAATT ACACAGGATT 61 DNA Sec iid Accessic 11	TCACAACACC ACATTGTTC ACATTGTTC ACACCATTGTTC ACACCATCGTTCTA GTAGTGTACT CCAGATTTGT CCAGATTTGC TTTTAATACC TTTTAATACC ACATTGACC ACATTGACC ACATTGACC ACATTGACC ACATTGACC ACATTGACC ACATTGACC ACATTAACTC ACATTAATACC ACATTAACTC ACATTAACT ACATTAACTC ACATTAACT ACATTAACTC ACAT	TOTGAATATG A ATTACTATT A AGTTATATA C TAGGAATATA C TAGAATAGTA C TAGAATAGTA T ATAATATGTT C TATTAGAATATT C CAGTCTCT C CATTAGAAT T CAGTTAGA T CAGTGATT C CAGTGATT T TTTTCTCTG C TTTTCTCTG	TITTAATGACA AGAAACAAAT ACCTATTIGGA GCTCCCTITI GCTAAACGCC ATTCCTATAT ATAGTTIGTA AGTATGAATTAA AGTATGAATTAA AGTATGAATTA AGTATGAATTAA TITTCCACTI TAAAAAAATGTT TAAAAAAAATGTT AAAAAAAATGTT AAAAAAAA	GAGCAATTAG AGGACATGTT TITITITANA CAAGGCATGG GAAGTGAAAA AATGAATAAT TATTATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTTGCT 51 A TAGAGGGTTT A TAGAGGGGTTT A TAGAGGAGG GAACAAGAG GAACAAGAGAG TAAAGAGCAGT TAAAGGAGAGAG A TAGATCCTT C AAGGAAAAAA A TTGATTCCTT G CCGCCACAGA	120 180 300 360 420 480 540 660 667
50 55 60	ITTITITIT ARACARAGT AGRAGTARGA AGCATTACCC AGRATGGGAG ARTTACTITG GCACATTARA TITARATARAC TARGTACAC Seq ID NO: Nucleic Ac 1: GACCTRAGRA CCTTTRAGT ARTCAGACTI CCATCTGRAT TIGAGGATCAG GGATARGAA CAGTGGCTTI CAGTGGCTT CAGTGGCTT CAGTGGCTT CAGTGGATACAC GGATARGAA CAGTGGCTT CAGTGGCTT CAGTGGCT CAGTGGCTT CAGTGGCT CAGTGGCT CAGTGCCT CAGTGCC CAGTCC CAGTC CAG	I TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT GATCTAGATA TGGTTAATT TGGTTAATT ACATGGATT TGTGGAATT 61 DNA Sec 1d Accessic 11 1 CTTATCAAAA TGGGATATC ACATGGATC ACATGGATC TGTGGAATTI TTTTTCTCACA TGGGGATATC TTTTCTCACA TGGGCCTATA	TCACAACACC ACATTGTTC ACAACCATC ACATTGTTC ACAACCATC ACATTGTTC ACAACCATC GTATAATTTC CCAGATTTGC TTTTTAAATC TTTTTAATTG TTTTTAATTG ACATCAGCA TCATTAACTC AACTCAGCA TCATTAACTC AACTCAGCA AATTCCAGCA ATTCCAGCAT ATTCCAGGCAT ATTCCAGGCA	TCTGAATATG A ATTACTATT A AAGTTATATA C AAGCACATA C TGGGAATG G GAATAGTA A CCAAGAGAC G GAATAGTA A ATTACTATA A ATTACTATA C TGGGAATGT G ATTACAGGAC equence 31 TATACAGGAC G TATACAGGAT C CAATGCTT C CAATACCTT C CAATACCTT C CAATAGCT C CACTGTT T TTTGTCTCG A CATGGGAGG C CATGGGAGG A CATGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGAGGAGG A CATGGAGGAGGAGG A CATGGAGGAGGAGG A CATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	TITTAATGACA AGAAACAAAT ACCTATTIGGA GCTCCCTITI GCTAAACGCC ATTCCTATAT ATAGTTIGTA AGTATGAATTAA AGTATGAATTAA AGTATGAATTA AGTATGAATTAA TITTCCACTI TAAAAAAATGTT TAAAAAAAATGTT AAAAAAAATGTT AAAAAAAA	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGANA AATGAATATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAACAGAG A TAAAGATCATC CAAGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCTT CCCCCACAGA A GATCGCTTGA	120 180 300 360 420 480 540 660 667
50 55 60 65	TTTTTTTTT AAACAAAGT AGAGTAAGA AGCATTACCC AGAATGGGAG AATTACTTTG GCACATTAGAA TTAAATAAAC TTAAGCTACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTTTAAGTC AATCAGTCT TGAGGACTAC TTGAGGACTAC CCATCTGGAAT TTGAGGACTAC GGATAAGAAC CAGTGGCTTC GCCCCAAAAAC	I TITITITAAA TTAATTTATA AAAATAAAA AATAGGCTAT AATGGCTATA AATGGCTATA AATGGCTATA AATGGCTATA AATGGCTATA AATGGCTATA AATGGCTATA AATGGATTAATT AAGTGGCTGA AATTTAATTC I TOTGGAATTI C CTTATCAAAA TTGTAGAAAA TGGGTTACT TCAGACCTAT TCAGACCTAT TCAGACCTATA TCAGAGGTG TCAGAGGTG TCAGAGGTG TCAGAGGTG TCAGAGGTG	TCACAACACC ACATCATAGE ACATCATAGE ACACCATTGTTC ACAACCATCG ACACCATCGTTC ACACCATCGTTC CCAGATTTGT CCAGATTTGC TTTTAATACC TTTTAATACC TTTTAATACC TATTAATACC ACACCACCACCACCACCACCACCACCACCACCACCA	TCTGAATATG A ATTACTATT A AAGTTATATA C AAGCACATA C TGGGAATG G GAATAGTA A CCAAGAGAC G GAATAGTA A ATTACTATA A ATTACTATA C TGGGAATGT G ATTACAGGAC equence 31 TATACAGGAC G TATACAGGAT C CAATGCTT C CAATACCTT C CAATACCTT C CAATAGCT C CACTGTT T TTTGTCTCG A CATGGGAGG C CATGGGAGG A CATGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGGAGG A CATGGAGGAGG A CATGGAGGAGGAGG A CATGGAGGAGGAGG A CATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATGCTGATTGT ATGCTATAT ATGCTATAT ATGCATTAT ATGCATTAT ATGCATTAT TATGCATTAT TATGCACTT TAAAAAATGT GTGTTAACT CAGAGGGGA TTGAAATACT AAATGATTAC CTGAAGTGGT	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGANA AATGAATATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAACAGAG A TAAAGATCATC CAAGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCTT CCCCCACAGA A GATCGCTTGA	120 180 240 300 360 420 480 540 660 667 60 120 180 240 360 420
50 55 60 65	ITTITITIT AAACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTITG GCACATTAAA TATAGTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac I' GACCTAAGAA CCTTTAAGTC AATCAGACTI CCATCTGAAT TGGAGTGGCTTC GCCCAAAAAC Seq ID NO:	TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT GATCTAGATT TGGTTAATT TGGTTTAATT ACATGGATT TGTGGAATT 61 DNA Sec 11 11 11 11 11 11 11 11 11 11 11 11 11	TCACAACACC ACATTGTTC ACAACCATC ACATTGTTC ACAACCATC GTATAATTTC CTATATCTC CTATATCTC CTATATCTC CTATATCTC TTTTATTG CTATATTTC CTATATTC CTATATCTC TTTTTATTG TTTTTATTG TTTTTATTG TTTTTATTG TTTTTATTC TTTTTATC TTTTTTC TTTTTTC TTTTTTC TTTTTTC TTTTTT	CACTOGRATA TO CACTOCT CACTOC	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATGCTGATTGT ATGCTATAT ATGCTATAT ATGCATTAT ATGCATTAT ATGCATTAT TATGCATTAT TATGCACTT TAAAAAATGT GTGTTAACT CAGAGGGGA TTGAAATACT AAATGATTAC CTGAAGTGGT	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGANA AATGAATATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAACAGAG A TAAAGATCATC CAAGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCTT CCCCCACAGA A GATCGCTTGA	120 180 240 300 360 420 480 540 660 667 60 120 180 240 360 420
50 55 60 65	TITITITIT ARACARAGT AGAAGTAAGA AGCATTACC AGAATGGGAG AATTACTITG GCACATTAAA TITAAATAAAC TATAGTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTTTAAGTC AATCAGACTT CCATCTGAAT TTGACGAACA GGATAAGAAA CAGTGCTTT GACGAACA GGATAAGAAA CAGTGCTTT GACGAACA GGATAAGAAA CAGTGCTT GCCCAAAAAC Seq ID NO Nucleic Ac Nucleic Ac	TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT AATGTGACT GATCTAGATA TGGTTTAATT AAGTGGATT TGTGGAATTI 61 DNA Secid Accessic 11 CTTATCAAAA TTGGTATA CTTGTGGAATTI CTTGTGAATT TTTTCACAA TTGTGAATA TTGTGAAAT TTGTGAAAA TTGTTACAAA TTGTGAAAA TTGTGAAAA TTGTGAAAA TTGTGAAAA TTGTCACAA TTGTGAAAA TTCAGACCTAI TAGGTCAA TTCAGACCTAI TCAGACCTAI TCAGACGTG TCAGAGGTG TCAGAGGTG TCAGAGGTG TCAGAGGTG	TCACAACACC ACATTGTTA AGAACCATG CACTTGTTA AGAACCATG CACTTGTTA AGAACCATG GTATAATTT CACAGATTGC CACATTTGTA CACATTGTTA CACATTGTTA CACATTTGTA CACATTTGAACC TTTTTAATTG AAATTCAAGC AAATTTAACC AAATTCACG AAATTCAAG AAATTCAAG AAATTCAAG CATTAACTC CAGATTAACTC C	CACAGGAGA T CAGAGATATA T CAGAGATATA T GGCAAATG T GGCAAATG T GAGAATAGT A CCAAGGACA T GAAATAGTA T AGTAACGG GAAATAGTA T AGTAACGGG Equence 31 G TATGAGAAT, T CCAGTCTT T CAATACCTT G CTTTTAAAA T CAGTAGCA T CACTGGTT T TITGTCTCG TATGAGGAG T GATTGGGAGG T GATTGTGCC	TITTAATGACA AGAAACAAAT CCTATTTGGA CCTACTTTGGA CGCTCCCTTTT GGTAAAGCC ATTCCTATAT AGTATCCTATAT AGTATCATATAT AGTATCATATAT AGTATCATATAT TAGCAATAT TAGCAATAT TAGCAATAT TAGCAATAT TAGCAATAT TAGCAATAT TTTCACACTT TAAAAAATGAT TAAAAAATGAT TTGAAATACT CAGGGGGGGGA TGGAATACCT AATTGATTTC CTGAGGTGGG ACTGTTACCC	GAGCANTTAG AGGACATGTT TTTTTTTANA AGGACATGG GAAGTGANA ANTGANTATT TATTATTCT AGCCCTTGGT TTTANTCATT ATTANTCATT AGGACAGAA ATTGATTCCTT GCCCCACAGA AGATCGCTTGA AGATCGCTTGA ACCTCAT	120 180 240 300 360 420 480 540 660 667 60 120 180 240 360 420
50 55 60 65 70	ITTITITIT AAACAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTITG GCACATTAAA TATAGTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac I' GACCTAAGAA CCTTTAAGTC AATCAGACTI CCATCTGAAT TGGAGTGGCTTC GCCCAAAAAC Seq ID NO:	TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT GATCTAGATT TGGTTAATT TGGTTTAATT ACATGGATT TGTGGAATT 61 DNA Sec 11 11 11 11 11 11 11 11 11 11 11 11 11	TCACAACACC ACATTGTTC ACAACCATC ACATTGTTC ACAACCATC GTATAATTTC CTATATCTC CTATATCTC CTATATCTC CTATATCTC TTTTATTG CTATATTTC CTATATTC CTATATCTC TTTTTATTG TTTTTATTG TTTTTATTG TTTTTATTG TTTTTATTC TTTTTATC TTTTTTC TTTTTTC TTTTTTC TTTTTTC TTTTTT	TTCTGAATATG AATTACTATTT AAGTTATATA CAACATAAA CTGGCAAATG CGCAAATG AATTACTATATA CTGGCAAATG CGAAAATG AATTACTATATA CACCAAGAGACC GAAATAGTAA CACCAAGAGACC GAATAGCAT CACTACCT CAATACCT CACTGCTT CAATACCT CACTGGTT TTTTCTCTG CATTGCCC CACCAGGCC CACTGGTT CAATGCGAGGCC CACTGGTT CAATGCGAGGCC CACTGGTT CATTGCCC CACCAGGTT CACTGGGAGGCC CACTGGTT CATTGCCCC CACCAGGTT CACTGGGAGGCC CACTGGTT CACTGGGAGCC CACTGGTT CACTGGGAGGCC CACTGGAGGCC CACTGGAGGCC CACTGGAGGCC CACTGGAGAGCC CACTGGAGACC CACTGGAGACC CACTGGGAGGCC CACTGGAGACC CACTGGAGACC CACTGGGAGCC CACTGGAGACC CACTGGAGACC CACTGGGAGCC CACTGGAGACC CACTGGACC CACTGGAGACC CACTGAGACC CACTGGAGACC CACTGAGACC CACTGAGACC CACTGAGACC CACTGAGACC CACTGACC C	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATGCTGATTGT ATGCTATAT ATGCTATAT ATGCATTAT ATGCATTAT ATGCATTAT TATGCATTAT TATGCACTT TAAAAAATGT GTGTTAACT CAGAGGGGA TTGAAATACT AAATGATTAC CTGAAGTGGT	GAGCAATTAG AGGACATGT TITITITANA CAAGGCATGG GAAGTGANA AATGAATATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTGCT 51 A TAGAGGGTTT A TAGAACAGAG A TAAAGATCATC CAAGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCT CAAGGAAAAAA A TTGATTCCTT CCCCCACAGA A GATCGCTTGA	120 180 240 300 360 420 480 540 660 667 60 120 180 240 360 420
50 55 60 65	TITITITIT ARACARAGT AGAAGTAAGA AGCATTACC AGAATGGGAG AATTACTITG GCACATTAAA TITATGTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTTTAAGTC AATCAGACTT CCATCTGAAT TTGAGGATCA CAGTGGATT GCCCAAAAAC Seq ID NO Nucleic Ac 1 1 1	TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT TAGTTAATTGATATGGTTAATTTGATTAATTGATATTGATTATT	TCACAACACC ACATTGTTA ACAACCATTGTTA ACAACCATTGTTA ACAACCATTGTTA ACATTGTTA GTATGTTA CTATGTTA CTATGTTA CTATGTTA CTATGTTA CTATGTTA CTATACTC TTTTTATTG ACATCAGCA ACATCAGCA ACATCAGCA ACATCAGCA CATAACTC CAGTAACTA ACATCAGCA CATAACTC CAGTAACTA CTATAACTC CAGTAACTA CTATAACTC CAGTAACTC CAGTAACT CAGTAACTC CAGTAACT CAGTAACTC CAG	CACTGGATTAGA T CACAGCATA A TTACTATT A AGTTATATA C CACACATAA T GGCAAATGT G GTGGTGTAAA A CCAAGAGACC G GAAATAGTA A ATAAATATT ATAAAACGGA EQUENCE 31 G TATGAGAATT T CCAGTCTT CAATACCTT CAATACCTT T CAATACCTT T CACTGGTT T TTTGTCTCG T CATTGGAGG T GATTGGCC 10 10 10 10 10 10 11 11 11	TITTAATGACA AGAAACAAAT CCTATTTGGA GCTCCCTTTT GCTAAACGCC ATGCTGTTGTC ATGCTGTCAT AGTATGATAT AGTATGATAT TATGCAATTAT CTAAGATTAT CTAAGATTACT CTAAGATGATTT CTAAGATGATTAT CTGAGGTGGG CTGTAATCCC	GAGCANTTAG AGGACATGT TITTITTANA CAAGGCATGG GAAGTGANAA AATGANTAATCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTTGCT 51 I ATAGAGGGTTT ATGAAGAGTT TATGAAGAGTT TATGAAGAGTT TATGAAGAGTT TAAAGGTCT TAAAGGAGT TTAAAGGTCT TAAAGGTCT AAGGAAAAAA A TTGATTCCTT GAGGAAAAAA A TTGATTCCTT GAGGAAAAAA A CGCCCACAGA GATCGCTAGA A CCTCAT	120 180 240 300 360 420 480 540 660 667 60 120 180 240 360 420 420 360 420 360
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50 55 60 65 70	TITITITIT AAACAAAAGT AGAAGTAAGA AGCATTACCC AGAATGGGAG AATTACTITG GCACATTAAA TITAAATAAAC TITATGTTACA TACATTAGAA AAATTATTAC GTACACA Seq ID NO: Nucleic Ac 1 GACCTAAGAA CCTTTAAGTCAAT CCATCTGAAT TGAGGACACA GGATAAGAAA CAGTGGCTTT GCCCAAAAAC Seq ID NO Nucleic Ac 1 1 TITITITITIT AAGGGATCAA	I TITITITAAA TTAATITTATA AAAATAAAA AATAGGCTAT GATCTAGATT AGTGGCTGA AATTTAATT AAGTGGCTGA TGGTTAATT AGGGATT GATTGGAATT 61 DNA Sec id Accessic 11 1 CTTATCAAAA TTGGTAATA TGGTAATATAACC TTGGAAATATACC TTGGAAATATACC TTGGAGAAA TGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAA TAGGCTAAAA TAGGCTAAAA TAGGCTAAAA TAGGCTAAAAAAAAAA	TCACAACACC ACATTGTTC ACATCATTGTTC ACAACCATTGTTC ACAACCATTGTTC ACATCATCTC GTATAATTTT CCAGATTTGC TTTTAATATTT CTATAATTT CTATAATTT CTATAATTT CTATAATTT CTATAATTT CTATAATT CTATAATTT CTATAACC CAGTTAACTA AATTCACCA CAGTTAACTA CAAATTAACCA CAGTTAACTA CAAATTAACCA CAGTTAACTA CAAATTAACCA CAGTTAACTA CAAATTAACCA CAGTGAGCTC CAGTGAGCT CAGTGAGCTC CAGTGAGCT CAGTGAGC CAGTGAGCT CAGTGAGCT CAGTGAGCT CAGTGAGCT CAGTGAGCT CAGTGAGCT CAGT	CAGTACTT CAGTACTT CAGTATATA CTGCGAAATGT GTGGTGTAAA CTGCGAAATGT GAAATAGTAT ACCAAGAGACC GAAATAGTAT AGTAACCGG CTATACAGT CAGTACCAGT CAATACCTT CAATACCTT CACTGGTT CACTGGTAGAAT CTCAGTAGCA CATGGGAAT CACTGGTT CACTGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGT CACTGGTT CACTGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGTT CACTGGT CACTGGTT CACTGGT CACTGGT CACTGGT CACTGGT CACTGGT CACTGGT CACTGT CACTGGT	TITTAATGACA AGAAACAAAT ACCTATTIGGA AGCCCCTITI GCTAAACGCC ATGCTACTATTAC ATTGCTATAT ATTGCTATAT AGTATGACAATT AGTATGACAATT TATGCAATTAC TTTTCCACTT TAAAAAATGTT CAAGAGAGAAT TTGAAATACC TTGTAAATACC TTGTAATACC CAGAGAGAGAAT TTGAAATACC CTGTATCCC 41 TAAATACT TAAATACT CTGAGGTGGG CTGTATCCC	GAGCAATTAG AGGACATGT TITITITAAA CAAGGCATGG GAAGTGAAAA AATGAATAAT TATTATTCT AGCCCTTGGT TITAATCATT ATGAACACTA TTATTTTGCT 51 A TAGAGGGTTT AATGAAGAGAG AACAAGCAGT TAAAGGTCT CAAGGAAAAAA ATTGATTCCT CAAGGAAAAAA ATTGATTCCTT CCGCCACGAA AGTCCCTTGA ACCTCAT 51 TTATACTCCA GCATTTATAAC	120 180 240 300 360 420 480 540 660 667 60 120 180 360 420 480 537
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	TGAAGGCTGT	CACAGTTCCT	GTGCAGAGAG	AGAGGGCACT	GCAGCACCCA	GGCGCTGACT	240 300
	AGTTTTTTCC	TCCTCTACAC	TCCCCATGCA	TGACTAAAGA	CCCAGGAGGA GTAGGAGGAG	TCAGCAAGGC	360
15	AGACATATAT	AGTACCCAGG	AGGTGGACAA	ACAACTGCCT	TGGTGGAAAC	TCTGTCCTTT	420 480
	CIGGACITAT	CCTGGTGCCA	AGGTCCCACA	GCAGATTTAG	ATCTACAATC AAGCATCACC	CGAAAGTGAG	540
	AATGCCTAGA	GGCAGGAATC	ATGGAGGCTT	CCTTAACCGT	CTGTCTGCAA	CAGCAGGTGC	600
20	TAGAGATGAC	ACTGCAGAGT	AGAGAACAAA	GGAATCTTAG	TAATTGTTCA ACAGCTTATC	CAAGGTTGCA	660 720
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	TTTCTCCTCC	CTTCATACCT	TGCAGGATCT	TTAACAGAAT	TTAAAAGGAG	TTTTTTTTTT	960
25	TGTTTTGATG	TATCTAATAA	AAGTCAAGGG	AGGGAGAGGG	CCAGTATAAG	CAAGAGTACA	1020 1080
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	AAATTGAAAA	AAAAAAA					1398
25		: 64 DNA Sec					
35	Nucleic A	cid Accessio	n #: Eos se 21	equence 31	41	51	
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	GGCACGAGG	A GAGAAACTC	ATCTCAAAA	CAAAACAAC	A CAAAACAAA A GCACACAAA	AAAGAAGAGA G AGGTCACGTG	60 120
40	AACACACAA'	T GAGAAGGAG	CTGCCTGCA	A GTTAAGAGAJ	A GAGGCCTCAC	CATGAAACCT	180
	GCCTTACTG	G CACTTTGGT	C TTGAACTTC	CAGCCTCTAL	A AACTGTGAG	A AATAAGTTTC	240 300
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45	TTTAGCTTG	T TTCTGTCTT G TTATAGCCC	T GGAGGAGGC C TGTGTTCTC	T GCATATITI A TTATCCAGG	T AAAATACCCC	C CAAAAGTACA G TTGGCCATTT	540
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	TTCATGTTT	C ATTCTGCAT	C CCTTCCCCC T GAGGCAGCT	A AGGGCTTCT G TTTGTTGAT	T TTGCTCAAT. T TTCTGGACC	A TGGGACTCAT A AATAATGTTC	660 720
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	TTACTATTT	T TAACTATTA	C AAATTATCT T CTCAGGTAT	T GCTAACACA G TATCTCAGA	T TTTTGTGCA G TGAAACTGT	T GTCTTTTGGT T TTATCACAGT	840 900
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55	GATGTAAAA	TATTCTCTT	A TGGCCTGGC	T CAGTGGCTC	A TGCCTGTAA	T CCCAGCATTT C CTGGGCAACA	1020 1080
33	TACTGAGAC	C CTCATCTCT	A CAAAAAAAA	a aaatttgtt	T AATTAGCTG	A GCTTGGTGGT	1140
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	ATATCTCCC	CA GTGCTATCO	C TCCCCCCTC	C CCCGACCCC	CA CAACAGTCC	C CAGAGTGTGA	1500
	ななかすりりりか	PT CCTCTCTCC	TOTAL A	'A TTGTTCAA1	T CCCACCTAI	NG AGTGAGAATA TT TCCAATTTCA	1560
65	TCCATGTC	CC TACAAAGG	NC ATGAACTC	AT CATTTTTI	AT GGCTGCATA	IG TAAAAATACA	1980
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	GGTCTTAA	AATAATAT TT	AA GGTTACAT	TG AAAATTGA	AAAAAAA AA	аа аааааааааа	2700
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5	1			31	41	51	
	 ATCACTARCA	GCAAATGCTC	COTTOCOLACTO	ATCTCTTCC	Treetreecccc	GGCTAAGGAG	60
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	GGCCAGTTCA	ACAGGGAAGG	GGCCGCTGGT	GTCTGGAAGA	TCTGCCCCAT	ACTGAAAGGT	420
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25		TCTTCTCCTT					1140
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	GTTGGGCAGT	TCAGCGACGA	CATCCAGCAG	ATGACCGGGC	AGCGGCCCAG	CCTGTACTGG	1560
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35	GTGACCTTCA	TOGOCACATO	CTACGGAGCC	ATGGTGCCCA	TCTATGCGG	CAACGCGCTG CTACAAGTTC	1740
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		TGGACAGAGG	GGAGGTGCGC	CAGTTCACGO	TCCGCCACTC	GCTCAAGGTG	1860 1863
	TAG						1003
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45	GAGTCTGGC	GCAGTCGCGC	CAGTGGTGG	CONNECCT	CAAAAGGCG	CCTCCGACTC CGCACCACTC	60 120
	CCGCTGGTT	CCGAAGGCAG	ATCCCTTCT	CCGAGAGTT	G CGAGAAACT	TCCCTTGTCC	180
	CCGACGCTG	AGCGGCTCGC	GTACCGTGG	AGCCGCAGG	TTCTGAACC	CGGGCCACGC	240
50						C ACGCTGGGGA CTGGACCTGG	300 360
50						C TGCTACCTGG	420
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	GCACCGGGG	C CCTGCGGGA	C GGCCAGCTG	GCGGGCCGC	G CGCCGGCGT A GGAGGGCTG	C TCCAAGCGAC C GAGGCCATCA	600
55	GCTTCCTCC	T GTCCCTCAT	C GACAGGCTG	G TOCTCTACT	G CGGGAGCCG	G CTGGGCAAAT	660
	ACTACGTCA	A GGAGAGGTC	T AAGGCAATG	G TGGCTTGCT	A TCCGGGAAA	T GGAACAGGTT	720 780
	ATGTTCGCC	A CGTGGACAA A TTGGGATGC	C CCCAACGGT	G GTGGGATCC	T GCGGATATT	C ATCTACTATC T CCAGAGGGGA	840
	AATCATTCA	T AGCAGATGT	G GAGCCCATT	T TTGACAGAC	T CCTGTTCTT	C TGGTCAGATC	900
60	GTAGGAACC	C ACACGAAGT	G CAGCCCTCT	T ACGCAACCA	G ATATGCTAT	G ACTGTCTGGT A ACTAGGAAAA	960 1020
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05	CTAACTCCA	G AAATTCCTG	C AGACATCCT	A CTCGGCCAG	C GGTTTACC1	G ATAGATTCGG	1320
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	ATGTATACI	T CCTGATTTC	A AAGGAGGAG	G TTTGAAAAG	A AAAAAATGO	A GGTGGTAGAT	1440 1500
70	AACAATTT	C AGATGTTCT	T AATCCAGG	C TGTTGGGG1	T TCTGGAGA	TATCACAACC	1560
	TAATGACAT	T AATACCTCT	A GAAAGGGCT	G CTGTCATAG	T GAACAATT	TA TAAGTGTCCC	1620
						C TCAGCTCCAT C TCCATTTCA	
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	GTGTTAAC	A CTGATAACT	TGGAAAGA(C TAGGTCTA	IT GATATACA AT GTGGGTGT	AT AAACATGTGT IC CIGITITITI	1920 1980
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5	ATAAGACATG TCACCATTAA TTCTCAACGA CTGCTCTATT TTGTTGTACG GTAATAGTTA TCACCTTCTA AATTACTATG TAATTACTC ACTTATTATG TTTATTGTCT TGTATCCTTT CTCTGGAGTG TAAGCACAAT GAAGACAGGA ATTTTGTATA TTTTTAACCA ATGCAACATA 2	460 520 580 640
	ARACTCAGTC TCCTACATTA GCATTCTARA ARARARARA ARARARARA ARARARARA ARARARARA ARARARARA ARARARARARA ARARARARARARA ARARARARARARA ARARARARARARA AR	2760 2770
10	Seq ID NO: 67 DNA Sequence Nucleic Acid Accession #: NM_139314.1 Coding sequence: 1961416 1 11 21 31 41 51	
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15		120
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		360
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	ATCCAGCAAC TCTTCCACAA GGTGGCCCAG CAGCAGCGGC ACCTGGAGAA GCAGCACCTG	600
25		660 720
23	CACAATGTCA GCCGCCTGCA CCGGCTGCCC AGGGATTGCC AGGAGCTGTT CCAGGTTGGG	780
		840
	1000104104 COLUMNICO INCOLUMNICO CITATO COLUMNICO COLUMN	900 960
30	TGGCTGGGTC TGGAGAAGGT GCATAGCATC ACGGGGGACC GCAACAGCCG CCTGGCCGTG	1020
		1080 1140
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25	CGCAGGGACA AGAACTGCGC CAAGAGCCTC TCTGGAGGCT GGTGGTTTGG CACCTGCAGC	1260
35	CHITCHICC ICHICOCCH CINCIPECT ICANICATION CONTINUES	1320 1380
	TTGATCCAGC CCATGGCAGC AGAGGCAGCC TCCTAGCGTC CTGGCTGGGC CTGGTCCCAG	1440
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		1740 1800
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65	CACAATGTCA GCCGCCTGCA CCGGCTGCCC AGGGATTGCC AGGAGCTGTT CCAGGTTGGG	780
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	TOGCTOGGTC TOGAGAAGGT GCATAGCATC ACGGGGGACC GCAACAGCCG CCTGGCCGTG	1020
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	GAGGACACGG CCTATAGCCT GCAGCTCACT GCACCCGTGG CCGGCCAGCT GGGCGCCACC ACCGTCCCAC CCAGCGGCCT CTCCGTACCC TTCTCCACTT GGGACCAGGA TCACGACCTC	1200
	CGCAGGGACA AGAACTGCGC CAAGAGCCTC TCTGGAGGCT GGTGGTTTGG CACCTGCAGC	1260
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	CTCAGTCACA TTGACTGACG GGGACCAGGG CTTGTGTGGG TCGAGAGGGC CCTCATGGTG	1740 1800
	CTGGTGCTGT TGTGTGTAGG TCCCCTGGGG ACACAAGCAG GCGCCAATGG TATCTGGGCG GAGCTCACAG AGTTCTTGGA ATAAAAGCAA CCTCAGAACA CTT	1843

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	AGCCCCTGGC	TCCCTCTGTT TGCTTCTGAT	GATCCCGGCC	CCTGCTCCAG	TECCHERATION	GCAACIGCIG	120 180
	TOTOTTEG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
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	CTGCACTGGG	TCCACGTGGT	TCACCTCAGC	ACCECTTE	CCAGAGTTGA	CGAGGCCTTG	840
20	GGGCGCCCGG	GAGGCCTGGC	COTOTTGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAAGAAAAC	900
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	TATGAGGGGT	CTCTGACTAC TGCTGAGTGC	ACCGCCCTGT	CACACCCTCT	CTCACCICGAC	GTGGGGACCT	1140
25	CAGACAGIGA	GGCTACAGCT	GAACTICCGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
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30	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	TTTTAAAATA	AATATTTATA	AT	1552
		70 DNA Seq		030.3			
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	CTTCTCTCTC	CATTCAGTGC	ACGCGTTACT	TTGGCTAAA	GGAGGTGAGG	GGCACTCTGC	60 120
40	CCTTCCAGAC	CAAGCATGGA	GCAACAGGAT	TTTCCCTCAT	TOPOUMADUR I	GCTGACGCTT TGGGTACAAC	180
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43	ATGGGATGC/	CAGGETETATE	TTCCAACGT	GACCITATO	r ACTTAGGGG	GCTGGCCCCT	540
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	ACTCTGATG	T TGCTGTTCT	T GAAGCTGGG	C TOTOTOTO	C CATGTTGG	TGTCACCAGA	1800
	CCCGAGTCA	A TTAAACAGO	T GGTCCTCCA	C TTTGCTGGT	T CAGCCTTCC	T GIGGCTCCIG	1860
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	AACCTGAGG	A ACAGGTTC	T GTGGAGACA	C TGAGTCAG	A TICTICATO	C AAATTATTTT	
	GTTAGTGG	A AATGGAATT	G CTTCTGTGT	A GTCAATAA	A TGAACCTG	T CACTITIC	2218
75							
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		Acid Accessi equence: 130		,1434.1			
	1	11	21	31	41	51	
80	1	1	1	- 1	1	1	
	GGCTGGTC	CC CTGACAGG	T GAAGCAAG	TA GACGCCCA	G AGCCCCGG	SA GGGGGCTGCA	60 120
	GTTTCCTT	C CCCCCCC	TO GCAGCGCT	C GCGCCCCC	NI CUCCUCIO	CT GOGOTAGOGG GG CGCAGGOCCT	
	ATGGGTGO	GT CCTGCGGG	T GCTTTGGT	CC CATTGGTO	GC GGGCTTGG	TG ATCTGCCTCG	

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	TGGTGTGCAT C	CAGOGCTTC	GCACAGGCTC	AGCAGCAGCT	GCCGCTCGAG	TCACTTGGGT	300
	GGGACGTAGC T	GAGCTGCAG	CTGAATCACA	CAGGACCTCA	GCAGGACCCC	AGGCTATACT	360
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	CACTGCTGCT G	ATTAGGGTT	TTTAAATTTT	TTTTTTTATT	TATTTAAGTT	CAAGAGAAAA	780
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	1 1	11	21	31	41	51	
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	AAAACCGCTT 1						240
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						CAATAATTTA	1740
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	ACCIGACCCT	TIMATCATGI	TATTIAIGC	ACCAAGGIIG	, IGGAICIIA	GGTATGTATG	2160
	GAAAGGAACT	CATTIATCA	ATTGIANGIA	T TO A TO A TO A A A A	r abcerrance	AGAGGTAAAT TTCACTGGAT	2220
55						ATTGTGACCT	2280
55				GILLICICA	3 MIIMOIGAA	MITGIGACCI	2308
	TAAATTTAAT	ACACATATAC	. IGCCICAG				2300
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60		11	21	31	41	51	
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	COMO L MORT		TOTAL	 TCCNNNTCT	 CATTCATTC	A TCTCATTATA	60
						A CAAGTGCTGG	120
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65						CATGTTGCATA	240
05						C @CTTTCCCGG	300
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						C GGGATTAGCT C AAGGCTGAGA	420
						G CGGGGCAGGC	480
70						A GGGCCAGAGC	540
, 0							600
						TTTGACCAGC G CCTTTTTATG	660
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				A GAAACACTA	TTGGAACTC	A AAAGTCATTT	60
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	WIGGIIWANG GWANACIG GILIGONACI CIRCUITATE	180 240
	ACTCACCTGG CTGGAATTAA CATGTCATAA AAAGGCAACT GCCCTCTCCT TGCGGTGGGT	300
_	AATCAAGGCA CCCATTTAGA GGCTTGCTGG TCAAAATGAA CCAACTCCAG TGTTCCATGC	360
5	TTGGAGCTCA ACACTAAGTC AGACTGCTCT GGCCCTGGAG CCAAAGCCAG TGACCGACCC	420 480
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10		
10	Seq ID NO: 75 DNA Sequence	
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	1 11 21 31 41 51	
15	TOTAL TRANSPORTED TO THE PROPERTY OF THE PROPE	60
13	ATCATTGCAG CCACGATTAA TAATGCCAGC ATGACTTCCC CAATTGACAA TGCTGGACTT GCAGCAGATG ACTTCAAAAT GAATGCATCC TTGCAGACAC AGATCTCCAC GGATGCTGAA	120
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	CATGAACTGC AGTCTGTCTT GGCCATGCAA AGCTCCCCAG AAGGAACCCT GGCTGACACA	240 300
20	GAAGCTGGCT ACGTGGCTCA GCTGTCAGAA ATTAAGATGT ATATCAGCAT CCTGGAGGAG CAGATCTGCC AGATCCGGGG CGAGACTGAA TACCAGAACA CAGAGTATGC ACAACTGCAG	360
20	GACATCAAGA CACGCCTGGA GGTGGAGATC GAGACCTACC ACCGCCTGCT CGGTGGAGAG	420
	CGACCTTCTG AGGCCAGAGA AGCTGAATCT AAAGGATGAT TCTCTGTGGA CTCCAAAGGA	480
	ATAACCAACA CAGCTCAATC GAGGGGAAGA GTCGCTTTTT AAAATTCACA TAAAAGCAGA GGAACCAGGC TGGTGACGGA TAATGACCAA CTAATTTCAT CTCAACACTG TTTCTGATGT	540 600
25	AAAATTCAAG AGTAAGATGC AGGCAGCTGA GTCCTGTCCC CAGGATGTAA ATGATGACAC	660
	CTARCARAGG CGTGCTGRAG CACTGCRACA RACCTGCGGC CACAGRGCTG CAGCTACTCC	720
	TGTAATCCTT TCTCAGATTC TTTTGTCTTA TTGGTTCGGT TTTGTCTTTA AATTGCAAAA TGTGTTTTCC TTCTTAATCA TTCTGTGTCG ATAAACTTTT TGCCTGTTGC AAATCAA	780 837
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	Coding sequence: 1022816 1 11 21 31 41 · 51	
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40	CAGCOGCCAA CTTCACAAGG TATAGCCAGC TAACTAGCTT GGATGTAGGA TTTAACACCA TCTCAAAACT GGAGCCAGAA TTGTGCCAGA AACTTCCCAT GTTAAAAGTT TTGAACCTCC	360 420
	AGCACAATGA GCTATCTCAA CTTTCTGATA AAACCTTTGC CTTCTGCACG AATTTGACTG	480
	AACTCCATCT CATGTCCAAC TCAATCCAGA AAATTAAAAA TAATCCCTTT GTCAAGCAGA	540
45	AGAATTTAAT CACATTAGAT CTGTCTCATA ATGGCTTGTC ATCTACAAAA TTAGGAACTC AGGTTCAGCT GGAAAATCTC CAAGAGCTTC TATTATCAAA CAATAAAATT CAAGCGCTAA	600 660
43	AAAGTGAAGA ACTGGATATC TTTGCCAATT CATCTTTAAA AAAATTAGAG TTGTCATCGA	720
	ATCAAATTAA AGAGTTTTCT CCAGGGTGTT TTCACGCAAT TGGAAGATTA TTTGGCCTCT	780
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	CTCCCTTACA CATACTCAAC CTAACCAAGA ATAAAATCTC AAAAATAGAG AGTGATGCTT TCTCTTGGTT GGGCCACCTA GAAGTACTTG ACCTGGGCCT TAATGAAATT GGGCAAGAAC	1440
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	ACTTGACCAT TCTGGATCTA AGCAACAACA ACATAGCCAA CATAAATGAT GACATGTTGG	1680
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65	AACACGCAAA CCCTGGTGGT CCCATTTATT TCCTAAAGGG TCTGTCTCAC CTCCACATCC TTAACTTGGA GTCCAACGGC TTTGACGAGA TCCCAGTTGA GGTCTTCAAG GATTTATTTG	1800 1860
0.5	AACTAAAGAT CATCGATTTA GGATTGAATA ATTTAAACAC ACTTCCAGCA TCTGTCTTTA	1920
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	AGAAGGTTTT CGGGCCAGCT TTCAGGAACC TGACTGAGTT AGATATGCGC TTTAATCCCT TTGATTGCAC GTGTGAAAGT ATTGCCTGGT TTGTTAATTG GATTAACGAG ACCCATACCA	2040 2100
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	GCTGGAGGAT ATCITTITAT TGGAATGITT CAGTACATCG AGTICTIGGT TTCAAAGAAA TAGACAGACA GACAGAACAG TITGAATATG CAGCATATAT AATTCATGCC TATAAAGATA	2400
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	TTATATTCCT TTTCCTTGAG GAGATTCCAG ATTATAAACT GAACCATGCA CTCTGTTTGC	2700
80	GAAGAGGAAT GITTAAATCT CACTGCATCT TGAACTGGCC AGTTCAGAAA GAACGGATAG	2760
	GTGCCTTTCG TCATAAATTG CAAGTAGCAC TTGGATCCAA AAACTCTGTA CATTAAATTT ATTTAAATAT TCAATTAGCA AAGGAGAAAC TTTCTCAATT TAAAAAGTTC TATGGCAAAT	2880
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	ATCACAATTA CATCTCTTCT AGGAAAATGT GTCTCCTTAT TTCAGGCCTA TTTTTGACAA	3000

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5	Nucleic Acid Accession #: Eos sequence 1 11 21 31 41 51	
	ATCAAGGAGG ACAGATITTA TATGCTTAAG ACTGGAGGGA GAGAGACCAG TTAGAAAGAC	60
	TOTACCTATA ATCCARGUA COCATACTAT GGGCTGGTTT GGTGGAGGTA GAGGAATGTU	120 180
10	CAGATTGGAG AAACAGGAAG TTAAAAATGG GCAGGGCTTG CTGACTGTTT GAAACTAGGG GGTGTGAAGG GAGGCAGCAC TCTAGGATAA ACACCAGACT TGCCGATTGT TTGGGAATAT	240
••	COLUMN TOTAL TOTAL CALCAL ACCADANCIA TARACTCARA AGRAGIGITA CACATAGATA	300 360
	ACTABATTAG TCATCTGTAG ATAGTACAAC ATATTCGTGT GTACAGAGAT CABAAGGGAC AGAAAGACCA AGGAGGCACT ABATATTCAC GGTACCCTAB ATACGTGAGA CATGAGGCAC	420
15	TCAGGATGCA GGAGGTTTCA ATTIGACAGG ATGGATGCAC ACTGCATGAC CCACAGTTCA GCTGGTGTGA TCATTCCACC CAACTTGCCC CCTCTCCCGT GTGTTGACCC ACCCCAGCAC	480 540
13	CIGCUICTG CITCUAGAA TOTGTTTTAC ATTTATTTAA TAAACGATGT TATTTGAGCA	600
	TITA	604
20	Seq ID NO: 78 DNA Sequence Nucleic Acid Accession #: Eos sequence	
20	1 11 21 31 41 51	
	TITITITITI TITITITITA AATGCTCAAA TAACATCGTT TATTAAATAA ATGTAAAACA	60
0.5	CATTOTERCA ACCACGACCO ACCTGCTGCG GTGGGTCAAC ACACGGGAGA GGGGCAAGT	120 180
25	TEGGTEGAAT GATCGATCAC ACCAGCTGAA CTGTGGGTCA TGCAGTGTGC ATCCATCCTG TCAAATTGAA ACCTCCTGCA TCCTGAGTGC CTCATGTCTC ACGTATTTAG GGTACCGTGA	240
	ATATTTAGTG CCTCCTTGGT CTTTCTGTCC CTTTTGATCT CTGTACACAC GAATACGTTG TACTATCTAC AGATGACTAA TTTAGTTATC TGTGTGTAAC ACTTCTTTTG AGTTTATTGT	300 360
	TTTCTGTCT TCTACAGCAG AATTGGATAT TCCCAAACAA TCTGCAAGTC TGGTGTTTAT	420
30	CCTAGAGTGC TGCCTCCCTT CACACCCCCT AGTTTCAAAC AGTCAGCAAG CCCTGCCCAT TTTTAACTTC CTGGTTTCTC AATCTGGACA TTCCTCTACC TCCACCAAAC CAGCCCATAG	480 540
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45	AAAGAAACAG CATTTCCTAC TTTTATACTG TCTATATGAT TGATTTGCAC AGCTCATCTG GCCAGAAGAG CTGAGACATC CGTTCCCCTA CAAGAAACTC TCCCCGGTG GAACAAGATG	300 360
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	ANANTCANTG TGAAGCAANT CGCAGCCCGC CTCCTGCCTC CGCTCTACTC ACTGGTGTTC ATCTTTGGTT TTGTGGGCAA CATGCTGGTC ATCCTCATCC TGATAAACTG CAAAAGGCTG	540
50	AAGAGCATCA CTGACATCTA CCTGCTCAAC CTGGCCATCT CTGACCTGTT TTTCCTTCTT ACTGTCCCCT TCTGGGCTCA CTATGCTGCC GCCCAGTGGG ACTTTGGAAA TACAATGTGT	600 660
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	CTGACAATCG ATAGGTACCT GGCTGTGTC CATGCTGTGT TTGCTTTAAA AGCCAGGACG GTCACCTTTG GGGTGGTGAC AAGTGTGATC ACTTGGGTGG TGGCTGTGTT TGCGTCTCTC	780 640
	CONGRATOR TOTTTACCAG ATCTCARARA GRAGGTCTTC ATTACACCTG CAGCTCTCAT	900 960
55	TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT AGTCATCTTG GGGCTGGTCC TGCCGCTGCT TGTCATGGTC ATCTGCTACT CGGGAATCCT AAAAACTCTG	1020
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	THE THE CONTROL OF THE PROPERTY OF THE PROPERT	2040
75	TATTGCTGGC AAAGACAGAA GCCTCACTGC AAGCACTGCA TGGGCAAGCT TGGCTGTAGA AGGAGACAGA GCTGGTTGGG AAGACATGGG GAGGAAGGAC AAGGCTAGAT CATGAAGAA	2160
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	AAGGAGGAGG AGGAGGTTTA GGTCAAGAAG AAGATGGATT GGTGTAAAAG GATGGGTCT GTTTGCAGAG CTTGAACACA GTCTCACCCA GACTCCAGGC TGTCTTTCAC TGAATGCTT	G 2580 C 2640
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		2760
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5	TOTAL TOTAL TOTAL AGRICATION AGRICATION OF THE STREET OF T	1380
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20	1 11 21 31 41 51	
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35		
	Seq ID NO: 88 DNA Sequence	
	Nucleic Acid Accession #: Eos sequence	
	1 11 21 31 41 51	
40	TOTAL TOTAL CONTINUES TO THE PARTY OF THE PA	60
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	COTOTOTAGO TOACATCAGO GGAGCAACGT GAACACAGGA AAATGGAAAT CAACATTTGA	240
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	TATTGGCTCA CAGA	0/4
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	Nucleic Acid Accession #: Eos sequence	
55	1 11 21 31 41 51	
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							720
	AGCGAGAGCC C	GGGAGCCAG (CIGGAIGGA (ACCRECETTE	CACACCCCCC	PACCAGCCAG	780
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	1 11 21 31 41 51	
	TOTAL STATE OF THE PROPERTY ACCOUNTS AC	60
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45	CGGACGCGTG GGCGGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACG AGTGGGCTG CATTCTGCGG AGGAAGACC CCAGCACAA GAGCCCACC TACTGATGG TCAGAGCATC CAGAAGAAGT	
45	CGGACGCCTG GCCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACG AGTGGGCCTG CATTCTGCGG AGGAAGACCC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC	120 180 240
45	CGGACGCGTG GGCGGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACG AGTGGGCCTG CATTCTGCGG AGGAAGACCC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGA GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAAGATG TTTCTGGCAG AAAGAACAGC ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCCC	120 180 240 300
45	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACCC CCAGCGACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC ACAAGCAAAG ATCTGGTAAC CCTAGCTGCC TCCAGTTTGA GGGAGAGAGAACAGACCCC CCCACACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGGTGG	120 180 240 300 360
	CGGACGCGTG GGCGGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACCC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG ACGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC TGCGCACCA GGGGCAGGAC ACTGGCTGG TGCAGAGCC TGCCCGGAT GTCGCGGAGG ACTCGCGGGC CGGTAGAACG CGCGGGGGCG TGCAGAGCC TGCCCGGAT GTCGCGGAGG ACTCGCGGGC CGGTAGAACG CGCGGGGGC	120 180 240 300
45 50	CGGACGCGTG GCCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACG AGTGGGCCTG CATTCTTGCG AGGAAGACCC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAAAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACTGGCTCG GTGCAGACGC TGGCCCGGAT GTCGCGGAG ACTGGCCGGC GCGCGGGGC CGGCGGCGGG AGGAAGACGCA GGGCAGCAC CCTTCCCACC ACCTCCCGCC	120 180 240 300 360 420
	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACCT CAGCGACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACACC ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGAGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACTGGCTGG GTGCAGAGCG TGGCCCGGAT GTCGCCGGAG ACTGGCTGG CGGTAGACG CGCGCGGGGG GCGGCGGGG CGGCGCGCG AGGAGAGCCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCGACGGGG CCGCCGCGCC GAGGAGACCC GGACAGGTGA CTCCTAGACG ACTGGCTCTC CCCTCCCCC GGGGGGAGTC CTTCTTCGC GGCCTCTGCC GCCCCTGGC TCCCCTCCT	120 180 240 300 360 420 480 540
	CGGACGCGTG GGCGACGGC TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCCTG CATTCTGCGG AGGAAGACCC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGGACATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGAACACCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACCTGCCTCCACCCCA GACATAGGAA GCAGTCCAC CTGGCACCCA GGGGAGGAC ACCTGCGGCGGGGGGGGGG	120 180 240 300 360 420 480 540 600
50	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGATTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCTG CATTCTGCGG AGGAAGACCT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTACTGATGG TCAGAGCAATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAGC ACAAGCAAAG ATCTGGTAAC CCTAGCTGCC TCCAGCTTGGA GGGAGGAGAGA AGGAACACGC CTCCACCACCCA GACATAGGAA AGCAGTCCAC CTGGCGACCA GGGGCAGGAC ACGTGGGTGG GCGGCGGCGG CGGCGCGGGA GGAGAGCGA ACTCCCCGC GCCGACGGGC CGGCGCCGG AGGAGACGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCGACGGG CGGCGCGCG AGGAGACCGC GGACAGGTAC TCCTTCAACG ACTGCGTCGC CCCTCCCCC GGCGGGAGTC CCTTCTTCGC GCCCTCCCGC GCCTTCCCAG AGTCTAACTC AGCCAAGCCC GCATCGCTTC GCCTCCTCCAC ACCACCGCAGAGACCAG AGCCTCCACA ACACACCCCC GCCTTCCCAGAAGAATACAAGAACCACCACACCA	120 180 240 300 360 420 480 540 660 720
	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCTG CATTCTGCGG AGGAAGACCT CAGCGACAA GCAGCCCACC TTACTGATGG TCAGAGCATC CAGAAGAAGT GGCAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACACC ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGAGAGA AGGACACCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGGTGG GGGGGGGG GGGCGGGGG AGGAGAGGCA GGTCAGCGC CCTTCCCACC ACCTCCGGC GCCGACGGG CGCGCGCGC GAGGAGACGCA GGTCAGGGG CTCTCAGACG ACTGCCGCC GCCCACGGG CCCCCCCC CAGGAGCCC GGCACAGGTGA CTCCTAGAGG ACTGCGTCG GGCTTCCCAC GGGGGAGGTC CCTTCTTCCC GGCCTCTCC GCCCCCTGC GGCTTCCAAG AGTCTGACCC GGCACGCTCTC GCCTCCTACA ACCACCCCC AGCGGGAGAGA GAATTACAGGG CCACGCTTAA TTACCCACCC CTCCTGTCAT CCGCGCGCCT CGGCGCGCT GGCCCAACGCC CTCCTGTCAT CCGCGCGCCT CGGCGCGCT AAGCACCCCC	120 180 240 300 360 420 480 540 600 660 720
50	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTC CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG AAAGAACAGC GCAAGCAAG ATCTGGTAC CCTAGGTGCC TCCAGCTAGAG AGGAGAGAGAG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGAGG TGGCCCGGA GGAGAGGAGGA ACTGGCTGG GCGCGGCGG CGGCGGCGG AGGAGAGCGCA GGTCACGCC CCTTCCACCC ACTCCCGCC GCCGACGGG CGCGGCGCG AGGAGACGCA GGCCAGGGA TCCCTCCGCC GCCGACGGG CGCGGCGCC GAGGAGCCCC GGACAGGGA CCTTCCACCC ACCTCCGGC GCCTTCCCCC GGGGGAGTC CTTCTTCC GGCCTTTCCC GCCCCTCCACC ACCTCCCCC AGCGGGAGA GAATTACAG GATTGCAGGG GCATGGCTTA TGCGCTCTAA TTACCCACCC CCGCGTGTCAT CCGCGGGCCC CGGGGGCCT CGGCGCCAGGC GCCGTAATTA AGACGCCGC CCCCTTCCTC CGGGCCCC CCCCCGGCCC CCCCCCCGG TCCCCCCCGC CCCGTGTCAT CCGCGGGCCC CCGCGGCCC CCCCCCGGG CCCCACGC GCCCACGCC CCCCTTCCTCCTCTCTCTCCCCC CCCCCCCGGG TCCCCCCCGGC CCCCCTCCCCCC CCCCCCCCCC	120 180 240 300 360 420 480 540 660 720
50	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGC TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCTC CATTCTGCGG AGGAAGACT CAGCTGTCCT CAAAGCAGA AGACAGAGT TTCTGGCAG AAAGAACAT GCAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCC CCCACACAAAGAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAG AGGACACCG CTCACCCCA GACATAAGAA AGCAGTCCAC CTGGCGACCA GGGGCAGGAC ACGTGGCTGG GCGGGGGG CGGCGGCGG AGGAGACGCA GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCGACGGG CGCGCGCGC GAGGAGACCC GGTCACGCC CCTTCCCACC ACCTCCCGCC GCCTCCCAC GGCGGGGGTC CCTTCTTCCC GGCCTTCCCA CCTCCCGCC GCCTCCCAC GGCGGGGGTC CCTTCTTCCC GCCCTCTCCA AGCCGAGAAA GAATTACAAG GATTGCAGGG GCACGCTTA TGCCCTCTCA AGCCGAGAAA GAAATTACAAG GATTGCAGGG GCACGCTTAA TTACCCACCC CCCCGTTCCT CGCGGGCGCT CGGCCACCCC CCACCTCCGC GTCCCCACCC CCCCGGTCCC GGAACCCTCC CTCCACCCA CCACCTCCGG GTCCCCACGC CCACTGCCTG CCACTCCTC CCGCCCTCTG GGACTGCCC CTCCACCCA GAAGGCTTA AGGCCTCACT GCGGCGAGAA CTTGGGGAGA CTGCAGCCCC CCCCTTCCACC CCACCTGCT AGGCCTCACT GCGGGCGAGA CTTGGGGAGC CCCTTCCACC CCCCTTACA AGGCCTCACT GCGGGCAGAA CTTGGGGAGCCC CCCACGCCC CCCCCTACAC CCCCTAATTA AGACCCCTA AGGCCTCACT GCGGGCAGAA CTTGGGGAGCCC CCCCTCCAC CCCCCTACAC CCCCTAATTA AGACCTCAC CCACTGCCTAC CCACCCAC CCACCCTCCC CCCTTACAC CCCCCTACAC CCCCTAACTAC AGGCCTCACT CCGGGGGAGAC CCCCCTCCACCCC CCCCTACACCCC CCCCTACCTCC CCCCTACACCCC CCCCTACCCC CCCCTACCCC CCCCTACCCC CCCCTCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGTG TTCTGGCAGAA AGAAGACTA CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTTGA GGGAGGAGAGA ACGTGGCTGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGAGGC TGGCCCGGAG AGGAGACGCA GTCAGCCC CCTTCCACC GCCGACGGGC CGGCGGCGGG AGGAGACGCA GCTCACCCC CCTTCCACC ACCTCCGGC GCCGACGGG CGCGGCGCG CGAGGACGCC GGACAGGTGA CCTCTCGGC CGCTTCCAG AGCTGACTC AGCCAAGCCG GCCCTTCCACC ACCTCCGGC GGCTTCCAGA AGTCTGACTC AGCCAAGCCG GCATGGCTA TTCCCACCC GGCGGAGAA GAAATTACAG GATTCCAGG GCACGGCTAA TGCGCTCTAA CCCCGTGTCAT CGCGGGGCT CCGCGGGGT GGGCCAAGG GCCGTAATTA AGACGCCGC CCCCTTCCC GGAACCCTCC CTTCGCACC CTCACCCAC CCACCTGGG TCCCCCGGG CCCACTGGCT GCAACCCTCC CTTCGCACC CTCACCCCA CCACCTGGG GGAGAGCTTA AGAGGCCTCACT GGGGCCAGAG CTTCAGACG GCCTTAATCA AGAGCCGCT AGGCCTCACT GGGGCAAGA CTTCGCAACC CCACCTGGG GGACCCACGG CCCACTCCCTG GGACCCTCC CTTCGCCACC CCACCTGGG GGAGAGCTTA AGAGCCCCCC CCCTTCACT GAACCCTCC CTTCGCCACC CCACCTGGG GGCCCACGG CCACTCCCTG GGACCCTCC CTTCGCCACC CCACCTGGG GCCCCACGG CCACTCCCTG GGACCCTCC CTTCGCACAC CCACCTCGG GGCCCCACGG ACCCCTCACTC CACCTCCTGG GGCCCACGGACCTCC CCCTTCACCT CAACCCCCC CCCTCCACCCACCACCCCGGGGCCCCACGGACCTCC CCCTTCACCCCC CCCTCCACCCCCCACGAGACCTCC CCCTTCAACCC CCCTCCACCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGATTGGGG TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCTG CATTCTGCGG AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGACGAGGTG TCAGGAGAACT GCCAAGCAAAG ATCTGGTAAC CCTAGCTGCC TCCAGCTTTGA GGGAGGAGGA ACGTGGCTGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGACGC TGGCCCGGAT GTCGCCGAGG ACTGCCGCGC GCCAGCGGCGCGCG AGGAGAGCCA GGTCAACGCC CCTTCCACC GCCAGCGGCGCGC GGGCGCGG AGGAGAGCCA GGTCAACGCC CCCACTGCGC CGGCCCGCG AGGAGACCCC GCCATGCGGC CGGCCCGCG AGGAGACCCC GCCATGCGG CGGCGCCGC CGGAGAGCCCG GCCTTCCCAC GCCCATGCC GCCTTCCACC GCCCCTCCACC GCCTTCCACC GCCCCCCCC GCCTGCCGC CGCCCCCCC CCCCGTCCCC GCCCACGCGCCC CTCCCACC CCCCGTCCCC GGACCCCTCCC CCCCGCTCCC GGACCCCTCC CCCCGCCCC CCCCGCTCCC GGACCCCTC CCCCGCCCC CCCCGCTCCC GGACCCCTC CCCCGCCCC CCCCCGCCC GGACCCCTC CCCCGCTCCC GGACCCCTC CCCCGCCCC CCCCCTCCCC CCCCCCCCC CCCCCTCCCC CCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020
50	CGGACGCGTC GGGCACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACTC CCAGGCACAA GCAGCCCACC TTACTGATGG TCAGGACATC CAGAAGAAGT GCAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTGA GGGAGGAGA AGAACAACGC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGGAA ACGTGGCTGG GTGCAGACGC TGGCCCGCAT GTCGCGACAC GTGCACCAC GGGCAGGAC ACCTGCCCCC GCCGCGGCGG CGGCGGCGGA AGGAGACGCA GGTCACGCC CCTTCCACAC ACCTCCGCC GCCGACGGG CGGCGGCGGA AGGAGACGCA GGTCACGCC CCTTCCACAC ACCTCCGCC GCCGACCGGC GGCGGCGGA AGCAGCCC GGACAGGTGA CCCCCTCCGC GCCTCCCCC GGGGGAGTC CCTTCTTCC GGCCTCTCCC AGCGCAGAAG AGAATTACAG GATTGCAGG GCATGGCTT GCCCCTCTG AGCGCAGAAG AGAATTACAG GATTGCAGG GCACGCCTA TGCCTCTAA ACACACCCCC CCCCTGTCAT CCGCGCCCT CCCCGGCCCT CCCCGCC GCCCTACCC CCCTCCACCC CCCCGTCCC GGAACCCTC CTTCGCACC CTCCACCCAC CCCCTCCGG AGGCCTACCT GCAACCCTC CTTCGCACC CTCCCACCCC CCACCTCCGG GTCCCCCAGG AGGCCTACCT GCAACCCTC CTTCGCAACA CCACCCCCC CCACCTCCGG GTCCCCCAGGA AGGCCTCACT GCGGCCAAAC CTTCGCAACA CCACCCCCC CCACCTCCAG GTCCCCCAGGA AGGCCTCACT GCGGCCAAAC CTTCGCAACA CCACCCCCC CCACCTCCAGC CCCCCACCACC CCACTGCGG CAACCCTC CTTCGCAACA CCACACCCC CCACTGCGG CCACCCTCC CTTCGCAACCA CCACCCTCCAGG GCCCTAACC CCACTGCGG CAACCCTC CTTCGCAACA CCACACCCCC CCACCTCCGG GCCCAACCC CTCCCCCCCACCC CCACCTCCAGG AGGCCTAACC CCACTGCGG CAACCCTCC CTTCGCAACAC CCACCCTCCAG CCCTCCACCCACCCCAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080
50	CGGACGCGTG GCGGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGTG TTCTGGCAGAA AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAAG ATCTGGTAGC CTAGGTGCC TCCAGCCCA GGGGCAGGAC AAAGAACAGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGCTGG GCGCGGCGC GGCGCGCGG AGGAGACGCA GCTCACCCC CCTTCCACCC ACCTCCGCC GCCGACGGG CGGCGGCGG AGGAGACGCA GGTCACGCC CCTTCCACC ACCTCCGGC GCCGACGGG CGCGGCGCG AGGAGACGCA GGCCACGGGA CCTGGCTCGG GCCTTCCCCC GGGGGAGTC CCTTCTTCG GGCCTTTCCACC ACCTCCGGC GCCTTCCAGA ACTCTGACTC AGCCAACCCA GCACCCTTC GCCCCTTCAA ACACACCCG AGCGCGAGAA GAAATTACAG GATTGCAGGG GCAAGGCG GCGTAATTA AGACGCCGC CCCGTGCTC GGAACCCTC CTTCGCCACC CTCCACCCA CCTCCCAGG CCCACTGCTG CCAACCCC CTTCGCCACC TCCACCCCA CACCCCCCGG CCCACTGCTG CCAACCCC CTTCGCCACC TCCACCCCA CACCCCCCAGG CCCACTGCTG CCAACCCCC CTTCGCCACC TCCACCCCC GGCCCAGGA CCACTGGCTG CCAACCCCC CTTCGCCACC TCCACCCCC GGCCCAGGA CCACTGCTG CCAACCCCC CTCCCCCGG TCCCCCCAGGA AGCGCCACTCCT CCAGCCACCA CCCCCTCGG GCCCCAGGA ATTCGTTGA CAGAAACAGT GAGGTCTTT GGAAAGATTA GGCACCACA AAGCCCCCC ACGCCCGCGA CCTCCCCCCCACCC ACCCCCCCCCCAGGAACCCC CCCCTTCAACC ACCCCCCCCCACCACCCCCCCCAGGAACCCC CCCTTCAACCC ACCCCCCCACACCCCCCCAGGAACCCC CCCCTTCAACC ACCCCCCACCACCCCCCAGGACCCC CCCCTCCACCCACCACCCCCAGGACCCC ACCCCCCACCACCCCCCAGGACCCC ACCCCCCACACCCCCCCC	120 180 240 300 360 420 540 600 660 720 780 840 900 900 1020 1020 1140 1200
50	CGGACGCGTG GGCGACGGG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCCTG CATTCTGCGG AGGAAGACT CCGCGCACAG AGGAGGCCCACC TTACTGATGG TCAGGACATC CAGAAGAAGT GCAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTGA GGAGGAGAG AGAACACACC CCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGAA ACGTGGCTGG GTGCAGACG TGGCCCGGAT GTCCCGGAGG ACTGCGCGC CGTTCCAACC ACCTCCACCCA GCGCGCGCGC GGCGCGCGC GAGGAGGCA GGTCACACC CCTCCAACCA CACTCCGGC GCCGACGGG CGCGGCGCC GAGGAGCGA GGTCACACC CCTCCAACCA CACTCCGGC GCCGACGGG CGCGGCGCC GAGGAGCGA GGCAGGAGGA ACTGCGTTG GGCTTCCCG GGCGGAGGT CCTTCTTCC GGCCTCTTCC GCCCCCTGC TCCCCACC AGCGCGAGAA GAATTACAG GATTGCAGG GCATCGCTT GCCCCCTTAA ACGCCGAGAA GAATTACAG GATTGCAGG GCACGCCTAC CCCTCCACCC CCCCGTGTCAT CCCCGGCCC CTTCCCACCC CCCCGTCCC GGACCCTC CTTCGCCACC CCCCGTCCC GGACCCTC CTTCGCCACC CCCCGTCCC GGACCCTC CTTCGCCACC CCACTGCCG GCAACTCCTC CTTCGCCACC CCACTGCTC GCAACCTCC CTTCGCCACC CCACTGCTG GAAGGTCTCT GCTGCAAGAA AGGCCCCAC GCCGAAACACT ATTTCGTGA CAGAAACAGT GAGGTTATT GGAAGACCCC ACAGCCCA GCCAGACCC CCACGCTGCG GAGGGCAACCC CCACTGCGG GCCCAACCC CCACCTCCGG GCCCAACCC CCACCTCCGG AGGGCCACAC ACAGCCCCC CCCCTGGCGCAGAA CTTCCCCCGGC CCTTCCACCCAC ACAGCCCCC CCCCTGGCGCAACCC CCCCTGGCGAACCTC CCCCAGGACCTC CCCCCGGCAACCTC CCCCAGGACCTC CCCCAGGACCTC CCCCGGCCCC CCCCCCGGAACCTC CCCCAGAACCTC CCCCGGCCCCC CCCCCCGCGAACCTC CCCCAGAACCCC CCCCCCCCACCCC CCCCCCAGAACCTC CCCCAGAACCCC CCCCCCCCCC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080
50	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCAGAAA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGTG TTCTGGCAGAA AGGAGACCT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTCTGGCAG AAAGAACAAG ATCTGGTAAC CCTAGGTGCC TCCAGCTACAG GGGGAGAGAG AAGAACAGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGAGGC TGGCCCGGAG AGGAGACGCA GTCAGCCC CCTTCCACCC GCCGACGGGC CGGCGGCGG AGGAGACGCA GCTCACCCC CCTTCCACCC ACCTCCGCC GCCGACGGGC CGGCGGCGC GAGGAGCCCG GGCCACGGC CGCTAGAGG ACTGCCTCC GCCGACGGGC CGCGGCGCC CAGGAGCCCG GGCCCAGGAC ACTGCCTCGGC GCCTTCCACC GGGGGAGTC CCTTCTTCG GGCCTTCCCAC ACCTCCGGC GCCGACGGAA GAATTACAG GATTCGAGGA GCACGCCTAA TGCCCTCTAA CCCCGGTGCTC CGAACCCCC CTTCGCACCC CCCCTCGG TCCCCCCGGG CCCACTGCCT GGAACCCTCC CTTCGCCACC CTCACCCCA CCACCTCGG GGCCCAGGA CCACTGGCTG CAACTCCTG CTCGCACCC CTCCACCCA CCACCTCGG GGCCCAGGA AGGCCTCACT GGGGCGAGAAC CTCGGAGGAG ACGGAGAGGGG CCCAGGGCC ACGCCCCAGAACCCCC CCCCCTGGAGAACAGT GGGACAGGAGACCCC ACCCCCCCCAGAACCCC CCCCCCCAGAACCCC ACCCCCCCCCAGAACCCC CCACCCCCCAGG GGCCCAGGACCCA AGGGCCCCCA CCCACCAGACCC CCCCCTCGAACCC ACCCCCCCCCCAGAACCC CCACCCCCCCAGAACCCCC ACGGCCCCCAACCCCC CCCCCCCGCGCCC ACGGCCCCCAACCCCC CCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1080 1220 1220 1250 1380
50 55 60	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTG CATTCTGCGG AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGAGGAGTG TTATGGAGGATC GCAAGCAAGA ATCTGGTAAC CCTAGCTGCC TCAGCTACGA GGAGGAGGACA ACGACCACCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGACGC TGGCCCGGAT GTCGCGGAGGAC ACGTGGCTGG GCGCGGCGGCG CGGCGGGGA GGAGGAGCAC GGTCAACGCC CCTCCACCC GGCGCGCGCG GCGCGGCGCGC GGGCGCGGA GGAGGACGCC GGTCAACGCC CCTCCACCC GCCATCGGCCGCCGC GGGGAGGCC GGCCGCGGGGAGAC ACTGCGTCCAC GCCATCGGC CGGCGCGCG AGGAGACCCC GGCCATGGGA ACTTCCACC GCCATCGGC CGGCGCCGC GAGGAGCCCG GGACAGGTGA CTCCTAGAGA ACTTCCGCC GGCTTCCCCC GGCGGAGGTC CCTTCTTCC GGCCTCTGCA CCCCCTCCGC CCCCGTCCCAC GGCGGAGACCC CCTCCACCA CCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 720 780 840 1020 1140 1200 1320 1320
50 55 60	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGCAGAA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCAC TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAGA AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTCCAC GGGGCAGGAC ACGTGCTGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGCTGG GCGCGGCGG CGCGCGCGG AGGAGGGCA GGTCACGCC CCTTCCACAC ACCTCCGGC GCCGACGGG CGCGCGCGC GAGGAGGCG AGTCAGGCC CCTTCCACAC ACTCCGGC GCCGACGGG CGCGGCGCC GAGGAGGCA GGTCACGCC CCTTCCACAC ACCTCCGGC GCCGACGGG CGCGGCGCC GAGGAGCCCA GGCACAGGCG CCCCTTGCACAC ACCTCCGGC GCCGACGGCG CGCGGCGCC CAGCCAGCC GCCCCTTGC TCCCCTCTG AGCCCCAGAGA GAATTACAG GATTGCAGG GCACGCCTTA TTCCCCCCC AGCCGAGAA GAATTACAG GATTGCAGG GCACGCCTA TGCCTCTAA TACCACCCC CCCCGTGTCAT CCCCGGCGCT CCCGGGCT GGGCCAACGC CCCCTTGCA ACACACCCCC CCCCGTCCC GGACCCTC CTTCGCCACC CTCCACCCA CCCCCTCGGC CCACTGCCG GCAACCTC CTTCGCCACC CTCCACCCC CCCCTCTGG GTCCCCCCTG AGGCCTCACT GCGCCAGAACACTC CTTCGCCAC CCCCACCCC CCCCTCTGGG GTCCCCCCTG AGGCCTCACT GCGCCAGAACACTC CTTCGCCAC CCCACCCCC CCCCTCTGG GTCCCCCAGGA AGAGCTCCT GCGCCAGAACACTC CTCGGAGAGA ACGAACCCGC TACACCCCA GCCAAACACAT GAGGTTATT GGAACACCCG ATTCGTGA ACAAACAGT GAGGTTATT GCAACACCCG CCCTTCAACC AAAGCACCCC AGGCAGGAG TACCCCCTT TGGCAACC CTCCCACCCA CCACCTCAGG GAGGGTAGA AAAGCACCC AGGCAGACTC CCAGACCCC TCGGAACGC CCTTCCACT CCCTAAACC AAAGCACCC AGGCAGGAG TACCCCCGT TGGGAACGAA GTTCCACCACACCA	120 180 240 300 360 420 480 540 600 660 720 840 900 1020 1140 1260 1320 1380 1440
50 55 60	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCAGAA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCT TCAGCAACGA AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTACTC CAAAGCAGGA AGACAGGATG TTTCTGGCAG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGACAAG ATCTGGTAAC CCTAGCTGCC CCCGTTTGA GGGAGAGAGAG CCCCCCCCCCCCA GACATAGGAA AGCAGTCCAC CTGCGCCACCA GGGGCAGGAC ACCTGGCTGG GTGCAGACGC TGGCCCGGAT GTCGCGGAGG ACTGCGCGCC CGGTAGAGAG GCGCGGCGGCG GGGAGAGCCCG GGGCACGAGC CCTTCCACCC ACCTCCACCCA GCCGACGGG GGGGGGGG AGGAGACGCA GGTCACACCC CCTTCCACC ACCTCCGCC GCCGACGGG CGGCGCGCGG AGGAGACCCG GGCCACGGC CGGTAGAGGG ACTGCGTCTG CCCCTCCCCC GGGGGAGATC CCTTCTTCG GGCCTCTCCACC ACCTCCGCC GGCTGCGAGA AGTCTGACTC AGCCAAGCCG GCATCGCTC GCCCCTCCGG TCCCCTCCTG GGCTTCCGAG AGTCTGACTC AGCCAAGCCG GCATCGCTCA ACACACCCCG CCCGGTCCA GGAACCCCC CTTCGCCACC CCCCCGTCAA TTACCCACCC CCCCGTCCC GGAACCCCC CTTCGCCACC CTCCACCCAC CCCCCTGGG TCCCCCAGGA AGCGCGAGAA CAATTCCTG CCGCCCCTTC GGACCCCCC CACCTCGGG GCCCCAGGA CCACTGGCTG CAACTCCTG CTCGCACCC CTCCACCCAC CACCTCCGG GAGAGCTGC CCCCGTCCT GGAGGCTCTC CTTCGCACC CTCCACCCAC CACCTCCGG GAGAGCTGA AGAGCCACCAC GGAACCTCC CTTCGAAGGA ACTGGGAGAG TGGGGGGGGC CAGGGACTT ATTCGTTGA CAGAAACAT GAGGTCTATT GGAAAGCTGG GCCCTCCACC ACGACCCCC AGGACCCCC CCCGACCCCT TCCATCCAC ACACCCCG GAGAGCCGA AGTCCGCCCA GGGCAGACTC CCAGACCCGC TCCTTCACAC CCCCTTAAACC AGGACCCCA GCCAGAACTC CCAGACCCGC TCCTTCACAC GCACCGAGAA AGGGAAGGGA	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1080 1140 1200 1320 1320 1440 1560
50 55 60 65	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGGGTG TCAGGAGCATC CAGTGGCAGA GCAAGCAATG ATCTGGTAAC CCTAGCTGCC TCAGTTGGA GGAGGAGGAGA ACTACGCAGA ATCTGGTAAC CCTAGCTGCC TCAGTTGGA GGAGGAGGAGA ACTACGCAGA ACTGGGTCAC TCAGCTTGCA GGGGAGGAGA ACGTGGGTGG GTGCAGACGC TGGCCCGGGA GGAGGAGCAG ACTGGCGGG GCGCGGCGG CGGCGGCGGA GGAGGAGCAG ACTGCCGCG CGCCGACGGG CGGCGCGCGA GGAGGAGCAGA ACTGCGGGC GCCCACGGGG CGGCGCGCG AGGAGACGCG GGACAGGTGA TCCCTCCACC GCCCACGGGG CGGCGCGCG AGGAGACCGC GGACAGGTGA TCCCTCTCCAC GCCCACGGGG CGGCGCGCG AGGAGACCGC GGACAGGTGA TCCCTCTGG GCCTTCCCCC GGCGGGAGTC CCTTCTTCG GGCCTCTGCG CCCCCTCGG TCCCCCC GGCTGCAGAA GAATTACAG ATTGCAGGG GGACGGTAA TGGGCTCTAA ACACACCCG CCCGTCCTA CCCCGGCCCT CCGCGGGCT GGGCCAAGGC GCGTAATTA AGACGCCGC CCCGTTCAT CCCCGGCCCT CCTCGGCGC GGCCAAGGC GCGTAATTA AGACGCCGC CCCGGTCCT GGACCCTCT CTTCGCCAC CCCCCACCAC CCACCTCCGG GTCCCCAGGA CCACTGGCT GCAACTCCT CCTCGGCAC TCCCACCAC CCACCTCCGG GTCCCCAGGA ACGACCTCTC CCCCGGGGT GGGCCAAGGC GCCTTAATA AGACGCGGT TACAGTCCTG GAAGGTCTTC GCTGGAAGA ACTGGCTTGA CAGAAACAGT GAGGCAGGAC TCCCCACCAC CCACCTCCGG GAGGACTTAT AAAGCCCCC GAACCTCC CTCGGGAGAA CCTCCACCAC CCACTCCGG GAGGACTTAT AAAGCCCCC GAGACCTTC CCTCGGAGAACACT GGGCCTCTTA GGCACCTCCC CCACTCCAC ACGACCTCCC CCCCCTTGACG GACCCTCCAC CCACCTCCAC ACGACCTCCC CCCCCTTTAACA GGCACGGAACCT ACGACTCCCC CCCCCTTGGCG GCAACTCC CCCCTTAACGGAACC ACGACTCCC CCCCTCGGG GGAAATTAC CTTCCTGCGA AGAAAGGTGA CACCCCCC ACAGAACCTC CCCCCTGGG GGAAATTAC CTTCCTGCGA AGAAAGGTGA CATCCCCGCC ACAGAACCTC CCCCCTGGG GGAAATTAC CTTCCTGCGA AGAAAGGTGA CATCCCCGCC ACAGAACCTC CCCCTTGGCG GCAAATTA AGGGGTAGG CTGCGAAGGAA AGGAAGGAA AGGCCCCGAACCTC CCACTGCGG CTTAACAGGAA GAGCACTGAA GAGACCTCCC ACGGAACTCC TCCCCTGGG GGAAATTAC CTTCCAGGGA AGGACCCTCTCCCCC ACAGACCTC CCCCTAGGG GAAATTAC CTTCAGGGTA CATCCCTGCC ACAGACCTCC CCCCAGAACTC CCACACCCC CACTCCAC CACTCTCCCC ACAGACCTC CCCCTCTCATC AGCAACTCTT CCCACACC CACTTTAACA GTCCCTTAACA GACACCACGC CCCCGAAGCCC CCCTCTCATCC CCCACACCC CCCCCCC CACTCCACCC CACTCTCACCC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1080 1140 1200 1320 1320 1440 1560
50 55 60	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGGCAGAA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG AAAAACAAG GCAAGCATA CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG AAAGAACAGG CCCCCCCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGCTGG GCGCGCGCGC GGCGCGCGG AGGAGAGGAC ACTGGCGCCCCC CTTCCACCCA GACATAGAAA ACCAGTCCAC GCGCGCGCGC GGCGCGCGC GAGGAGGCCGC GGCCGACGGA CACGTGCTGG GCCGCGCGCGCGCG CGGCGCGCC GAGGAGGCCG GGCCCCTCCCACCAC ACCACCCCCA ACCGCGAGGA GAATACAG CCTTCTTCCC GGCCTCTCCC GCCGCCGCCGCCC GAGGAGCCCC GGCCCCTCCCACCAC ACCTCCGCC CCCCGTCCCCC GGCGGCGCC CCGCGCCCC GCCCCCCCC	120 180 240 300 360 420 480 540 660 660 720 780 840 1020 1080 1140 1200 1320 1320 1440 1560 1620 1620
50 55 60 65	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGC TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTTC CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGGATG TTATGGGCAGA AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTATGGGCAGA ACAAGCAAGA ATCTGGTAAC CCTAGCTGCC TCCAGTTGA GGAGAGAGAGA ACGTGGCTGG CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGGGCACCA GGGGCAGGAC ACGTGGGTGG GTGCAGACGC TGGCCCGGAT GTCGCCGAGG ACTCGCGGC CGGTAGAAGG ACGTGGGTGG CGCGCGGCGG CGGCGGGGA GGAGAGGCA GGTCACGCC CCTTCCACC CACTGCGG CGCGAGGGG CGGCGCGGG AGGAGACGCG GGCACAGGGA ACTTCGCGC CGCCACGGGG CGGCGCGCG GAGGAGCCCG GGCACAGGGA ACTTCGCGC CGCCACGGGG CGGCGCGCG AGGAGACCCG GGCACAGGGA ACTTCCCACC GGCTTCCCCC GGCGGAGTC CCTTCTTCGC GCCCTTGCAC ACCTCCCGC CGCCACGGG CGGCGCCGC CAGGAGCCCG GGCACAGGGA ACTTCGCTCT GGCTTCCAGA AGTCTGACTC AGCCAAGCCG GCCATCGCT GCCCCTCTGAAGA ACTCCCCGC CCCCGTCCCA CCCCCCCC CTTCGCCACC CCCCCTCCACA ACACACCCCG CCCGTCCAC GGAACCCTC CTTCGCCACC CCCCCACCAC CCACTCCGG GCCCCAGGA CCCCTGGCG GGACCCTCC CTTCGCCACC CCCCCTCCACC CCCCTCCAGA CCCCTGGCG GGACCCTCT GGACCCCC CCACCTCCGG GCCCCAGGA CCCCTGGCAGACACTC CCCCCCACC CCACCCAC CCACCTCCGG GCCCCAGGA AGGCCTCACT GGAGGCCTCT GCGCCCTCT GGACGCCCCC CCACTCCAC CCCCTAAACC AAAGCCACG GAACCTTC GCCCCCTT GGACGACCCC CCACTCCAC CCACTCAGA AGGCCTCACT GGAGGCAGAA TACCCCCTT TGGCACCC CCACTCCAC CCCCTTAACC ACGACTCCT CCCCTGAGG GGAAATTAC CTTCAGCGAA AGGAAGGGAA AGGAACTCCC CCCCCTGGG GGAAATTAC CTTCAGCGCA AGGAACGTGA AAAGACACG ACGGAACTTC CCAGACCCCC TCGTTCACAC CCTTCAACC ACGACTCCC CCCCTGGG GGAAATTAC CTTCAGGGAA AGGAAGGGAA AGGAAGGGAA GGGAATTAC CTTCAGGGAA GGGCACGAAA GGGAAGGAA AGGACCCCCC TCCTCCACCC CTTCCACCC CACCACCAC CCACTAAGGGAA AGGACCCCCC TCCTGGCG GGAAATTAC CTTCAGGGAA AGGAAGGAACGAAGACACACACACACACACAC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1220 1320 1440 1500 1620 1680 1780
50 55 60 65	CGGACGCGTG GCGCACGGC TGGCCGCGTG AGGAGTGGGG TGATGATGCC ACTGCAGAA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAGA AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG ACAAGCAAAG ATCTGGTACC CCTAGGTGCC TCCAGCTAGA GGAGGAGAGA ACGTGGCTGC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GCGGCGGCGG CGGCGGCGGG AGGAGGACGA GCTCCACCC CCTCCACCCCA GCGCCGCGCGC GCCGACGGG CGCGGCGGC GAGAGACGCC GGCCACGGC CCTCCCACCCA GCGCGAGGAC GCCGCGCGCCGC GAGGAGCCCG GAGAAGCCCC CCCCTCCCCC GGGGGAGGACGC CTTCTTCGC GCCTCCCCC GGGGGAGGACGC CCTTCCTCCACC ACCTCCGCC AGCGCGCGCCGC CGCGCCGCC GAGGACGCC GGCCCACCGC CCTTCCACC ACCTCCGCC AGCGCGAGAA GAATTACAG GATTGCAGGAG GCATGCCTC GCCCCTTCACA ACACACCCCG AGCGCGAGAA GAATTACAG GATTGCAGGAG GCATGCCTC GCCCCTTCACA ACACACCCCG ACCGCGCCCC CCACCTCCACCCAC CCACCTCACA ACACACCCCG CCCCTGTCAT CCCCGGGGGCT CCGCGCGCT GGGCCAACGC CCACCTCCAC ACCACCCCG CCCATGCTG CCAACTCCTG CCCCCCTTTGCCACC CCACCTCCAC CCACCTCACA ACACACCCCG ACGCGCCCCCC CCACCTCCTG GGACCAGCCC CCACCTCCAC GCCCCAGGA ACACCCCC CCACCTCCC CCACCCCCC CCACCTCCAC ACACACCCCG ACACGCCCACCCCC CCACCTCCAC CCACCTCCAC CCACCTCACA ACACACCCCG ACACGCCCACCCCC CCACCTCCAC CCACCTCCAC CCACCTCACCAC ACACGCCCACCCCC CCACCTCCAC CCACCTCCAC CCACCTCACCAC ACAGCACCCC CACCTCCACCCCC CCACCTCCAC CCACCTCCAGGA ATTCCGTCAC ACACACCCCC TCCCCACCAC CCACCTCCAG GAGGAGTATT ACACCCCCAC ACCACACCCC CCCCTCCACCCAC CCACCTCCACCAC ACAGACCCCA ACCACACCCC TCCCCCACCCCC TCCCACCACCACCACCACCACCACCACCACCACCACCACC	120 180 240 300 360 420 480 600 660 720 840 900 1020 11200 11200 1140 11200 11500 11500 11500 11600 11740 11800 11
50 55 60 65 70	CGGACGCGTG GGCGACGCG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTACTC CAAAGCAGGA AGACGAGGATTCTTCTGCGA AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGGATG TTTCTGGCAG AAAGAACAGG CCAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTGA GGGAGAGAGAG ACCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGACGC TGGCCCGGAT GTCGCGGAGG ACTGCGCGC GCGCGGCGCG CGGCGCGCGG AGGAGAGCCA GGTCACACCC CCTCCACCCC GGGGGAGAGACGA CCTTCCACCC GCCGACGGGG CGGCGCGGC GAGGAGCCCG GGCACAGGC CGTTAGAGG ACTCCCGCC GCCGACGGGG CGGCGCGCG GAGGAGCCCG GGCACAGGC CCCTTCCACC ACCTCCCGC GCCTACCGG GGGGGAGGA CCTTCTTCG GGCCACTCGG TCCCCTCTG GCCTCCCCG GGGGGAGGC CCTTCTTCG GGCCTCTCCAC ACCTCCCGC GGCTGCGAGA GATCTGACTC AGCCAACCCG GCATCGCTC GCCCCTCTGG TCCCCTCCTG GCCTACTCGAG AGTCTGACTC AGCCAACCCG GGCCACGGC GCGGAAATATA AGACGCCGC CCCCGGTCCT GGAACCCTCC CTTCGCCACC TCCCACCCCTCCGG GTCCCCCGG CCCCGGTCCT GGAACCCTCC CTTCGCCACC TCCCACCCC CCCCCTCGG GTCCCCGGG AGGCCTCCTG GAACCCTCC CTTCGCCACC TCCCACCCC CCCCCTCGG GTCCCCAGGA AGGCCTCACT GGGGGCAGAG CTGCGAAGGCG CCCTTCCACC CCCCCAGGA AGGCCTCACT GGAGGCTCTC CCTGGAAGACTC CCCCCACCAC CCCCCCAGG GAGGACTA AAAGCCACG AGGCCAGGA CTGCGAAGAG CCGAAGCCG CCCTTCCACC CCCCCAGGA AGTCCCCCA GGAGCCTCC CTTCGCACC CTCCACCCC CCCCTCCAG GAGGACTT AAAGGCACGA AGGGAAATTA GAGGTCTATT GGAAAGTTAG CCCCCTAAACC ACGACCACC ACGAACCTC CCAACCCCG TTCGTACAC GCCACCACC ACGAACCAG AGGCCAGCCT CCCAACCCCC TCCTTCACCC ACGAACCAG AGGCCAGCACT CCCAACCCCC TCCTTCACCC ACGACCCCA GCCAAACTC CCAACCCCC TTCTTCACCA AGAAAGGGA CTGCTGAGGGA AGTCCCCCA GCCAAACTC CCAACCCCC TTCTTCTCCCAC GCCCACCACC ACGACCACCAC GCCAAACTC CCAACCCCC TTCTTCACCA GCCACCACC ACGACCACCAC GCCAAACTC CCAACCCCC TTCTTCACCC CACCTCCCCCCACCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1140 1200 1320 1320 1440 1500 1620 1680 1740 1800 1860
50 55 60 65	CGGACGCGTC GGCGACGCG TGGGCGGCTC AGGAGTGGGG TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCCTG CATTCTGCGG AGGAAGACT CAGGACACA GCAGCCCACC TTACTGATGG TCAGGACACC CAGGACACA GCAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGCTAGG GGAGGAGAG AGAACACCC CCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGAG AGCAGCCCC CTCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGAG ACGTGCTGG GCGGCGGCG CGGCGCGGG AGGAGAGCA GCTCACCCC CTTCCACCCAC ACCTCCACCCCAGACGCCGCGCGCGCGCGCGCGCGCGCGC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1220 1320 1350 1440 1500 1620 1680 1740 1620 1680 1740 1690 1690 1690 1690 1690 1690 1690 169
50 55 60 65 70	CGGACGCGTG GGCGACGGC TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGGCAGA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGACGG TTACTGGGCTG GCAAGCATA ACTGGTACA CCTAGGTGCC TCCAGCTAGA GGAGGAGACT CCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGAGAGA ACGTGGCTGG GTGCAGACG TGGCCCACG TGCCCCACGA GGACACCACCA GGGGCAGGAC ACCTGGCTGG GCGCGGCGG CGCGCGCGG AGGAGACGCA GCTCCACCCC CCTCCACCCA GACATAGGAA GCAGTCCAC GCCGACGGGG CGCGGCGGG AGGAGACGCA GCTCACCCC CCTTCCACCCA ACCTGGCTGG GCCGCCGCGCGCGC GAGGAGCCCG GGCCACGCC CCTTCCACCCA ACCTCCCGCC GCCGACGGG CGCGGCGCG AGGAGACGCA GCTCACCCC CCTTCCACCAC ACCTCCCGCC GCCGACGGG CGCGGCGCG AGGAGACGCA GGTCACGCC CCTTCCACCAC ACCTCCGCC GCCGACGGG CGCGGCGCC CAGCAGCCCG GGCCCACGG CCCCCTTCCACC ACCTCCGCC GCCGTCCCAG AGTTCACTC AGCCAACCCG GCACCACCTC GCCCTCACACCAC ACCTGCAGA AGAATTACAG GATTGCAGGAG GCATGCCTT GCCTCCTACA ACCACCCCG CCCGTGTCAT CCCCGGGGGCT CCGCGGCGC GGCCAAGCG GCCGTAATTA AGAGCCCCG CCCCTGCCC GCAACTCCTG CTCCGCCGCC CCCCCTCCGG TCCCCCCGCG CCCCTGCCC GCAACCCCC CTCCCCCCCAC CCACCTCGG GCCCCAGGA CCACTGCTG CCAACTCCTG CCGCCCCTT GGACCACCCC CCACCTCGG GCCCCAGGA ACTCCCCCGC CCACCACCCC CCCCCTCGG GCCCCAGGA CCACTGCCG CCAACACCCC CCCCTTCGCACCCA CCACCTCGG GCCCCAGGA ATTCCCTCTA CAGCAACCAG CCGCAGAACCCC CCACCTCGG GCCCCCAGGA ATTCCCTCTA CAGCACCCC TCCCCCCCTA CCCCCTCGG GCCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 1020 1140 1200 1150 1560 1660 1740 1860 1920 1980
50 55 60 65 70	CGGACGCGTG GGCGACGCG TGGCCGCTC AGGAGTGGGG TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCT TCAGCAACGG AGTGGGCTG CATTCTGCGG AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGACAGGATT TTCTGGCAG AGGAAGACT CAGCTGTCCT CAAAGCAGGA AGACAGGATG TTCTGGCAG ACAAGCAAGA ATCTGGTAAC CCTAGCTGCC CCCAGTTTGA GGGAGGAGAGA ACCAGCCAAGA ATCTGGTAAC CCTAGCTGCC CCCAGTTGA GGGAGAGAGAGA CCCCCCCCCCCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACTGGCTGG GTGCAGACGC TGCCCCGGAT GTCGCGGAGG ACTGCGCGCC CGGGGCGGAGA ACTGGGTGG GCGCGCGCGC GGGGGCGGG AGGAGACGCC GGTCAAGAGG GCGCGGCGGC GCCGACGGGC CGGCGCGCGC GAGGAGCCCG GGCCACGCC CCCTTCCCACC ACCTCCGCC GCCGACGGG CGGCGCGCGC GAGGAGCCCG GGCCACGCC CCCTTCCCACC ACCTCCGCC GCCGACGGG CGGCGCGCGC GAGGAGCCCG GGCCACGGC CCCTTCCACC ACCTCCGCC GCCGACGGG CGGCGCGCGC GAGGAGCCCG GGCCACGGC CCCTTCCACC ACCTCCGCC GCCGACGGG AGTCTGACT AGCCAACCCG GGCCACGGG ACTCCTTCG GCCTTCCAGA AGTCTGACT AGCCAACCCG GCCCACGCG GCCCCTGCG TCCCCTCCTA ACCGCGAGAAA GAAATTACAG GATTCCAGGG GCACGCTAA TGGGCTCAA ACACACCCG CCCCGTGCT CCCACCCCCC CTCCCCCCCC CCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800 1860 1920 1980 2040 2100
50 55 60 65 70	CGGACGCGTG GGCGACGGC TGGCCGCTG AGGAGTGGGG TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCAC TCAGCAACGG AGTGGGCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG ACAAGCAAAG ATCTGGTACC CCTAGGTGCC TCCAGCTAGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGA	120 180 340 340 360 420 480 540 600 660 720 780 840 1020 1080 1140 1200 1560 1620 1680 1740 1800 1800 1900 1900 1900 1900 1900 190
50 55 60 65 70	CGGACGCGTG GGCGACGCG TGGCCGCTC AGGAGTGGGG TGATGATGCC ACTGCGAGAA GCAGGCGCCC TGGCCCAAGG AGGAGGCCCAT CTAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAACGG TCAGTGGCTG GCAAGCATA ATCTGGTAAC CCTAGCTGCC CTCCACCCCA GACGTAGGAGA ACCAGCAAGA ATCTGGTAAC CCTAGCTGCC CTCGACCCA GGGGCAGGAC ACAGCAAGA ATCTGGTAAC CCTAGCTGCC CTCGACCCA GGGGCAGGAC ACCTGGCTGCG GTGCAGACGC TGGCCCGCGT GTCGCCGAGG ACACGGGGCAGGAC ACCTGGCTGG GTGCAGACGC TGGCCCGCGT GTCGCGACGA GACCACCCC CCCACCCCA GACATAGGAA AGCAGCCCC GCCGACGGGC CGGGGCGGG AGGAGACGCC GTCACACCC CCCTCCACCC GCCGACGGGC CGGCGCGCGC GAGGAGCCCC GGACAAGCCC CCCTTCCCACC GCCGACGGG CGGCGCGCGC GAGGAGCCCG GGCACGGC CGGTAGAAGG ACCTCCCGCC GCCGACGGG CGGCGCGCGC GAGGAGCCCG GGCCACGCC CCCTTCCACC ACCTCCGCC GCCTACCCC GGGGGAGTC CCTTCTTCG GGCCTCTGC CCCCCTCTGG GCCTCCCGG AGCTCCCC CCCCCCCCCCCCCCCCCCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1140 1220 1380 1440 1560 1620 1680 1740 1800 1860 1740 1800 1860 1920 1980 2040 2160 2220
50 55 60 65 70	CGGACGCGTG GGCGACGGG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCGAGA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTTCTGGCAG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTTCTGGCAG ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTGA GGCAGGAGAGA ACGTGGCTG CCCCCCCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGAC ACGTGCTGG GCGCGCGCG CGCGCGCGG AGGAGAGGA GGTCACACCA GGGGCAGACA CCTGCCCCC GCCGACGGG CGCGGCGCG AGGAGAGCAC GGTCACACC CCTCCACCCCA GACGACGCC GCCGACGGCG CGCGGCGCG AGGAGAGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCTCCACC ACCTCCGGC GCCGACGGC CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCTCCACC ACCTCCGGC GCCGACGGC CGCGGCGCC CAGGAGAGCAC GGACAGCTC CCCTCTTCT GGCTTCCAGA ACACACCCC AGCGCGAGAA GAATTACAG GATTGCCAC GCCCCTCTGC TCCCCTCTG AGCGCGAGAA GAATTACAG GATTGCACC CTCCACCCCA CCCCCTGAG TCCCCTCTG AGCGCGAGAA GAATTACAG GATTGCCCC CTCCACCCCA CCACCTCGGG CCCACTGCTC CAACCCCCT CCCGGGGCT GGGCCAACGC CCCCTGTCCT CGCACCCC CTCCCACCCC CCACCTCGGG GTCCCCACCC CCCCTGCTCC GCAACCCCC CTCCCACCCC CCACCTCGGG GTCCCACCCC CCACTGCTG CAACTCCTG CCGCCCTTG GGACTGCCC CCACCTCCGG GTCCCACCCC CACCTGCGC CCAACCCC CCCCCTCGGG GTCCACCCC CACCTGCGC GCAAACCAC CCCCCTTTGGCACAC CCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020 1140 1220 1320 1440 1500 1560 1680 1740 1860 1980 2040 2160 2220 2280 2340
50 55 60 65 70	CGGACGCGTG GGCGACGGC TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCGAGA GCAGGCGCCC TGGCCCAAGG AGGAGGCCACC TCAGCAACGG AGTGGGCTTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTCTGGCAG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACAGAGTG TTTCTGGCAG AAAGAACAAG ATCTGGTAAC CCTAGGTGCC TCCAGCTAGAGGAAGAGAGAGAGACTCCC CCCACCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGGAC ACGTGGCTGG GTGCAGAGG TGGCCGGAG AGGAGACGCC CTGCACCCCA GGGGCAGGAC ACGTGGCTGG GCGCGGCGG CGGCGGG AGGAGACGCA GTCCACCCC CCTTCCACCCA ACCTGGCTGG GCCGACGGG CGCGGCGGG AGGAGACGCA GTCGCGCCC CCTTCCACC ACCTCCGGC GCCGACGGG CGCGGCGGC GAGGAGCCGC GGCCAAGGC CCCTCCACCCA CACCTCCGGC GCCGACGGG CGCGGCGCG AGGAGACGCA GGTCACCC CCTTCCACC ACCTCCGGC GCCGACGGG CGCGGCGCC GAGGAGCCCG GGCCAAGGC CCCTTCCACC ACCTCCGGC GCCGACGGG CGCGGCGCC GAGGAGCCCC GGCCAAGCCC CCCTTCCACC ACCTCCGGC GCCGACGGG CCGGCGCCC CAGGAGCCCC GGCCAAGCCC CCCCTTCCAC ACACCCCG GCCGACGGA GAAATTACAG GATTGCAGGG GCATGCCTT GCCTCCTACA ACACACCCCG GCCGTGCAT CCGGGGGGCT CCGCGGGGCT GGGCCAAGC GCCGTAATTA AGACGCCGC CCCGTGCACT CGGGGGGCT CCGCGCGGCT CCCCCTCCACCCAC CCACCTCGG TCCCCCAGGA CCCACTGGCTG CCAACTCCCT CTCCGCACCC CCACCTCGG TCCCCCAGGA CCCACTGGCTG CCAACTCCCT CCCCCCACCACCACCCTCGG TCCCCCAGGA CCCACTGGCTG CCAACTCCCT CCCCCCACCACCCAC CCACCTCGG TCCCCCAGGA CCCACTGGCTG CCAACTCCCT CCCCCCACCACCCC CCACCTCGG TCCCCCAGGA ATTCCGTCCA AGGAACACTC CTCTGGAAGAG ACTGGGAGAG TGGGGAGAGG CCCAAGGGGC CAGGGCCT ATTTCGTTGA CAGAAACAGT GAGGTCTTT GGGAAGAAGCCG CCCTTCCACCCAC ACGGCCCCAC ACCGAACTC CAGACCCC TCCCACCCCC CCACCTCGG TCCCCCAGGA AGGCCCCAACCCC CCCCCCCCT TCCGGAAGAA ACGGGAAGCGG CCCAGGACCT ACGGCCCCACACCC CCCCCCCCC TCCCGACCCC TCCTTTAACA GCACCGAACT ACGGACCCCAACTC CCACCCCCGC TCCTCAACCCA ACGGACCCCAACCC CCCCCCCCC TCCTCCACCCAC ACCACCCCCCCC	120 1800 360 3600 420 4800 540 6600 6600 720 780 8400 1020 1080 11400 1260 1320 1440 1500 1620 16800 1740 18000 18600 1920 1980 20400 21600 22280 23400
50 55 60 65 70	CGGACGCGTG GGCGACGGG TGGGCGGCTG AGGAGTGGGG TGATGATGCC ACTGCGAGA GCAGGCGCCC TGGCCCAAGA AGGAGGCCCACC TCAGCAACGA AGTGGGCCTG CATTCTGCGG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTTCTGGCAG AGGAAGACTT CAGCTGTCCT CAAAGCAGGA AGACGAGGT TTTCTGGCAG ACAAGCAAAG ATCTGGTAAC CCTAGGTGCC TCCAGTTGA GGCAGGAGAGA ACGTGGCTG CCCCCCCCCA GACATAGGAA AGCAGTCCAC CTGCGCACCA GGGGCAGAC ACGTGCTGG GCGCGCGCG CGCGCGCGG AGGAGAGGA GGTCACACCA GGGGCAGACA CCTGCCCCC GCCGACGGG CGCGGCGCG AGGAGAGCAC GGTCACACC CCTCCACCCCA GACGACGCC GCCGACGGCG CGCGGCGCG AGGAGAGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCCCACCAC ACCTCCGGC GCCGACGGG CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCTCCACC ACCTCCGGC GCCGACGGC CGCGGCGCC CAGGAGACGCA GGTCACACCC CCTCTCCACC ACCTCCGGC GCCGACGGC CGCGGCGCC CAGGAGAGCAC GGACAGCTC CCCTCTTCT GGCTTCCAGA ACACACCCC AGCGCGAGAA GAATTACAG GATTGCCAC GCCCCTCTGC TCCCCTCTG AGCGCGAGAA GAATTACAG GATTGCACC CTCCACCCCA CCCCCTGAG TCCCCTCTG AGCGCGAGAA GAATTACAG GATTGCCCC CTCCACCCCA CCACCTCGGG CCCACTGCTC CAACCCCCT CCCGGGGCT GGGCCAACGC CCCCTGTCCT CGCACCCC CTCCCACCCC CCACCTCGGG GTCCCCACCC CCCCTGCTCC GCAACCCCC CTCCCACCCC CCACCTCGGG GTCCCACCCC CCACTGCTG CAACTCCTG CCGCCCTTG GGACTGCCC CCACCTCCGG GTCCCACCCC CACCTGCGC CCAACCCC CCCCCTCGGG GTCCACCCC CACCTGCGC GCAAACCAC CCCCCTTTGGCACAC CCCCCCCCCC	120 180 360 360 360 420 480 540 660 660 720 780 840 1020 1080 1140 1200 1320 1380 1560 1620 1680 1740 1800 1860 1740 2000 2160 2210 2210 2210 2210 22460

	GCTGTCTCC	CCCCTTCAGA	CTGGGGCCTC	CCCCAAAGGA	CAGGGACTGT	GTCTCCCCTG	2580
	GGACTAGGTT	CTTTGTGTCT	TCTGCATCAG	ACAGATTCCC	ATGAGGACAG	GGCTGTCTCC	2640 2700
	CCCTCCATCT	GGAGCTCCCT	GAAGGCAATG	CACCCATTCC	TCCCAGGACA	CATTIGUACE	2760
5	CCACCCCACC				ICCCMOUNCH	CCATTIOTCA	2800
,	CGCTTTGATG	Midwacii	ACIMOODOO.				
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10	Coding sequ				44	51	
10	1	11	21	31	41	1	
	AACACATTTC	ATCTGGGGTT	CTTAAATCTA	AATCTTTAAA	ATGACTAAGT	TTTCTTCCTT	60
	TTCTCTGTTT	TTCCTAATAG	TTGGGGCTTA	TATGACTCAT	GTGTGTTTCA	ATATGGAAAT	120
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15	CCGACATCAC	GTTTGTGGAG	GTGTTCTGAT	TGATCCACAG	TGGGTGCTGA	CAGCAGCCCA	240 300
	CTGCCAATAT	COGTTTACCA	AAGGCCAGTC	CCACACIGIG	GTTTTAGGCG AAATTTATAC	CATTCTCAAG	360
	ACTTACATCA	GATCCTCAAT	CARATGATAT	CATGCTGGTT	AAGCTTCAAA	CAGCOGCAAA	420
	ACTCAATAAA	CATGTCAAGA	TGCTCCACAT	AAGATÇCAAA	ACCTCTCTTA	GATCTGGAAC	480
20	CAAATGCAAG	GTTACTGGCT	GGGGAGCCAC	CGATCCAGAT	TCATTAAGAC	CTTCTGACAC	540
	CCTGCGAGAA	GTCACTGTTA	CTGTCCTAAG	TCGAAAACTT	TGCAACAGCC	AAAGTTACTA	600
	CAACGGCGAC	CCTTTTATCA	CCAAAGACAT	GGTCTGTGCA	GGAGATGCCA	AAGGCCAGAA	660 720
	CGATTCCTGT	COTCATCART	CAUGUGGGCCC	CACABACCCT	AAAGGTGTCT GGAATCTACA	CCTGTTAAC	780
25						ATTAAGTTAC	840
	AAATAATTTT	ATTGGATGCA	CTTGCTTCTT	TTTTCCTAAT	ATGCTCGCAG	GTTAGAGTTG	900
	GGTGTAAGTA	AAGCAGAGCA	CATATGGGGT	CCATTTTTGC	ACTTGTAAGT	CATTTTATTA	960
				TGATGTATT	CTACCATGCT	GGTTTTATTC	1020 1040
30	TAAATAAAT	TTAGAAGACT					1040
50	Sea ID NO:	94 DNA Seq	uence				
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25	1	11	21	31	41	51	
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	GRATCIGCIG	GTCCCACT	CATCCTCAT	CONTRARAGAC	CTCCTATTTC	AACCCAGGCA	120
	GAGCAAGAAG	CAAAAACCC	TCAAACTTC	ACAGACTCA	TCTCCAAAGA	AGGCAACACA	180
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40	TGGAGTGATC	CTCCTCAGG	ACAAGTTCA	GAAACAGTC	A GAGAGACAA1	CTCTTGCAGC	300
						GACCACAACA	360
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45	GAGACTATGI	CCCCAGGTG	GTTCTCAAG	CATCTCCCC	A AGGATGCTCC	TGCTGACTTC	600
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50	AACTATTCG	CTCAAGAAA	r TIGCICIGI	A GATACGGAA	C TGGCAGAAGG	TCAAAACAAA A GACACAAGTG	840 900
50	TCTGAGACT	r CAGTGTCTA	C GTGCAAAAG	C AGCAAGGAO	G GCAACTCAG	CATGTCCCCT	960
	CTTTTTATC	A GTACTTTCA	C CTTGAACAT	T TCACACACA	G CTAGTGAAG	G TGCCACAGGA	1020
	GAAAATCTA	G CCAAGGTGG	A GAAATCCAC	C TACCCACTG	G CCTCCACAG	T ACATGCTGGC	1080
55	CAGGAGCAG	C CAAGCCCCA	G CAACTCAGG	A GGGCTTGAT	G AAACACAGC	CCTTTCTTCT	1140
55						G TCCTAGTGCC	1260 1260
						C TTGGGAGAAG C TGTTACCATT	1320
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	GGTTTCTGC	A GTAATTCCC	C TOTTCAGG	A CACAATTY	Y ABGBABGAG	A GAGCCAGACT G AAGTGAAACA	1680
	DESCRIPTION	G TOCAGCAGO	A GAGCCTGTC	C CAGCAGGG1	T CTCTTTCTG	C ACCTGATTTC	1740
65	CAACAAAGT	T TGCCTACGA	C ATCTGCTG	LA CAAGAGGAA	A GAAACTTGG	T GCCCACGCCC	1800
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						G GGAGGCAGGC	
70	CTCACAAGCTG	T CTGAGAGC	A GGCATCAG	C CCTCCTC	A TAATTOOT	C ACCACGACAA A CAAGGTCTGG	
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75						A GITATCTGTC	
75						LA CAATGTGAGT LA AAAGTTTCTG	
	CAAGACUAG	AAAAAAAA w	A GTCCTCT	TA GATOCOAT	IG ATGAGATA	AG TGTGATAGAG	
	TACACCAGO	G CTGGAAAA	C AGAGCCCT	CT GAAACCAC	AC CACAGGGC	C CAGAGAAGGA	2580
00	GGTCAATC	VA ATGACGGA	AA CATGGGCC	AC GAAGCGGA	AA TCCAGTCG	SC CATTITGCAA	2640
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						C CATTIGGCAA	
						AT AGGCCAAATA GA CAAAGCAGAA	
	TTGATTTC	C CCACTTCA	CC TCTTTCTA	GT TGTCTTCC	AA TAATGACTI	CA CTCTTCTCTT	

	GGGGTTGACA CGC	CACAACTC C	ACAGGCCAA A	TTCATGACG T	CCCTGAAAA 1	GACATAGTT	3000 3060
	GAGCCCAGAA AGC GAGCGTGGGA AAC	CGTCAGTA T	GIGITICEI G	ITTTCACAGA A	AAGGGGAAC 1	ATTGAGAAT	3120
	CCTGAAGGAA ATC	GTCACAGA C	TTTTTGATA A	GCCACAAAA I	GGAGGAACC 1	AAAATAGAG	3180
5	GTGCTTCAAA TTC	GGGGAAAC C	AAACCCCCA A	GCTCATCTA G	CTCCTCAGC (SAAGACCTTG	3240
	CCATTTATTT CAC	GGAGAACG 1	CACTTAGAG A	VAAGCCCCTA A	LGTTACTGCA (GATCCATGT	3300
	CAAAAGGGCA CC	CTGGGCTG 1	rgcgaaaaag 1	CCAGGGAGA G	SAGAGAAGTC (CTGGAAGCC	3360 3420
	CGAGCAGGCA AA	TCGCCAGG (SACCCTCACA (CONGREGORACIO	AADAADAAT	ATTTTGTCC	3480
10	ACCOMPANDED TAKE	CTGAGGCT (RABACTGGAA (GAAAAGGAAA A	ATATCAGAAA (GAACTCAGCC	3540
	TITCTTAAAA AG	ATGCCCAA A	ACTCGAAACA 1	CATTATCAC A	ACACAGAAGA	GAAACAAGAC	3600
	CCADADAGC CA	TCTTGCAA A	NACAGAAGGA A	AGAGCTCCAG 1	TATTACTGAA .	AAAAATCCAA	3660
	GCTGAGATGT TC	CCTGAACA	CTCTGGAAAT (GTAAAATTAA (CTGCCAATT	TGCAGAAATT	3720 3780
15	CATGAAGATT CT. AGTGCAGGGG AC	ACTATCIG (CTGGACAAAA (GOCATOGTGC	AAGCCAGTCC	GAAGGACCAG	3840
1.5	CCACTCTATT AC	TGCTGCAT	CAAGAACAGC '	TACCGAAAAG :	TGACTGCTGA	ATTTAACCTC	3900
	ACAGCTGAAG TT	CTCAAACA	GCTGTCAAGT (CGCCAGGATA (CTAAAGGATG	TGAAGAGATT	3960
	CAATTCACCC AA	CTCATCTT (CAAAGAAGAC '	TTCCTCCATG A	ACAGCTACTT	TGGGGGCCGC	4020 4080
20	CTGCGTGGTC AG	ATCGCCAC	GGAGGAGCTG	CACTITGGAG	AAGGGGTTCA	TECTTETET	4140
20	CTTAAGGTGC AC	CARTGCCAT	TGCCTATGGG	ACCAGAAATA	ATGATGAGCT	CATCCAAAGG	4200
	AACTACAAAC TO	CCTGCCCA	GGAATGCTAT 1	GTTCAAAATA :	CTGCCAGGTA	TTATGCCAAG	4260
	ATCTACGCTG CI	GAAGCACA	GCCTCTGGAA	GGCTTTGGAG	AAGTACCTGA	GATCATTCCT	4320
25	ATTITICITA TO	CATCGGCC	TGAGAACAAT	ATCCCGTATG	CTACAGTGGA	GGAGGAGCTG	4380 4440
25	ATTGGAGAAT TT GAATCAGAAG CT	PGTGAAGTA	ATCTTCCACC	TTCCAGCACT	CCCTCTACCA	GAAAACAAGT	4500
	GGCTGCCTCC TO	GTGACGGA	CATGCAAGGT	GTAGGAATGA	AGCTAACTGA	CGTTGGCATA	4560
	GCAACGCTGG CT	TAAAGGGTA	CAAGGGATTT	AAAGGCAACT	GTTCCATGAC	CTTCATTGAT	4620
20	CAGTTTAAAG CA	ACTACACCA	GTGTAACAAG	TATTGCAAAA	TGCTGGGACT	GAAATCCCTT	4680
30	CAAAACAACA AC	CCAGAAACA	GAAGCAGCCG	AGCATTGGGA	AAAGCAAAGT	CTAACCACAC	4740 4800
	TCTATGACAG TA	AAAGAAGGC	CCCTACCAGC	ACACAATCTC	GCCAGGGAAA	ATCTGAGGCC	4860
	ACACAGGAGA GI	DATATAA	CCTGCAGAGA	GTGCGTGGCA	ATCCTTACCC	CCAGCCGACT	4920
	GTGCGCCAAG A	TGCTTCTAA	ACCCATCACC	TGCTGTCTTC	ACTCAAATGA	TTTCAGAACA	4980
35	GGATTTGCGA C	CAGGTTTAT	GGGGAGATTG	AATCAACGAT	TGGTCTCAAA	GACAGGCCAT	5040 5100
•	TCTTTATATA C	ACGTTTAGC	CONCURRENCE	CTCBCBBGBG	TCTCTTCACA	GCCARARTTC	5160
	TTCCCACTGT C	ATTCCTAAC	CTGGGATTTC	TAGACACATC	CTGCTGTGAT	GTAAACAGAA	5220
	ATCACGAATT C	GCTCACTGG	ATCAAGTTGT	TCCACTGGTG	TCTAATACGC	TATTGTTGCC	5280
40	GGAGGTGGGT T	CTGTGACGT	GAAGCCATTT	CCCATCATTC	AACAGCCAGT	TACAATTTTC	5340
	TGTTTAATTA A	ATTCATATT	TARACARARA	AAAA			5375
	Seg ID NO: 9	- NA Com					
			uence				
	Nucleic Acid			421.1			
45	Nucleic Acid Coding seque	Accession ence: 527.	n #: NM_134 .1108				
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	Nucleic Acid Coding seque 1 1 AGCTTCTGCC AGGGGGGACGA G	Accession ence: 527. 1 AGGGTGGGG	n #: NM_134 .1108 21 	31 AGGCGATCCG CGACCCGCAC	CTCGTTCCTC	CCAGGGCCAT GCCAGACGCG	60 120
45 50	Nucleic Acid Coding seque 1 1 1 AGCTTCTGCC A GGGGCGACGA G CCACCTTCCC C	Accession ence: 527. 1 AGGGTGGGG GGAGAGCCCT	n #: NM_134 .1108 21	31 AGGCGATCCG CGACCCGCAC TTAAAATGAG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG	120 180
	Nucleic Acid Coding seque 1	Accession	n #: NM_134 .1108 21	31 	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC	120 180 240
	Nucleic Acid Coding seque 1 1	Accession ence: 527. 1 AGGGTGGGG AGGTGGGGT AGGTGAAATG	n #: NM_134 .1108 21	31 	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC	120 180 240 300
50	Nucleic Acid Coding seque 1	ACCESSION ACCESSION ACCESTAGE	n #: NM_134 .1108 21	31 	CTCGTTCCTC CGCGACCTGG GACAGCTCCAA CTCCCTGGAG CCAGCTCCAA	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAAGGAG	120 180 240
	Nucleic Acid Coding seque 1 1 1	Accession ence: 527. 1 LAGGGTGGGG GGAGAGCCCT LGGTGAAATG TCTAGTGGC CTCTGCAGC CTGCAGCTGG	n #: NM_134 .1108 21	31	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCCCTGGAG CCAGCTCCAA CCTTAGCTGG	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCA AGAGAAGGAG GGTCAGACCC CGGTCAGACCCT CTGCTGAAAA	120 180 240 300 360 420 480
50	Nucleic Acid Coding seque 1	Accession ince: 527. 1 AGGGTGGG GGAGAGCCCT CGGTCGCGGT TCTAGTGG AGCCTCGCC TTTCTGCAGC TGGGAGCTGG	n #: NM_134 .1108 21	AGGCGATCCG CGACCCGCAC TTAAAATGAG GGAGGAACA GTTGGCTGTT CGCTCCATT CGTTCTCAGG	CTCGTTCCTC CGCGACCTGG GACAGCTCCTA CTCCTGGACC CCAGCTCCAA CCTTAGCCCAC CTAGCCCTCCA GCCGCCATGC	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA GCAAACAGAA	120 180 240 300 360 420 480 540
50	Nucleic Acid Coding seque 1	Accession ince: 527. AGGGTGGGG GGAGAGCCCT AGGTGAAATG FICTAGTGGC AGCCTCCGCC CTCCTGCAGC CTGCAGCTGG CTGCAGCTGG CTGCAGCTGG CTGCAGCTGG	n #: NM_134 .1108 21	AGCOGATCOG AGGCOGATCOG AGGCOGATCOG AGGCAGCAGCAGC AGGAGAACAA AGTTGGCTGTT CAGCTCCATT AGGCTCCATT AGCTCCAGG ACCTGCGGGAACAA ACCTGCGGGGAACAA ACCTGCGGGAACAA	CTCGTTCCTC CGCGACCTGG GACAGCTCCTA CTCCCTGGAG CCAGCTCCAA CCTTAGCTCCA CCTTAGCCTGG CGCCGCATGC AACACGGAGT	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA TCACCGACCA	120 180 240 300 360 420 480 540
50	Nucleic Acid Coding seque 1 1 1	Accession ince: 527. 1 LAGGGTGGGG GGGGAAATG GGCTGAAATG FICTAGTGG AGCCTCGGCC TTCTGCAGC TTGCAGCTGGAGCTGG GGGCCCGAGG GGGCCCGAGG	n 8: NM_134: .1108 21	31	CTCGTTCCTC CGCGACCTGG GACAGCTCCA CTCCCTGGAC CCAGCTCCAA CCTTAGCTGGA CCTAGCCCCA GCCGCCATGC AACACGAGT CCAACCGGCC	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA GCAAACAGAA TCACCGACCA	120 180 240 300 360 420 480 540
50	Nucleic Acid Coding seque 1	Accession ince: 527. AGGGTGGGG GGAGAGCCCT XGTGAGATG AGGTGAAATG TTCTAGTGGC TTCTGCAGCT TTCTGCAGCT TTCTGCAGCT AGGTGACT AGGTGACT AGGACTCAC TTCTGCAGCACT AGGACTCAC TTCTGCAGCACT ATCCGCACCAACT ATCCGCACCA	n #: NM_134 .1108 21	31 GGGGATCGG GACCGGAC TTAAAATGAG GAAGACAGCT GGGGAAACA GTTGCGTTCTCAGG GCCGCGCA CCTGCGGGAG CAAGACTGC CAAGA	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCCGCGCC CCTAGCTGCA CCTTAGCCTCC ACCCGCCC AACACCGAGT CCCACCGGCC GGCGACGCCT AACACGAGGCC AACACGGCCCCC AACACGGCCCCCCCC	CCAGGGCCAT GCCAGACGCG CCCTTGGGGG AGCCCCGCAC GTTCTGACCC AGAGAAGGAG GGTCAGACT CTGCTGAAAA GCAAACAGACA ACCTGACGACA CACCTGACGT TCCCGGACGT TCCCGGGAGTT TCCCGGGAGTT	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Nucleic Acid Coding seque 1	Accession ince: 527. 1 1 AGGGTGGG GGAGAGCCCT AGGTGAANTG TCTAGTGGA AGCCTCGCC TTCTGCAGC TGGAGCTGG TGGGACTCAC GGGCCCGAGG AGAGGATCA TTCCGCACCT TTCCGCACCT	n #: NM_134 .1108 21	AGGCGAACGC TTAAAATGAG GAAGACAGCT CGGGGAACA GTTGGCTGTT CAGCTCCATTCAGG CGCTCCATCAGG CCTCCTCCAGGCGCAC CCTGCGGGAG CCTGCGGGAGCA CCTGCGGGAGCACCACGCCACG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCGTGGAC CCAGCTCCA CCAGCTCCAA CCAAACCGAGT CAAACCGAGT CCAACCGAGC CCACCGGCC GGCGACGCTC ACCATCGACG ACCATCGACG	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCCCCAC GCCTTGGGGG AGCCCCCAC AGAGAGGAG GGTCAGACCA CTGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGACCA ACCTGACCGACA ACCTGACGAT CCAGGGGGTT CCAGGGGGTT AGTGGCCTT AGTGGGCCTT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Acid Coding seque 1	Accession ince: 527. 1 MGGGTGGGG GGAGAGCCCT MGGTGAAATG FTCTAGTGG GGCCTGGGGC TTCTGGAGC TTCTGGAGC TTGGGACTGAGC TTGGAGCTGAATG TTGGGACTGAGC TTGGAGCTGAGC TTCTGGAGC TTGGAGCTGAGC TTCTGGAGC TTGGAGCTGAGC TTGGAGCTGAGC TTGGAGCTGA	n #: NA_134 .1108 21	BI GGCGATCGG GAGCGGACGG GAGCGGGAACA CCTGCGGGAACA CCTGCGGGAACA CCTGCGGGA CCTGCGGCA CCTGCGGGAGGA CCTGCGGGAGGA CAGGAGGGGAGG	CTCGTTCCTC GGCGACTGG GACAGCTCCT CTTGGTCCAA CTCGTGGAC CCTTAGCTGG CTAGCTCCA CCTTAGCTGG ACACCGAGG CCCACCGGCC GGCGACGCT ACCACGGGC GGCGAGGCT ACCATCGAC CAGAGGCT ACATCGAC CAGAGGCT CAGAGAGCT CAGAGGCT	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCCGCAC AGCCCCCAC AGAGAAGGAG GGTCAGACCT CCGCAGACAT GCAAACAGAA CCCAACCAC CCCAGCGT CCCAGCGT CCCAGGTCGC TCCGGGAGTT AGTGGGCCTT CTGGAGATCT CTGGAGATCT CTGAGATCT TTGAGATCT TTGAGATCT TTGAGATCT TTGAGATCT TTGAGATCT TTGAGATCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Acid Coding seque 1	Accession cnce: 527. 1 AGGGTGGGG GGAGAGCCCT CGTGCAAATG GCTTCTGCAGC CTTCTGCAGC CTGCAGCTGGGGACTCAC GGGCCGAGGGACTCAC CTGCAGGCTGGAAAGATAC AAGAAGATC CTTCGGACCT CTGAGCGTG GACCTGAGCGTG	n #: NM_134 .1108 21	AGGCGAACAC CAAGGCGGAC CAAGGCGGAC CAAGGCGGAC CAAGGCGGCC CAAGGCGCCC CAAGGCGGCGCC CAAGGCGGCGCC CAAGGACGC CAAGGACGC CAAGCACGCC CAAGGACGC CAAGCACGCC CAAGGACGC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCGGACCTCCC CCAGCCCCCC CCAGCCCCCCC CCAGCCCCCCC CCACCGCCCCCC CCACCGCCCCCC CCACCGCCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCGC GCCTTGGGGG AGCCCCGCAC GTTCTGACC AGAGAAGGAG GGTCAGACCT CTGCTGAAAA GCAAACAGAA ACCTGACCGT CCGAGCT TCCGGGACT AGTGGGCCTT TCTGGGGCTT AGTGGGCCTT TGGGGAGTTGGG AGTCCACCCC GGAGAGTCGG GGAGTTGGGGGGGTGGGGGGGGGG	120 180 240 300 360 420 480 540 600 720 780 840 900 960
50 55 60	Nucleic Acid Coding seque 1	Accession Ince: 527. Ingggregge GAGAGCCCT GGTGGCGT AGGTGAANTG TCTAGTGGC AGCCTCGCC TTCTGCAGC TGGGGCTCAC GGGCCCGAGC TGGGGACTCAC CGGCCCGAGC TCTCCGCCCCT TCCAGCC TCCGCCCCGACC TCCAGCGTGGACC TCCAGCGTGGACC TACAAGATCA	n #: NM_134 .1108 21	A CATCAGCOG GARGAGACC GARGAGAGC GARGAGAGC GARGAGAGC GARGAGC GARGAGAGC GARGAGAGC CATTCAGC GARGAGAGC CATTCAGC GARGAGACC CATTCACC CATTCACC GARGAGC CATTCACC GARGAGC GARGAGAGC GARGAGAGC GARGAGAGC GARGAGACC GARGACC GARGACACC GARGACC GARGACACC GARGACC GARGACACC GARGACACC GARGACACC GARGACACC GARGACACC GARGACC GARGACACC GARGACACC GARGACAC GARGACACC GARGACACC GARGACA	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCCTTAGCTGG CCAGCGCCTCC GCGCCATGC AACACGGAGT ACCATGACT ACCAGGG CCACAGGAGATGAC CCGAGAGATGAC ACCAGGAGATGAC AACAATGACA	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCCCCAC GCCTTGGGGG AGCCCCCAC GTTCTGACC AGAGAGGAG GGTCAGACCT CTGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGACA ACCTGACCGACA ACCTGACCGT CCAAGTTCGC TCCGGGAGTT AGTGGCCTT TGGGAACACGC AGTCCACCCC GCAAACTGCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Acid Coding seque 1	Accession cince: 527. 1 1 AGGGTGGGG GGAGAGCCCT CGTTGCAGG CTTCTGCAGG CTTCTGCAGG CTGCAGCTGGAGATTC CGGCCCGAGG GAGCTCGCCC CTGCAGCTGGAAGATTC CTGAGCGTG GACCTTGCAGG CTTCCGACCT CTGAGCACCT CTGAGCACCT CTGAGCACCT CTACAAGATG ACAACAAG ACAACAAG ACAACAAG ACAGCACAGT ACAGCACAGACAAG ATTCATCAGACAAGA AGTGCCAGTC AGTGCCAGTC ACAGCACAAGACAAG	N #: NA_134 .1108 21	BI AGGCGATCG GGACCGCAC TTAAATGAG GAAGACAGCT GCGGAAACA GTTGGCTGTT GCGCGGAGC CATCCAGGCGCAC CTTCCAGG CAAGGACTCG CAAGGACTCG CAAGGACTCG CAAGGACGC CAAGGACGC GCAAGGACGCC GGACGACCCCTCC GGACGACCCCTCC GAGCGCGCCCCTC GAGCGCGCCCCTC	CTCGTTCCTC GGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTTGGTCCAA CCTTAGCTGG CTAGCCCTCC GCCGCCATGG AACACGGACT ACACGGACT CAGAGCTCCA CCGAGGACT CAGAGCTCCA CAGAGGACT CAGAGGACT CAGAGGACT AACACGACT CAGAGGACT AACACGACT CAGAGGATT AACATGACC TGGACAGCT	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCGCAC GCTTGGGGG AGCCCGCAC GGTCAGACCT CCGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGT CCGGGGGTT AGTGGCCTT AGTGGCCTT AGTGGCCTT GCGAAATTGCC GGAAACTGCC GGCAAACTGCC GCCAGAGAACA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Acid Coding seque 1	Accession ince: 527. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	N #: NM_134 1108 21	AGGGGGATCG GGAGGGGGGGGGGGGGGGGGGGGGGGGGG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCGTGGAC CCTAGCTGG CCAGCTCCA CCTAGCTGC CCACCGGCC CCACCGGCC CCACCGGCC CCACCGGCC CCACCGGCC CGCGACGCTC ACCATCGACT ACCATCGACT ACCATCGACT ACCATCGACT ACCATCGACT ACCATCGACT ACCATCGACT ACCATCGACT CACAGAGATG CCCGAGAGATG CCCGCCCCC ACCCCCCCC CCCCCCCC CCCCCCCC CCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAC GCCTTGGGGG AGCCCCCAC GCAGAAGAGGG GGTCAGACCA CCTGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGACCA ACCTGACCGACCA ACCTGACCGACCA ACCTGACCACCC GCAAACTGCC GCAAACTGCC GCCAACTTCCC GCCAACTTCCACCC GCCAACTTCCACCC GCCAACTTCCACCC GCCAACTTCACCACCAC ACCTGCCAGTG CCAGAGAACA AATCGTTCCTG	120 180 240 300 360 420 540 660 660 720 780 840 900 1020 1080
50 55 60	Nucleic Acid Coding seque 1	Accession ceres: 527. 1 UNGGGTGGGG SGAGAGCCCT SGGTGAAATG STCTAGTGGG GGCCTGGGC CTGCAGCTGGAC CTGCAGCTGAGC CTGCAGCTGAGC CTGCAGCTGAC CTGCAGCTGAC CTGCAGCTGAC ACAAGAATC TACAAGATGA ACTACAAGATGA ACTACAAGATGA ACTACAAGATGA ACTACAAGATGC CTCAGGGCC TACAAGATGC TACAAGATGC TCCATGAGC TCCAGGGC TCCAGGGC TCCAGGGCC TCCAGGGCC TCCCCCGGGCC CCCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCCGGGCC CCCCGGGCC CCCCGGCC CCCCGGGCC CCCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGCC CCCCGCGCC CCCCGGCC CCCCGGCC CCCCGGCC CCCCGGCC CCCCGGCC CCCCGGCC CCCCGCGCC CCCCGGCC CCCCCGGCC CCCCCGCGCC CCCCCGCC CCCCCC	n #: NA_134 .1108 21	BI AGGGGATCGG CGACCGGAACAA CCTGCGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CCTGCGGGAACAA CGGGGACGGG GATGAAGATGAACCGG GGAGGACGGG GGAGGACGGGGAACAAAAAGATGAAAGGTGGAACGGGGAACAAAAAGATGAAAAGGTGGAACGG GGAGGAAAAAAGATGAAAAGGTGGAACGG GGAGAAAAAGATGAAAAGGTGAAAGATGAAAAGGTGAAAGGTGAAAGATGAAAAGGTGAAAGATGAAAAGGTGAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAAGATGAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAAA	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCCCTGGAC CCAGCCCTCC CTAGCCTCC CTAGCCTCC CTAGCCTCC CCACCGCC CCACCGCC CCACCGCC CACCGCC CACCGCC CACCGCCC CACCGCCC CACCGCCC CACCGCCC CACCGCCC CACCGCCC CACCGCCC CACCGCCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CACCGCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CACCACGCC CCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCAT AGAGAAGGAG GGTCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCAT CCAGGTTCGC TCCGGGAGTT CTGGAGCTT CTGGAGCTT CTGGAGCTCT TCGAGCCTC TCGAGCTCCC TCCAGCTCCC TCCAGCTCCC TCCTCCACTC TCCTCCACTC TCCTCCACTC TCCTCCACTC TCCTCCACTC TCCTCCACTC TCCTCCACTC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1200
50 55 60 65	Nucleic Acid Coding seque 1	Accession cince: 527. 1 1 AGGGTGGGG GAGAGCCCT AGGTGAAATG AGCTCGGGT CTTCTGCAGG CTTCTGCAGG CTGCAGCTG GAGAGACTCA GAGAGACTCA CTGCAGCTG GAGCTGAAGATG CTGCAGCTG CTGCAGCTG CTGAGCTG CTGAGCACCT CTGAGCACCT CTGAGCACCT CTGAGCACCT CCCGACCGACG CCCGACCGACG CCCGACCGACG CCCGACCGA	N #: NM_134 .1108 21	BIL PAGGOGATOGA GARAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CTCGTTCCTC GGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCGGACCTCGA CCTTAGCTGGA CCTTAGCTGGA CCAGCGCCTCG CCAGCGCCATGG AACACGGACT ACACGGACTCCA CAGAGCTCCA CAGAGGACTC ACGAGGACTC ACGAGGATTGA CCAGAGGATTGAC ACATCGACC TAGAGACTC ACGAGGATTGAC ACATCGACC TAGACAGGATTGAC ATCGTCCGGC TTGGACAGTTGACGACC CCGGCCCGGG CCCGGCCCGG	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCGCAC GCTTGGGGG AGCCCGCAC GCTCAGACCA GCTAGACCT CCGCTGAAAA GCAAACAGAA TCACCGACCA ACCTGACCGT CCGAGCAT AGTGGCCTT AGTGGCCTT AGTGGCCTT CTGGGAGTT AGTGGCCTT CTGGAGATTGC GCAAACTGCC GCAACTGCCCC GCAAACTGCC GCAACTGCCCC GCAAACTGCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTGCCCC GCAACTCCC GCACCCC GCAACTCCC GCACCCC GCAACTCCC GCACCCC GCAACTCCC GCACCC GCACCC GCACCC GCACCC GCACCC GCACCC GCACCC GCCC GCC GCCC GCC GCCC GCC GCCC GCC G	120 180 240 300 360 420 480 540 660 720 840 900 1020 1020 1140 1200 1200
50 55 60	Nucleic Acid Coding seque 1	I Accession ceres: 527. 1 UNGGGTGGGG SGAGAGCCCT SGTCGGGGT GGGTGAAATG STCTAGTGGG GGCCTGGGGC CTGCAGC CTGCAGC GGCCCGAGG GAGTGAAAGATG TTCCGGACC TTCCGGACC TTCAGGAGC TTCAGGAGC TTCAGGAGC TTCAGGAGC TTCAGGAGC TTCAGGAGC TTCAGAGC TTCAGAGC TTCAGAGC TTCAGAGC TTCAGACAAG AGGGACCAAG AGGGATGTGC CCCCGGGCC CCTGACCAAG AGGGAATGTG	n #: NA_134 .1108 21	BI AGGCGATCG CGACCGCAC TTANANTGAG GAAGACAGCT CGCGGAAACA GTTGGCTGTT CAGGCGCGCCA CAGGCGCCCA CAGGCGCCCA CAGGCGCCCA CAGGCGCCCCA CAGGCGCCCCC CGCAAGACAC CGCGCCCCC CGCAAGACAC CGCGCCCCC CGCAAGACAC CGCGCCCCC CGCAAGACAC CGCGCCCCCC CGCAAGACACCC CGCGACCCCCCCC	CTCGTTCCTC GGCGACCTGG GACAGCTCCA CTCGCTGGAC CCAGCTCCA CCTCGCACCTCC CCAGCCCATGC CCAGCCCATGC ACCACGGCG CCAGCGCATGC ACCACGGCG CCAGCGCGCT ACCACGGCG CCAGCGGCT ACCACGGCG CCAGCGGCT CACCAGGAGTC ACCAAGGAGT ACCATGGACT ACCATGGACT CACCAGGGGT CACCAGGGGT CACCAGGGGT CACCAGGGGT CACCAGGGGGT CACCAGGGGGT CCGGCCCGG CCGGCCCGG CCGGCCCGG CCGGCCCGG CCGGCCCGG CCGGCCCGG CCGGCCCGG CCGGCCCGG CCTGCCCGG CTCTGCTCTGGT CCAGGGAGGACT CCAGGAGGACT CCGGCCCGG CCGGCCCGG CCGGCCCGG CCTGCCCGG CCGGCCCGG CTCTTGGTT CAGGGAGGAC CTCTTGGTT CAGGGAGGAC CTCGCCCGG CTCTTGCTT CAGGGAGGAC CTCTTGGTT CTCTTGGTT CAGGGAGGAC CTCTTGGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTGTT CTCTTT CTCTT	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCAC GCCTTGGGGG AGCCCCCCAC GCGAACACCAC CCTCGACCAC CCCAGCACAC CCCAGCACAC CCAGCACAC CCAGCACC	120 180 240 300 360 420 480 540 660 720 780 840 1020 1140 1260 1320 1320
50 55 60 65	Nucleic Acid Coding seque 1	Accession cince: 527. 1 1 AGGGTCGGG SGAGAGCCCT SGTCGCGGT SGTCGCGGT TTCTGCAGG CTTCTGCAGG CTTCCGCGC GGGACTCAC GGGCGACG GAGCTCGCC CTGAGCGTG GACCTGAC CTGAGCGTG GACCTGAC CTGAGCAC CTGAGCAC CTGAGCAC CTGAGCAC CCCGAC GACCAG CCCGAC GACCAG CCCGAC CCCGCCC CCGGCCC CCCGAC CCCGAC CCCGCCC CCCGCCC CCCGCCC CCCGCCC CCCGCCC CCGCCC CCGCCCC CCGCCCC CCGCCCC CCGCCCC CCCCCC	N #: NM_134 .1108 21	BIL AGGCGATCG GGACCGCAC TTAAATGAG GAAGACAGC GTTGGCTGTT CAGCTCCATT CAGCTCCATT CAGCTCCATT CATTCTCAGG CAAGCAGCC CTACCGCAG CAAGCAGCC GAAGACTGG GAAGACTGG GAAGACTGG GAAGCCCTC GGAGGGCCC GGAGGGCCC GGAGGGCCC GCAAGAGTG GTTCACTGAC GGAGGGCCC GGAGGGCCC GGAGGGCCC GGAGGGCCC GCAAGAGTG GCAAGAGTG CTCCCCTCACG GGCGGGACGC CTCCCCTCACG GGGGGAGGCC TCCCCTCACG GGGGGAGAC TCCCCAAGTGAC CGCAAGGGAGAC TCCCAAGTGAC CGCAAGGGACAC TCCCAAGTGAC CGCAAGTGAC CCCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CCCAAGTGAC CCCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CCCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CGCAAGTGAC CCCAAGTGAC CGCAAGTGAC CCCAAGTGAC CGCAAGTGAC CCCAAGTGAC CGCAAGTGAC CGCAAGTCAC CGCAAGTGAC CGCAAGTCAC C	CTCGTTCCTC GGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCGGACCTCGC CCTGGACCTCCC GCCGCCATGC AACACGACGC CAACAGGACT CAACAGGACTCCA CAGAGCTCCA CAGAGCTCCA CAGAGCTCCA CAGAGCTCCA CAGAGCTCCA CAGAGCTCCA CAGAGCTCCA CAGAGGACTCC CAGAGGATTGAC CAGAGGATTGACCA CAGAGGATTGACCAGCC CTGGACAGGTC CAGGCCCGG CTTCTTGGGACGCCC CTCTGGGCCCGC CTCTTTGGGACGCC CTCTTTGGGACGCCC CTCTTTGGGACGCCC CTCTTTGGGACGCCC CTCTTTGGGACGCCCCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCGCAC GTTCTGACCC AGAGAAGAGG GGTAAACAGAA TCACCGACCA ACCTGACCGT CTGGGGAGT AGTGGCCTT AGTGGCCTT CTGGGAGTA AGTGGCCT GGAAACTTGC GAATTGGC GCAAACTGCC GCAGGAGTCA ATCGTTCCAGTC GTCCCAGGCT GGCTCCCAGGCC CTCCCGAGGCT AGGGGACCTC AGGGGACCTC AGGGGGGACCA AGGGGGGGACCA AGGGGGGGACCA AGGGGGGGACCA AGGGGGGGACCA AGGGGGGGG	120 180 240 300 360 420 480 540 660 720 840 900 1020 1020 1140 1200 1320 1380 1440
50 55 60 65	Nucleic Acid Coding seque 1	Accession ince: 527. luggettees seaglectees seaglecte	n #: NM_134 .1108 .1108 .21	AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CGTGACCTCCT CTTGGTCCAA CCAGCTCCAACCGCCC CCTAGCCTCC CCCACCGCCC CCCACCGCCC CCCACCGCCCC CCCACCGCCCCCC CCCACCGCCCCCC CCCACCGCCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAC GCCTTGGGGG AGCCCCAC AGAGAGGGG GGTCAGACCA AGAGAGGGG CCTGCTGAAAA CGCAAACAGAA TCACCGACCA AGCTGACCGT TCAGGGGCT AGTGCACCCC GGCAAACTGCC TCCGGGGATT AATGGCCT TCGGGAGTCOT TCGGGAGTCOT TCGGGGATT AATGGTCACCCC TCCGGGGCT TCCGGGGCT TCCGGGGCT TCCGGGGCT TCCCGGGGCT TCCCGGGGCT TCCCGGGGCT TCCCGGGGCT TCCCGGGGCT TCCCGGGGCT CCCGTGCGCT TCCCGGGGCT CCCGTGCGCT CCCGGGGCT CCCGTGCGCT CCCGGGGCT CCCGTTCCATT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1320 1380 1440 1560
50 55 60 65 70	Nucleic Acid Coding seque 1	I Accession cnee: 527. 1 UNGGGTGGGG SGAGAGCCCT SGTCGGGGT GGGGAAATG STCTAGTGGG GGCCTGGGGC CTGCAGC CTGCAGC GGCCCAGAG GACTGGAGC TTCCGGCC GAGGGACTCAG GACCTGGACC TTCAGAGC TTCAGACAAG AGGGACC CCTGACCAAC AGGGATGTG GGGAGCTCAC CGGGCCCATG GAGGGTATA CGGAGGTATA AGCCGCTTTG AGCCGCTTTG AGCCGCTTG AGCCGTTTG AGCCGCTTG AGCCCCTTG AGCCGCTTG AGCCGCTTG AGCCGCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCCTTG AGCCCCTTG AGCCCCTTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTTG AGCCCCTT	n #: NM_134 .1108 21	BIL AGGCGATCG GGACCGCAC TTANATGAG GAAGACAGCT GCGGAAACA GTTGGCTGTT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATT CAGCTCCATC CAAGCTGGAC CAAGCTGGAC CAAGCTGGAC CAAGCTGGAC CAAGCTCCATC CAAGCTCCCTCCC GCAAGACTCC CTCCCTCACT CCAAGCTGAC TCCCCGTCCACT CCAAGCTGAC TCCCCGTGCACT TCCCCGTGCACT TCCCGTGCACT TACTGTGGTC TACTGCGGTCC TACTGCTGCC TCCCGTGCACT TCCCGTGCACT TACTGTGGTC TACTGTGCACT TACTGTGGTC TACTGTGGTC TACTGTGGTC TACTGTGGTC TACTGTGTC TACTGTGGTC TACTGTGGTC TACTGTGCACT TACTGTGCACT TACTGTGGTC TACTGTGGTC TACTGTGCACT TACTGTGGTC TACTGTGCACT TACTGTCACT TACTGTC	CTCGTTCCTC GGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCGTCGAC CTCGTGGAC CCAGCTCCA CCAGCCCTCC CCAGCCGCC CCAGCGCCATGC AACACGACG CACACGGCG AACACGACG CACACGGAG CACACGAGGACT ACCATCGAC CACAGAGGAG CACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCC GCCTTGGGGG AGCCCCCCAC GCAGAACAGCA ACCTGACCT TCCAGGACA ACCTGACCT TCCAGGACT AATACACAA ACCTGACCT TCCAGGACT GCACCCC GCAAACTTCC GCAAACTTCC GCAAACTTCC GCAGGACT TCCAGGGCT TCCAGGGCT TCCAGGGCT TCCCAGGGCT AATATACAAA ACTCTTCCAG GCAGGACTC CCCCCCCC CCCTTCCAG	120 180 240 300 360 420 480 540 660 720 780 840 1020 1140 1120 11320 11440 1500 1500
50 55 60 65	Nucleic Acid Coding seque 1	Accession cince: 527. 1 AGGGTCGGG GAGAGCCCT AGGTCGAAATG AGCTCCGCC TTCTGCAGC TTCAGAGCTGA AGGAAGATCT TTCAGCACCT GACCTGACC CTGAGCACC AGGACAAG AGGACACAAG AGGACACAG GTGCCGTTT CCCCGGCCC GGGCCCATG GGGGCCAAG GAGGGTATAA AGCCGCTTG TGAAGTGGAA AGCGCTTTA	N #: NM_134 .1108 21	A CATCACCOCT GAGGGGGCC GAAGGCGCC THANATGAG GAAGACAGCT GGGGAAACA GTTGGCTGTT CAGCTCCATT CAGCTCCATT CATTCTCAGG CAAGCTCCAT GATCAGCCGC GAAGACTGGC GAAGACACCCTC GAGGGCCCC GAGGGGCCC GAGGGGCCC GCAAGACTCC TCCCCTACC GGCAGGGCCC TCCCCTCACC GCAAGACTCC TCCCCTCACC GCAAGGACCC TCCCCTCACC GCATCACCCC TCCCCTCACC TCCCTCACC TCCCACTCC TCCCACTCC TCCCACTCC TCCCACTCC TAGCTCCCCT TAGCTCCCCT TAGCTCCCCT TAGCTCCCCT TAGCTCCCCT TAGCTCCCCT TAAATCACCCC TAAATCACCCC TAAATCACCCC TAAATCACCCC TAAATCACCCC TAAAATCACCC TAAACTCACC TAAACTCACC TAAACTCACC TAAACTCACCC TAAACTCACC TAAACTCACCC TAAACTCACCC TAAACTCACCC TAAACTCACCC TAAACTCACC TAAACTCACCC TAAACTCACCC TAAACTCACCC TAAACTCACC TAA	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCTCGGACCTCG CCTAGCTGC CCTAGCTGCA CCTTAGCTGC CCTAGCTGCAG CCAGCGCCTGG AACACGAGGT CAGCGGCCTG CAGCAGGAGGTT AACATGACT AACATGACT AACATGACT CAGCAGGAGTT AACATGACT CAGCAGGAGT CACCAGGAGT CAGCAGGAGT CAGCAGGAGAGT CAGCAGGAGT CAGCAGGAGGAGT CAGCAGGAGGAGT CAGCAGGAGGAGT CAGCAGGAGGAGT CAGCAGGAGGAGGAGT	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCA AGCCCCCAC AGAGAGGG GGTCAGACCA ACCTGACCA ACCTGACCA ACCTGACCA ACCTGACCAT AGTGGCCTT CTGGGAGTA AGTGGCCT CTGCTGAAA ATTGCC GCAAACTTGC GCAAACTGCC GCAACTTCCC GCAGCACT AGTGGCCTT CTGGGGAGT AGTGGCCT TCCCGGGGC CCAGGCACT GCAGCACCCC CCCCCAGGCC AGGGCACCT CCCCCAGGCC CCCCTCCATTT AGTATATAAAA T CTGACTGCCT	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1200 1260 1380 1440 1500 1560 1660
50 55 60 65 70	Nucleic Acid Coding seque 1	I Accession cnee: 527. 1 Ingogreege Scagageccc Scagagecccc Scagageccc Scagagecccc Scagageccc Scagag	N #: NM_134 .1108 21	A GARGACACC GAAGACACC TRANATGAS GAAGACACC TRANATGAS GATGCTCATT CAGCTCCATT CAGCACCCTCCATT CAGCACCCTCCC GAAGACTGC TCCCCTCACC GAGCAGCCC TCCCATCCATT TACTGTGTT ACTGTGCT TACTGTGTC ACCTTGCCTACC TACCCTCCC CAGCCCCTCCCC CAGCCCCTCCCCC CAGCCCCTCCCCC CAGCCCCTCCCCC CAGCCCCTCCCCC CAGCCCCTCCCCCC CAGCCCCTCCCCCCCCCC	CTCGTTCCTC GGCGACCTGG GACAGCTCCT CTTGGTCCAA CTCGCTGGAC CCAGCTCCA CTAGCCTCC CTAGCCTCC CTAGCCTCC CTAGCCTCC CTAGCCTCC CACACCGCC CACACCGCCC CACACCGCCC CACACCGCCCC CACACCGCCCC CACACCGCCCC CACACCGCCCC CACACCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGCCAC GCCTTGGGGG AGCCCCCCAC CCGCAC CCCTGACCCT CCGCACAC ACCTGACCCT CCGCACACAC ACCTGACCCT CTCGCGACAC ACCTGACCCT CTCGCGACAC ACCTGACCCT CTCGCGACAC CACCCCC GCAAACTGCC GCAAACTGCC GCAAACTGCC CTCCCGGGCCT CTCCCGGGCCT CTCCCGGGCCT CTCCCGGGGCT CTCCCGGGGCT AGGGCCCTC CTCCCGGGGCT CTCCCGGGGCT CTCCCGGGGCT CTCCCGGGCCT CTCCCGGGCT CCCGGTCCT CTCCCGGGCT CTCCCGGGCT CTCCCGGGCT CTCCCGGGCT CTCCCTCC	120 180 240 300 360 420 480 540 660 600 660 720 780 840 1080 1140 1260 1320 1380 1440 1500 1680 1680 1780
50 55 60 65 70	Nucleic Acid Coding seque 1	Accession cnee: 5271 .1 .1 .1 .1 .1 .1 .1 .1 .1 .1 .1 .1	N #: NM_134 .1108 21	A CARCECTORA GARGACACT THANATGAG GARACAGCT GAGGANACA GTTGCTGTT CAGCTCATT CCCAGCTCAC GAGGAGACA CTCCCTCAC GGTTCAAGTC CTCCCTCAC CCCTCAC CCCTCAC CCCTCAC CCCTCAC CCCTCACC CTCCCTCACC CCCTCACC CCCTCACC CTCCTCACC CTCCTCAC CTCCTCAC CTCCTCAC CTCCTCAC CTCCTCAC CTCCTCAC	CTCGTTCCTC CGCGACCTGG GACAGCTCCT CTTGGTCCAA CCCTCGGAC CCAGCTCCAA CCCTCGGAC CCAGCTCCAA CCCTAGCTGC AACACGAGCT CAGCAGCTCCA CAGCAGCAGCT CAGCAGCTCCAA CAGCAGCTCCAA CAGCAGCTCCAA CAGCAGCTCCAA CAGCAGCTCCAACAGCTCCAACAGCTCCAACACCAACATCACACCACCAGCCCGGC CCGGCCCGGG CTCGCCGGGCCCGGG CTCGTCGGCCCGG CCTGGGCCGGG TTCTTGGTT CAGCAGCTCGGCCCGCCCTCCTTCTTT ATTTAATGCC CGCTTGGGCAC CGCTTGGTTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGGG CCCTGAGCCCGG CCCTGAGCCCGG CCCTGAGCCCGG CCCCTGAGCCCGGG CCCCTGAGCCCGGG CCCCTGAGCCCGGG CCCCTGAGCCCGGG CCCCTGAGCCCGGG CCCCTGAGCCCCGGG CCCCTGAGCCCCGGG CCCCTGAGCCCCGGG CCCCTGAGCCCCGGG CCCCTGAGCCCCCGGG CCCCTGAGCCCCGGG CCCCTGAGCCCCGGG CCCCTCCCCCCGGGCCCGGG CCCCCCCCCC	CCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAT GCCAGGGCCAC AGAGCAGGG GCTTGGGGG AGCCCCAC AGAGAAGAGG GGTAAACAGAA TCACCGACCA AGTGGGCT CTGGGGAAT AGTGGGCTT CTGGAGATGGC GCAGATTGGC GCAGACTGCC GCAGACTGCC GCAGACTGCC TCCCGGGGA ATCGTCCCG GCAAACTGCC CTGCTGCAGTG ATCGCTTCCAGGC CCAGGCACTC CTGCTGCAGTG GCCTTCCAGTG CTGCCTTCCAGGC CCCGTCATTT TAATATATAAA TCTGACTGCC GTGATTTTAT GTGTATTTAT TGATTGGTC TTGATTGGTC TTGATTGATC TTGATTGGTC TTGATTG	120 180 240 300 360 420 480 540 660 720 840 900 1020 1180 1200 1560 1560 1680 1740 1860
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5	GCAGCGGCCC G						240
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10	AGGACTGCCC C						540
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15	TGAAGATGCC G						840
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20	AAGAGTGGAT G						1080
20	GCACCTGCCC G						1140 1200
	CCCTCACGCC T						1260
	AGGAGACCAG G						1320
	CAAGTGACTC T						1380
25	CCGTGCATGG C						1440
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40	GGTCAAACAT						180
40	ATTAATAACA						240
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	CCATCTGCAG	GTTAAACAAA	AGCAATTAGC	ATGCTTGTGC	ACATGGCAGG	CCAGAGACCC	480
45	TGATTGTCCC	CCTTCCACTA	AGGTGGTCCT	CCAGTCGACC	AGGCATGGGC	TGCATGGTAG	540
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5	CACCCCGGAG GAGCCAGAGC CAGAGCTGGA AGCTGAGGCC TCTAAAGAGG CTGAACCGGA GCCGGAGCCA GAGCCAGAGC TGGAACCCGA GGCTGAAGCA GAACCAGAGC CGGAACTGGA	660
,	GCCAGAACCG GACCCAGAGC CCGAGCCCGA CTTCGAGGAA AGGGACGAGT CCGAAGATTC	720
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10	AAACTCCGGA GGGTCGGACG GGACCTGGGC TCTCTCCACG ATTCTGGCTG TTTGCCCAGG	900 960
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	AGCTGAACAT GGAGCAAGGG GAGGGTGACT TCTCTCCACA TAGGGAGGGC TTAGAGCTCA	1200
15	CAGCCTTGGG AAGTGAGACT AGAAGAGGGG AGCAGAAAGG GACCTTGAGT AGACAAAGGC	1260
	CACACACATC ATTGTCATTA CTGTTTTAAT TGTCTGGCTT CTCTCTGGAC TGGGAGCTCA	1320 1380
	GTGAGGATTC TGACCAGTGA CTTACACAAA AGGCGCTCTA TACATATTAT AATATATTCG CTTACTAAAT GAAAAAAAA AAAAAAAAA A	1411
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	1 11 21 31 41 51	
25	GGCGAGAGGC GGGCTGAGGC GGCCCAGCGG CGGCAGGTGA GGCGGAACCA ACCCTCCTGG	60
	CCATGGGAGG GGCCGTGGTG GACGAGGGCC CCACAGGCGT CAAGGCCCCT GACGGCGGCT	120
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	AGGCCGTCAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA	240 300
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50	TGGGCATGGT GGCTGCGTCC TTTTGCCGGA GCATCATCCA GGTCTACCTC ACCACTGGGG	420
	TCATCACGGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT	480
	ACTICAGCAA GOGGOGOCCC ATGGCCAACG GGCTGGOGGC AGCAGGTAGC CCTGTCTTCC	540
35	TOTGTGCCCT GAGCCCGCTG GGGCAGCTGC TGCAGGACCG CTACGGCTGG CGGGGGGGCT	600 660
33	TCCTCATCCT GGGCGGCCTG CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC TGGTGGTCAC GGCCCAGCCG GGCTCGGGGC CGCCGGGACC CTCCCGGCGC CTGCTAGACC	720
	TGAGCGTCTT CCGGGACCGC GGCTTGTGC TTTACGCCGT GGCCGCCTCG GTCATGGTGC	780
	TGGGGCTCTT CGTCCCGCCC GTGTTCGTGG TGAGCTACGC CAAGGACCTG GGCGTGCCCG	840
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	ANACCACCTC CTGAGGGCTC AGCTCTGCCC CCGCCCTGGG CTGCAGGCTC TGCACGCAAG	5100
25	CACCAGGCAT CCTTTGTGTT GTCAACTCCG TGTAACCAGT AACTACAGCC ATTTACAATT	5160
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	ATGAAATCTG AAAAAAAA	5239
20	Seq ID NO: 106 DNA Sequence	
30	Nucleic Acid Accession #: NM_004585	
	Coding sequence: 62556	
	1 11 21 31 41 51	
25	CCTTCAGCAT AAAAGCTGAT CCACAAACAA GAGGAGCACC AGACCTCCTC TTGGCTTCGA	60
35	GATGGCTTCG CCACACCAAG AGCCCAAACC TGGAGACCTG ATTGAGATTT TCCGCCTTGG	120
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	TGAGTACCCC GGGGCTGGCT CCTCCAGTGT CTTCTCAGTC CTGAGCAACA GTGCAGAGGT	240
	GAAACGGGG CGCCTGGAAG ATGTGGTGGG AGGCTGTTGC TATCGGGTCA ACAACAGCTT	300
40	GGACCATGAG TACCAACCAC GGCCCGTGGA GGTGATCATC AGTTCTGCGA AGGAGATGGT	360 420
40	TGGTCAGAAG ATGAAGTACA GTATTGTGAG CAGGAACTGT GAGCACTTTG TCGCCCAGCT	480
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	AAAAGCAACA GCCTGAAGCA GCCACAAAAT CCTGTGTTAG AAGCAGCTGT GGGGGTCCCA	660
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45	TCTCTAGATC CTTTCCTCTG TTTCCCTCTC TCGCTGGCAA AAGTATGATC TAATTGAAAC	768
	AAGACTGAAG GATCAATAAA CAGCCATCTG CCCCTTCAAA AAAAAAAA	700
	0 - TD NO 103 DWA Co-10000	
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50	Coding sequence: 1831646 1 11 21 31 41 51	
	CTTGGCTCTT ACAATGCTCA CTTGTTTTCA CAATGCAGCA AAATGAAATG	60
	AGAGTAACAT TCCAGAAAAC GGTGTAATTT ATTTTTCTTC CTTAATTGCC CCATCTGTGG	120
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	TCATGCTGAA GAGGGAGGGG AAGGTCCAAC CTTACACTAA AACCCTGGAT GGAGGATGGG	240
	GATGGATGAT TGTGATTCAT TTTTTCCTGG TGAATGTGTT TGTGATGGGG ATGACCAAGA	300
	CHICATION AND AND AND AND AND AND AND AND AND AN	300
	CTTTTCCAAT TTTCTTTGTG GTCTTTCAAG AAGAGTTTGA AGGCACCICA GAGCAAATIG	360
	CTTTTGCAAT TITCTTTGTG GTCTTTCAAG AAGAGTTTGA AGGCACCTCA GAGCAAATTG GTTGGATTGG ATCCATCATG TCATCTCTTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA	
60	GTTGGATTGG ATCCATCATG TCATCTCTTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGGTG	360
60	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC	360 420
60	GTTOGATTGG ATCCATCATG TCATCTTCT GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGGTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TTCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT	360 420 480
60	GTTOGATTGG ATCCATCATG TCATCTTCT GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGGT GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TTCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCAAAAAACG ATTGGCTCTT TCTACAGCTA TTGCCCGTTC TGGGATGGGA	360 420 480 540 600 660
	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTG GCCACAAGTA TTCCTTTTCT TTGTGTACT ATGGGACTTC TACCCGGTTT GGGTCTGCT TTCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCAAAAAACG ATTGGCTCTT TCTACAGCTA TTGCCCGTTC TGGGATAGGGA CTGACTTTTC TTTTGGCACC CTTTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT	360 420 480 540 600 660 720
60	GTTOGATTOG ATCCATCATG TCATCTTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AMACTACCT CCATTCTTGG GCCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TTCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCAAAAAACG ATTGGCTCTT TCTACAGCTA TTGCCCGTTC TGGGATGGGA	360 420 480 540 600 660 720 780
	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTGTTTTTGTGCACAT ACTTCGAGAG AAAACTACCT CCATTCTTG GCCTTTCGTT GTTACTGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACAAAAAACG ATTGCCTCT TCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCTACAAGAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TATTTGGAGC TATCCCATTG AATTTGGTGC CTTCTAGATGA CCCATCCATTAT TCAAAAGTGA GACAATTCT GGTATTAAAG ATAAAGGGAG CGCTTATGT CACAAGTAG CCCATCCATTC	360 420 480 540 600 660 720 780 840
	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTACCT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TTCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCAAAAAACG ATTGGCTCTT TCTACACATA TTGCCCGTTC TGGGACAGGA CCCACTTTTC TTTTGGACCC CTTTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TATTTGGAGC TATCGCATTG AATTTGGTGC CTTCTAGTAT GCTCTTAAGA CCCATCCATA TCAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGCAG AGGTCTACC ATCAGAGCACA ACAACTGCTC CAGAGGCACA TGCAACAGAA ACACACTCCC ATGAGACAGA AGAGTCTACC ATCAAGGCA	360 420 480 540 600 660 720 780 840
	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGCACAT ACTTGGAGGA AMACTACCT CCATTCTTGG GCCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAGGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACCCGGTTT GGGTCTGCT TCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCTAAAAACG ATTGGCTCTT TCTACAGAT TTCCCGGTTC TGGGATGGGA	360 420 480 540 600 660 720 780 840 900
65	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTGTTTTTTGTGCACAT ACTTCGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GTATACTGGTA CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TCAAAAACG ATTGGCTCT TCTTACACA ATTGGCTCT TCTACAGCTA TTGCCCGTTC TGGGACAGGA GCCCTTATTTTTTTGGCACC CTTTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TATTTGGAGC TATCCCATTG AATTTGGTGC CTTCTAGTAT GCTCTTAAGA CCCATCCTATT CAAAAAGTGA GACAATTCT GGTATTAAAG ATAAAGGCAC CAGTTTTTTTTCAAAAAGTAG CACAACTGCC ATGAGACAGA AGAGTTACC ATCAAGGACA GACACTCCC ATGAGACAGA AGAGTCTACC ATCAAGGACA AATCAAAGAGTCA CAACAAGAAAGTG AACAGAAAACTGAC AACACAACAGA AATCAAAGAGAAAATTTAAC AGAGTCTAC AAAAGAAAAG	360 420 480 540 600 660 720 780 840 900 960
	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAGTA TTCCTTTTCT TTGTGTACCT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCAAAAAACG ATTGGCTCTT TCTACAGCTA TTGCCCGTTC TGGGATAGGA CTGACTTTTC TTTTGGACCACC CTTTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGCAG CGGTTTGTCT GCACATGGTC CAGAGGCACA TGCAACAGAA ACACCACTCCC ATGAGACAGA AGAGTCTACC ATCAAGGACA GAGGTTCTA CAATGGGCCT AACAGGACA GACTGTTATT AAAAGGTGA AATCAAAGTG AACAGGTTAT TTCGTGGACC TGCAAACAAC TGTTTGACAT TTCCTCTTT AGAAATCCT	360 420 480 540 600 660 720 780 840 900 960 1020 1080
65	GTTOGATTOG ATCCATCATG TCATCTCTTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AMACTACCT CCATTCTTGG GCCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAGGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TACCCGGTTT GGGTTCTGCT TCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCTAAAAACG ATTGCCTCTT TCTACAGCTA TTGCCCGTTC TGGGACAGGA CCCCTTATAT TATTTGGAGC TATCGCATTG AATTTGGTGC CTTCTAGTAT GCCCTTAAGA TCAAAAGTGA GAACAATTCT GGTATTAAAA ATAAAAGCAG CAGTTTGTCT GCACATGGTC CAGAGGCACA TGCAACAGAA ACACACTCCC ATGAGACAGA AAGTTACAC CACACAGGA AAGGTTCTA CAATGGGCCT AACAGGAACA GACTGTTATT AAAAGGTGAT GAAGAAAGTG AAAAGGTTAT TCGTGGAGC TGCAAACAAC GACTGTTATT AAAAGGTGAT GAAGAAAGTG TCTTTTCTACAT ATTTACTTGG TCTTTTTCCC TCAGTCAGTT AACCACTCCCT TCTTCTACAT ATTTACTTGG TCTTTTTCCC TCAGTCAGTT AACCACTCCTC	360 420 480 540 600 660 720 780 840 900 960 1020 1080
65	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTGTTTTTTTTGTGCACAT ACTTCGAGAG AAAACTACCT CCATTCTTGG GCCTTTCGTT GTTACTGGTG GTATACTGGTA CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TCAAAAACG ATTGGCTCT TCTACAGCA TTCCCTGTT TCTGAGAGAGA GCCCTTATACT TCTACAAAACG ATTGGCTCTT TCTACAGCA TTCCCGATTG ACTTCTGATTG CTGGACAGGA GCCCTTATAT TCTACAAGGAG TATCCGCATTG AATTTGGTGC CTTCTAGTAT GCTCTTAAGA CCCATCCTATAT TCAAAAGTGA GACAATTCT GGTATTAAAG ATAAAGGCAC CAGTTTTGTCT CAGCAGGACA GCACACGCA ACACCTCC ATGAGACAGA AGAGTCTACC ATCAAGGACA GACGATCTAC AAACACAGCA GACGTTTAT AAGAGGTCTA CAACAGGACA GACGATTAT AAGAGGTGAT GAACAAACAC TGTTTGACAT TTCCTCTTT AGAAATCCTT TCTCTTCTACAT ATTTACTTGG TCTTTTCTCC TCGGCAGTA ACCAACACT GGATTGACAT CACTGAGAGCC TCTTACCTTG	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
65	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTATTTTGTGCATA ACTTGGAGAGA AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGGAGCTGG GCCACAGATA TTCCTTTTCT TTGTGTACA ATGGGACTTC TCAAAAAACG ATTGCTCTT TCTACAGCAA TTGCCCGTTT GGGTTGCTCT TCTACAGCAA TTGCCCGTTC TGGGACAGGA CCCATTATAT TTTTGGCACC CTTTACACAAA TTCCTGATAG ATCGGTATGA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACACTTC GGTATTAAAG ATCAGGACAG AGGTCTACC ACCACGGA ACACACTCC ATGAGACAGA AGGGTCAAC ATCAAGGACA GAGGTCTACC ATCAAGGACA AAACACTCC ATGAGACAGA AAACAACTGT CTCTCTACATA TTCCTGATAG AAAACACACTCC ACGGACAA ATCAAAGTG AAAAACACTGT TCCTCTACATA ATTACCTGTA AAAACACCTGT TCCTCTTAAAAGTGAA AACACACTCC TCTTTGACAT TCCTCTTT AGAAAACCTCT TCACCTGGT AGCACAGACC AAAACACTGG GGATTGACAT CATGGACACC TCTACCTCT TCACCTGGT AGCACAGACCC AAAACACTGG GGATTGACAT CATGGAGCCC TCTACCTCT TCACCTGGT AGCACAGAGCC AAAACACTGG GGATTGACAT CATGGAGCCC TCTACCTCT TCACCTGGT AGCACAGAGCC AAAACACTGG GGATTGACAT CATGGAGCCC TCTACCTGT TCCCTGTAGCA AGGGTCACT CATGGAGACCA TCTACCTGT TCCCTGTAGCA AGGGTCACT CATGGAGACAC TCTCTCTCTTACACTGT TCACCTGGT AGCACAGAGCC AAAACACTGG GGATTGACAT CATGGAGCCC TCTACCTGT TCCCTGATCACTG GGACAGATCAT TTCCTGCTGATC CTTACCTGGT TCTCTTTACCTG GGACAGACCA GACGATTACT TTCCTGATGG CTTGCTGATC	360 420 480 540 660 720 780 840 900 960 1020 1140 1260
65 70	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAGA AMACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAGGTA TCCCTTTTCT TTGTGTGACT ATGGGGCTTC TACCCGGTTT GGGTTCTGCT TCTTATACC AAGTGGCTGC TGTGGTAACT ACCAAATACT TCTAAAAACG ATTGCCTCTT TCTACACGCTA TTGCCCGTTC TGGGACAGGA CTGACTTTTC TTTTGGACC CTTTACAAAA TCCTGATAG ACTCGTATGA CTCGTATAGA CCCATTCATAT TATTTGGAGC TATCGCATTG GATATAAAG ATAAAGGCAG AGGTTTGTCT GCACATGGTC CAGAGGCACA TGCAACAGAA ACACACTCCC ATGAGACAGA AAGTTTACC AGAGGTTCTA CAATGGGCCT AACACGAAA CACACTCCC ATGAGACAGA AAGTTCACA AATCAAAGTG ATAAGGTTAT TCCTGGAGC TGCAACAGAA CACTTCTCTCTCTTAAAAGTTA CATCGAGGACA TCCTAGCTAGCA CTACCTAGCA AAAATTTAAC AGTCTCACAA AATCAAAGTG TATAAGGTTAT TCCTGGAGC TGCAACAACA TGCTTGACT TCCTCTCTTT AGAAAACCT TCTTCTTCACT ATTTACTTGG TCTTTTTCCC TCAGTCAGTT AGCATTACTC ATCCCTACCT TTCACCTGGT AGCCAGAGCC AAAACACCTG GGATTGACAT CATGGATGCC TCTTACCTG TTTCTTACAG AGGTACCT AAGACACG GGATTGACAT TCCTCTGATGG GTTGCTGACT TAAAACTGGAT TAAGAAGTAT CATTACCACA AGTCTTACCT CATCCTTGCTGG GGATGACTAC AAAACTGGAT TAAGAAGTAT CATTACCACA AGTCTTACCT CCTCTGCTGGC GGCATCACTA	360 420 480 540 600 660 720 840 900 960 1020 1080 1140 1260 1320
65	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTATTTTTTTGTGCACAT ACTTCGGAGGA AAAACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTACA ATGGGACTTC TCAAAAACG ATTGGCTCT TCTACAGCA TTCCCTGTT GGGACAGGA GCCCTTATATTTTTTGGCACC CTTTACACAAA TTCCTGATAG ATCGGTTAT CTAAAAGTGA TATCGCATTG AATTTGGTGC CTTCTAGATA GCCTCTAAAGGA CCCATCCATATTTCAAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGACA AGAGATCACC ATCAACAGAA ACAACTCCC ATGAGACAGA AGAGTCTACC ATCAAGGACA GAAGATCAT AACAGAGACA GACGATTTATTAACACA GAAGATTAT TCCTTACATA ATTTACTTGG TCCCTACCT AACAGGACA AGAGTCTACC ATCAAGGACA AACAACTCC TCCCTCTACATA TTTCCTTACAT ATTTACTTGG TCCTTTTCCCTCACT ATCAACGACAC TCCCTACCA AAAACACTGC TCCCTCGT AGCAGACCA AACACACTGC TCCCCTGGT ACCAGAGCC AAAACACTGC GGATTCACTT ACCAGAGACA AAACACTGC GGATTCACT ACCAGAGCA AAAACACTGC GGATTCACT ACCTTACCTT	360 420 480 540 600 660 720 780 840 900 960 1020 1140 1260 1380
65 70	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT ACTTGGAGAG GCCACAGTA TTCCTTTTCT TTGTGTACCT ATGGGACTTC TACCCGGTTT GGGTCTGCT TCTTATACC AAGTGGCTGC TGTGGTACCT ACCAAATACT TCAAAAAAGG ATTGGCTCTT TCTTACACAA TTCCTGATTG CTGGACAGGA CCCATCTTTC TTTTGGACCC CTTTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAG ATCAGTATA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGCAG CAGTTTGTCT GCACACGGAA ACACCACTCCC ATGAGACAGA AGAGTCTACC ATCAAGGACA GTACTACGCA GAAGGCTGGA CTACCTAGCA AAAATTTAAA AGTCTCACCAA AATCAAAGTG AAAAGGGTTAT TACGTGGGCC AACAGAAA GACTGTTATT AAAAGGTGAT GAACAAACTGT TCTCTACAT ATTTACTTGG TCCAAACAAC TGTTTGACAT TCCTCTTT AGAAATCCT TTCCTGTGG AGCCAGAGCC AAAACACTGG GGATTGACAT CATGGATGC TCTTACCTT TTCTCTGTAGC AGGGTATCCTT GAGACACGA GGATTGACAT CATGGATGC TCTTACCTT AAAACTGGAT TAAGAAGTAT CATTACACCA AGTCTTACCT CATCCTCCG GGCATCACTA ACCTGCTTGC TCCTTTTAGCC ACCACATTTC CACACACTCA CACCACATCA TCTTGTTTGC CCATCTTTGC TGGTGGTAC CTGGCATTGA TACCCTCCTGC TCTTTCTCTTTTACCTTTG CACCTACCTC CATCCTTGCT CTCTTTTTCTCTTTTGCC TCCTTCTTTTTCTCTTTTG CACCTCCCC ACCACATTCC CATCCTTGT ACCTCTCCTTTG CCATCTTTGC TCGTTTTAGCC CCCACTTTA TACCCTGT ACTCGTTGAT CTTGTTTTGCTTTTG CCATCTTTGC TGGTGGTAC CTGGCATTGA TACCCTCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTGC TGGTGGTTAC CTGGCATTGA TACCCTCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTGA TACCCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTGA TACCCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTGA TACCCTGT ACTGGTTGAT CTTGTTTGACACC ATCTGTTTGAC CTGGTTTGAT CTGTTTTGCTTTGC TCGTTTTAGCACA ATCCTCTTGT ACCTGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTGAT TACCCCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTGAT TACCCTGT ACTGGTTGAT CTTGTTTTGCTTTTG CCATCTTTTGC TGGTGGTTAC CTGGCATTTA TACCCTGT ACTGGTTGAT CTTGTTTGACT CTGTTTTGCTTTTGC CTATCTTTTGC TGGTGTAC TTGTTTTGCTTTTG CCATCTTTTGC TGGTTTGATTTTTTTTTTTTTTTTTTTT	360 420 480 540 600 660 720 780 840 900 1020 1080 1140 1260 1320 1380
65 70	GTTOGATTOG ATCCATCATG TCATCCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTGG GGCTTTCGTT GTTACTGGTG GATATCTGAT CAGCAGCTGG GCCACAAGTA TTCCTTTTCT TTGTGTACA ATGGGACTTC TACCCGGTTT GGGTTCTCT TCTTATACC AAGTGGCTGC TGTGGTACCT ACCAAATACT TATTGGAGC TATCGCCTTT TCTACAAAA TTCCTGATAG ATCTGTATGA CTGGACAGGA GCCCTTATAT TATTTGGAGC TATCGCATTG AATTTGGTGC CTTCTAGTATG CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAA ATAAAGGCAG CAGTTTTGTC CACAGGGACA AACACATCCC ATGAGACAGA AGGTCTACC ACCAACAGAA ACCACATCCC ATGAGACAGA AGGTCTACC ACACAGAA ACCACATCCC ATGAGACAGA AGAGTCTAC AATCAAAGTG AAAAGGTTCTA CAATGGGCCT AACAGGAACA GACTGTTATT AAAAGGTGAT GAACAAAGTGT TCTCTCTACAT ATTTACTTGG TCTTTTCTCC TCAGTCAGT AGCATACCT ATCCCTACCT TTCACCTGGT AGCCAGAGCC AAAACACTGG GGATTGACAT TCCTCTCTTT AGAAATCGT TTCTGTAGC AGGTATCCTT GAGACACTG GGATGACAT CATGGATGCC TCTTACCTG TTCACCTGGT AGCCAGAGGC AAAACACTGG GGATGACAT CATGGATGCC TCTTACCTG AAAACTGGAT TAAGAAGTAT CATTACCACA AGTCTTACCT CACTCTTGCAGC AGCACACTACACAAAACTGG GCATTACTT TCGGATGC TCTTACCTG ACACGGTTG TCCTTTTAGCC ACCACATTC CACTCCTTA ATCCCTTGCC GGCATCACAC ACTGCTTTGC TCCTTTTTGCC TCGGCATGCA TACCCCTGTTAGCT TCTTGTGTAGCA ACTTGCTTTGC TCCTTTTTGCC ACCACATTC CACTCCTTC TCTGGTTGACA TCTGTGTTAGCA ACTTGCTTTGC TCCTTTTTGCC ACCACATTC CACTCCTTC TCTGGTTGACA TCTGGTTTGC ACTCTTTTGC TCGTGTTACC TCGGCATTCA TCCCTGT ACTGGTTGAC TCTGTGTAGGA ATTCTACAGT AAAACGGTTT TTGGGACTTG CACTTTCTT TGCGGATGC TCTGTGTTGACAT TCTGTGTTGAGA ATTCTACAGT AAAACGGTTT TTGGGACTTG CACTTTCTT TGCGGATGC TCTGTGTTGAC TCTGTGTTGACAT TTGTGTTGAGA ATTCTACAGT AAAACAGGTTT TTGGGACTTG CACTTTCTT TGCGGATGC TCTGTGTTGAC TCTGTGTTGACAT TTGTGTTGAGA ATTCTACAGT TTGGGATGC TTTGGGATGC TCTGTGTTGAC TCTGTGTTGAC TCTGTGTTGAC TCTGTGTTGAC TCTGTGTTGACAT TTGTGTTGACAT TCTGTGTTGACAT TTGTGTTGACAT TTGTGTTGACAT TCTTTTCTTT	360 420 480 540 660 720 780 840 900 960 1080 1140 1260 1320 1380 1480
65 70	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTTTTTTTTT	360 420 540 660 720 780 900 900 1020 1080 1140 1260 1320 1380 1440 1560
65 70 75	GTTOGATTOG ATCCATCATG TCATCCTTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTGTGACAT ACTTGGAGAG AAAACACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT ACTTGGAGAG GCCACAGTA TTCCTTTTCT TTGTGTACA ATGGGACTTC TACCCGGTTT GGGTTCTGCT TCTTATACC AAGTGGTGC TGTGATACA ACCAAATACT TCAAAAAAGG ATTGCCTTT TCTACAGCTA TTGCCCGTTC TGGGACAGGA CCCATTATA TATTTGGAGC TATCCCATTG AATTGGTGC CTTCTAGATA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGCAG CAGTTTGTCT GCACAGGAC GTACTACGCA GAAGGCTGGA CTACCTACAA AACACCACCC ATGAGACAGA AGAGTCTACC ATCAAGAGCA AGAGGTTCTA CAATGGGCCT AACAGAACA CGACTGTTATT AAAAGGTGAT CAATGGGCCT ATAAGGTTAT TTCGTGGAGCC TACCAGACAA AAACACCTGC TCTTCTCTTT TCTCTCACAT ATTTACTTGG TCCAAACAAC TGTTTGACAT TTCTCTCTTT AGAAATCCT TTCCCTGGT AGCCAGAGCC AAAACACCTGG GGATTGACAT CATGGATGC TCTTCCTTT AAAACTGGAT TAAGAAGTAT CATTACACA AGTCTTACCT CATGCATGCC CATCCTTTGC CCATCTTTGC TCGTTTAGCA CACCACTTC CACCACTTAC TCTCTTCTTTC AAAACTGGAT TAAGAAGTAT CATTACACCA AGTCTTACCT CATCCTCTCG CCATCTTTGC TCGTTTAGCA CCCACATTCC CACCACTTAT TCCTGTGACA ATTCTACAGT AAACACGGTTT TTCGGGACTG CCATCTTTACTTC TCTGGACCACC TCTTACCTC CACCACTTTC TCCTTTTTTCTTTTCCTTTTC CCATCTTTTGC TCGTTTAGCA CACCACATTCC CACCACTTTC TGCCTGACCACC ATTCCTTTGC CCATCTTTTGC TCGTGGTTAC CTGGCATTGA TACCTCCTGC TCTTTCTTTTCCTTTTC CCATCTTTTTCTTTTTCCC TCCACTTTTTTTCTTTTC	360 420 540 660 720 780 960 1020 1080 1140 1240 1320 1320 1440 1500 1620
65 70	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTGTTTTTTTTGTGCACAT ACTTCGAGAGA AAAACACCTC CCATCTTGG GCCTTTCGTT GTTACTGGTG GTACTCTTGT GAGAGCACAG ACTCTTGTT GCTTTCGTT GTTACTGGTG GTCACACAGATA TTCCTTTTCT TTGTGTGACT ATGGGACTTC TCAAAAACG ATTCGCCTTT TCACAGATA TTCCTGATAG ACTGGTAGCT GTGACTTTTCTTTT	360 420 540 660 720 780 840 900 1020 1080 1140 1200 1260 1320 1380 1440 1560 1660
65 70 75	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTATTTTGTGCATA ACTTGGAGAGA AAAACACTCCT CCATTCTTG GGCTTTCGTT GTTATCGGTG GATATCTGAT CAGGAGCTGG GCCACAGATA TTCCTTTTCT TTGTGTACT GTTATCGGTG GCCACAGATA TTCCTTTTCT TTGTGTACT ATGGGACTTC TCAAAAAACG ATTGCCTCTT TCTACACAA TTGCCCGTTC TGGGACAGGA GCCCTTATATTTTTTGGACC CTTTACACAA ACTCCTACTA ACTCCTGCTAGA ACACACTCC ATGAGACAGA ACACACTCC ACAGGACAA GCCCTTATATATCACAAGAGAACAA CACACACTCC ATGAGACAGA ACACACACAA ACACACACAA ACACACACA	360 420 540 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1560 1620 1680
65 70 75	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTA TTTTGTGACAT ACTTGGAGAG AAAACTACCT CCATTCTTG GGCTTTCGTT GTTACTGGTG GATATCTGAT ACTTGGAGAG GCCACAGTA TTCCTTTTCT TTGTGTACT GTTACGGACTTG TACCCGGTTT GGGTCTGCT TCTTATACC AAGTGGTGC TGGGAAGAGA CCACATTCTT TCAAAAAACG ATTGCCTTT TCTTACACAA TTCCTGATTA CTGGACAGGA GCCCTTATAT TATTTGGAGC TATCCCATTG AATTGGTCC CTTCTACATA CTGGACAGGA GCCCTTATAT TCAAAAGTGA GAACAATTCT GGTATTAAAG ATAAAGGCAG AGGTCTACC ACCACGGAA CCACACCCC ATGAGACAGA AGAGTCTACC ACCACAGAA ACACACTCCC ATGAGACAGA AGAGTCTACC ATCAGGACA GTACTACGA GAAGGCTGGA CTACCTACACA AAAATTTACA AGTCTCACAA AATCAAGGTA TTCACTGGT TCCATCGGACC TACCAGACA AGAGTCTACC ATCAGGACAGA AAACAGGATTA TTCGTGGAGCC TACCAGACA GACTGTTATT AAAAGGTGAT GAACAAAGTG TTCTCTACAT ATTTACTTGG TCCAACACAA GACTGTTACT TCCTCTCTT AGAAATCCT TTCTCTGTAGC AGGGTCA TCACACACACA GCACTGTACA TCCTCACCT TTCTCTGTAGC AGGGTACACACACACACACACGG GGATTGACAT CATGCATGCC TCCTACCTT AAAACTGGAT TAAGAAGTAT CATTACACAC AGTCTTACCT CATCCTTGC GCCATCCACC ATTCTCTTGC TCCTTTAGCA CACCACATTC CACCACATTC TCCTCTCTTG CCACTCTTGC TCGTGGTTAC CTGGCATTGA TACCACCC ATCTGCTTGACAT CATGCTGGAC ATTCTACAG AAACACGTTT TGGGACTTG CACACACACAC AGTCTTTCTTC CCACCTTTGC TCGTGGTTAC CTGGCATTGA TACCACCC ATCTGCTTGACACC ATCTGCTTGACACC ATCTGCTTGACACC ATCTGCTTGC CCATCTTTGC TCGTGGTTAC CTGGCATTGA TACCACCCA ATCTGCTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTTGACACC ATCTGCTTGACACC ATCTGCTTTGACACC ATCTGCTTTACACCA ATCTGCTTGACACC ATCTGCTTTGACACCACC ATCTGCTTTACACACCACC ATCTGCTTGACACCACC ATCTGCTTTACACCA ATCTACTTTGACACCAACACAACA	360 420 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740
65 70 75	GTTOGATTOG ATCCATCATG TCATCTCTC GTTTTTGTGC AGGTCCCCTG GTTGCTATTATTTTGTGCATA ACTTGGAGAGA AAAACACTCCT CCATTCTTG GGCTTTCGTT GTTATCGGTG GATATCTGAT CAGGAGCTGG GCCACAGATA TTCCTTTTCT TTGTGTACT GTTATCGGTG GCCACAGATA TTCCTTTTCT TTGTGTACT ATGGGACTTC TCAAAAAACG ATTGCCTCTT TCTACACAA TTGCCCGTTC TGGGACAGGA GCCCTTATATTTTTTGGACC CTTTACACAA ACTCCTACTA ACTCCTGCTAGA ACACACTCC ATGAGACAGA ACACACTCC ACAGGACAA GCCCTTATATATCACAAGAGAACAA CACACACTCC ATGAGACAGA ACACACACAA ACACACACAA ACACACACA	360 420 540 660 720 780 840 900 1020 1180 1260 1380 1440 1500 1560 1620 1740 1860

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	AGCATGTGAC / CTTCTGCCCT ( TGTGTACAAA / TAAAAAAAAA / Seq ID NO: Nucleic Acid	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA  quence n #: NM_14	ATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
<b>45 50</b>	AGCATGTGAC // CTTCTGCCCT ( TGTGTACAAA // TAAAAAAAAA // Seq ID NO: : Nucleic Acid Coding seque	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA  112 DNA Se d Accessic ence: 286.	GTTTAGTTAC CATAGTATAC CCTATTTGAA ATTTATGAA  quence n #: NM_14 .1521	ATTAGGCTTT G TGTGTCACTC A ATGTGTTATA C CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA	4020 4080 4140
	AGCATGTGAC // CTTCTGCCCT ( TGTGTACAAA // TAAAAAAAAA // Seq ID NO: : Nucleic Acid Coding seque	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic	GTTTAGTTAC CATAGTATAC CCTATTTGAA ATTTATGAA  quence n #: NM_14 .1521	ATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA	GCTATATCCC GTGGTTGGTG ATACAAACAA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT	4020 4080 4140
	AGCATGTGAC // CTTCTGCCCT ( TGTGTACAAA // TAAAAAAAAA // Seq ID NO: Nucleic Acid Coding seque	GGGTTTTGTT ACAGGACAGG GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA  equence n #: NM_14 .1521 21	ATTAGGCTTT G TGTGTCACTC A ATGTGTTATA CCATGACCAA 7187.1	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA	4020 4080 4140 4160
	AGCATGTGAC / CTTCTGCCCT / TGTGTACAAA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequit	GGGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAGAA ATTTATGAA  equence in #: NM_14 .1521 21	ATTAGGCTTT G TGTGTCACTC A ATGTGTTATA CCATGACCAA  7187.1 31   T CTTATTTATT	GCTATATCCC GTGGTTGGT ATACAACAA ATTAAATATG 41   GTCACCAACC	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA  51   TCTGGTGGAA	4020 4080 4140 4160
50	AGCATGTGAC / CTTCTGCCCT TGTGTACAAA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequi 1 1 GCGCTTGCGG	GGGTTTTGTT ACAGGACAGC TTCAAAGGTC ATACTTATGT AAAAAAAAA 112 DNA Se d Accessic ence: 286. 11 { AGGATTGCGT CACATTGGAT	GTTTAGTTAG CATAGTATAG CCTATTGAA: ATTTATGAA:  Gquence in #: NM_14' .1521 21   TQACGAGAC T CTGATTGGC	TATTAGGCTTT TGTGTCACTC ATGTGTTATA CCATGACCAA  7187.1  31	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG 41   GTCACCAACC TGACGCCTGC	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG	4020 4080 4140 4160
	AGCATGTGAC / CTTCTGCCCT ( TGTGTACANA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG TGAAAGTACA	GGTTTTGTT ACAGGACAGC BTTCAAAGGTC ATACTTATGT AAAAAAAAA  112 DNA Se d Accessic ence: 286. 11	GTTTAGTTAC CCTATTGAA ATTTATGAA  Quence on #: NM_14 .1521 21   TOACGAGGAC CCCCAGTCAC CCCCAGTCAC	ATTAGGCTTT TG TGTGTCACCA ATGTGTTATA CCATGACCAA 7187.1 31	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG  41   GTCACCAACC TGACGCCTGC TAAATCAGCA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA  51   TGTGGTGGAA CCCGAGGCAG CGCGCCCGA	4020 4080 4140 4160
50	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Acic Coding seque 1   GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGCA	GGTTTTGTT ACAGGACAGC TTACTATGT ANAAAAAAAA  112 DNA Se d Accessic ence: 286. 11 1 AGGATTGCGT CACATTGGAT GCCGCCGCCGCAT ACAGGACTGCGAT	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  GUENCE N #: NM_14' .1521 1 TUACGAGAC C CTGATTCGC C CCCAAGTCA	ATTAGGCTTT TO THE TOTAL TH	GCTATATCCC GTGGTTGGTG ATACANACAA ATTAAATATG  41   GTCACCAACC TGACGCCTGC TAAATCACGA GCCCCGATCTA	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGGGCCGGA CTTTAAGGC CTTTAAGGC	4020 4080 4140 4160 60 120 180 240
50	AGCATGTGAC / CTTCTGCCCT / TGTGTACANA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequi 1 1 GCGCTTGCGG / TTTGCAGTTG / TGAAGTACA / GAACCCCGCA / TGAAACCCAC /	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA  112 DNA Se d Accessic ence: 286. 11    AAGATTGCGT CACATTGGAT GCCGCGCCGA ACCTCTGCGA	GTITAGTIAG CATAGTATA CATAGTATA ATTTATGAA ATTTATGAA  ATTTATGAA  1521 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTAGGCTTT  A ATGTGTTATA CCATGACCAA  7187.1  31   1 CITATTTATT C CCGCCCGAA G CCTGGACACA A CACCGACGAT A GGGTTCCCTA	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41   GTCACCANCC TGACGCCTGC TANATCAGCA GCCCGATCTAC CCGCCATGCA	CAGGCCAAAT TCCTTTCATG GGAAGCACAT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGGCGGA CTTTAAGGGC ACAACGGGGA ACAACGGGGA	4020 4080 4140 4160 60 120 180 240 300
50	AGCATGTGAC / CTTCTGCCCT ( TTGTGTACANA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding seque 1   GCGCTTGCGG TTTGCAGTTG TGAAAGTACA ( GAACCCGCA TGAAACCCAC CAGAACGCCC	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTITAGTIAG CCTATTIGAN ATTIATGAN  GQUENCE on #: NM_14' .1521 21 1 TGACGAGAC CCTATTICGAC CCCAAGTCA CCCACAAAAT A GACTATAAG CGGGGGCCCG CGGGGCCCG CGAGGCCCG CGCAGCCCCC CGCGGCCCCG CGCGGCCCCG CCCAAAAT CGCGGGGCCCG CGGGGCCCG CGCGGCCCG CCAAAAT CGCGGGGCCCG CGGGGCCCG CGCGGCCCG CCAAAAT CGCGGGGCCCG CGGGGCCCG CGCGGCCCG CCAAAAT CGCGGGGCCCG CGCGGCCCG CGCGGCCCCG CCACAAAT CCCCCCCCCC	ATTAGGETTT  TOTAL  TOTA	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTANATATG  41   GTCACCAACC TGACGCTTGC GCCCATGGA GCCCATGGA GCCCAGGACC	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC ACAACGGGGA ACAACGGGGA CAGGGGGGCAG CCAGGGAGGCAG CCGCGCCGGA CCCGCCGGCACACACGGGGA ACAACGGGGA ACAACGGGGA	4020 4080 4140 4160 60 120 180 240 300 360
50 55	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Acic Coding sequi 1   GGGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGCA TGAAACCCAC CGGGGAGCCA	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  GUENCE N #: NM_14' .1521 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTAGGCTTT  TOTAL  TOTA	GCTATATCCC GTGGTTGGTG ATACANACAA ATTAAATATG  41   GTCACCAACC TGACGCTGG GCCCATGGA GCCCATGGA GCCCATGGA CTGCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	CAGGCCAAT TCCTTTCATG GGAAGCACT AAACCTATA  51   TGTGGTGGA CGGGGCGGA CTTTAAGGC ACAACGGGGA CAGGAGCAG CAGGAGCAG CGGGCCGGA CTTAAGGC ACAACGGGGA CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGCAGCAGCAG CAGCAGCAG CAGCAG CAGCAGCAG CAGCAGCAG CAGCAG CAGCAGCAG CAGCAGCAG CAGCAG CAGCAGCAG CAGCAGCAG CAGCAG CAG	4020 4080 4140 4160 60 120 180 240 300 360 420
50	AGCATGTGAC / CTTCTGCCCT TGTGTACAAA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequi 1 1 GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGC GAGACCCCC CGGGAGCCA CTGCTGTTGG	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA  d Accessic ence: 286. 11    AGGATTGCGT CACATTGGAT GCCGCGCCGCGCCG GGGCCTGGGCT GGCCTGGGCT TCTCAGCTGG	GTTTAGTTAG CATAGTATAG ATTTATGAA: ATTTATGAA: ATTTATGAA: ATTTATGAA: ATTTATGAA: ATTTATGAA: ATTTATGAA: ATTTATGAA: CATAGAAGAAGAAC CATAGAAGAAGAAC CACAAAATCA CACAAAATAAAG CAGGGGCCCG CACGGGTCCC CAGGGTCCC CAGGGTCCA CAGGTCCA CAGGGTCCA CAGGTCCA CAGGGTCCA CAGGTCCA CAGGGTCCA CAGGTCCA CAGGGTCCA CAGG	ATTAGGCTTT  TOTAL  TOTA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG  41	CAGGCCAAT TACTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGGGCCGGA CTTTAAGGGC ACAACGGGAGCGG CAGGCGGGGC CAGGCGGGGC CTCCCCAGCAG CTCCCCAGCAG	4020 4080 4140 4160 60 120 180 240 300 360 420 480
50 55	AGCATGTGAC / CTTCTGCCCT ( TTGTGTACANA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding seque 1   GCGCTTGCGG / TTTGCAGTTG TGAAAGTACA ( GAACCCGCA / TGAAACCCAC ( CGGGGGCCC CGGGGGCCCA / TGCTGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGCCCCCC	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAA  112 DNA Se cence: 286. 11    AGGATTGGGT CACATTGGAT GGCCGGCCG ATCTCTGGGC GGGCCTGAGG TCTCAGCTGG TCTCAGCTGG TCTCAGCTAG TCACACAAA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG GUENCE ON #: NM_14' .1521 21 1 TGACGAGAC CCCAAGTCAG CCCACAGTCAG CGGGGCCCG CGGGGCCCG CGGGTCCCAAGAGTCAG AGACTTATAGG AGACTTATAGG AGACTTATAGG AGACTTATAGG AGACTTATAGG AGACTTATAGAG AGACTTATAGAG AGACTTATAGAG AGACTTATAGAG AGACTTATAGAG AGACTTATAGAG AGACTTCAGTCT AGACTTCAGTCT AGACTTCAGAGAGTCCAGAGAGTCCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCAGAGTCAGAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGAGTCAGAGTCAGAGTCAGAGTCAGAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGAGTCAGAGTCAGAGAGAG	ATTAGECTTE TOTAL T	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTAAATATG  41	CAGGCCAAT TACTITCATG GGAAGCACT AAACCITATA  51   TGTGGTGGAA CCGAGGCAG CGCGCCGGA CTTTAAGGGC ACAACGGGGA CTTTAAGGGC CAGGGAGGCGG CCGGGGGGCGG CCGGGGGGGG	60 120 180 4140 4160
50 55	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA Seq ID NO: Nucleic Acic Coding sequu 1   GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGCA GAACCCCAC CGGGGAGCCA CTGCTGTTGG AGAGCGCCC CATATCTCAG	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CATAGTATAG CATAGTATAG ATTTATGAG ATTTATGAG  GUENCE  # : NM_14' .1521  # TGAGGAGAC CCCAAGTCAG CCCAAGTCAG CGGGGCCCG GGGGCCCG AGGGTCCGAG GGGGCCCGAG GGGGCCCGAG AGGGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGATTGCAT	ATTAGGCTTT TO THE TOTAL TH	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41   GTCACCAACC TGACGCTGG GCCCATGGA GCCCATGGA GCCCATGGA CTGCTGTTGT AAGACCTAGC ATTGTGTCC ATGGACAGGACC ATGGACAGGACC ATGGACAGGACC ATGGACAGACC ATGGACAGGACA	CAGGCCAAT AAACCTTATA  51 TGTGGTGGA CGGGGCGGA CTTTAAGGC ACAGGGGG CGCGCCGGA CAGGGGGG CGCGCCGGA CAGGGGGGGG	4020 4080 4140 4160 60 120 180 240 300 360 420 480 540 600
50 55	AGCATGTGAC / CTTCTGCCCT TGTGTACAAA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTGCAGTTG TGAAAGTACA GAACCCCGCA TGAAACCCAC CAGAACGCCC CGGGAGCCA CTGCTTGTGG AGAGCGGCCC CTGTTGGA AGAGCGCCC CATATCTCAG CACTGGAATG	GGTTTTGTT ACAGGACAGC ATACTTATGT ANAAAAAAA  112 DNA Se d Accessic ence: 286. 11	GTTTAGTTAG CATAGTATAG ATTTATGAA: ATTTATGAA CACAAAAAAAAAAAAAAAAAAAAAAAAAA	ATTAGGETTT  TOTAL  TOTA	GCTATATCCC GTGGTTGGTG ATACAAACAA ATTAAATATG  41	CAGGCCAAT TACTTCATIG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC ACACGGGAGCCGA CAGGGAGCCGA CAGGGAGCCGA CAGGGAGCCGA CACACGGGA CACACGGGA CACACGGCACCCT TCCCCAGCAG CACACGGCACCCT TCCCCAGCAG CACTAGACCAC TCTAAGGCACT TGAAGTGGAG	60 120 180 4140 4160
50 55 60	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Cding seque 1   GCGCTTGCGG TTTGCAGTTG GAAACCCAC CAGAAACCCAC CAGAAACCCAC CAGAACCCCC CAGGAGCCA CTGCTGTTGC AGAGCGCC CATATCTCAG CACTGGAAT CTAAGTCCCT CTAAGTCCCT CTAAGTCCCT CTAAGTCCCT	GGTTTTGTT ACAGGACAGC ATACTTATGT ANAAAAAAAA  112 DNA Se ence: 286. 11   AGGATTGGG CACATTGGA ATCTCTGGG GGCCTGAGG ATCTCTGGC GGCCTTGGGC TCTCAGCTG TCTCAGCTG TCTCAGCTG TCTCAGCTG AACACAAA AAGACGGTM ACCTCCTTT ACCACCACTA ACGCCCTTT	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  GUENCE M #: NM_14' .1521 21 1 TGACGAGAC CCCAGATAAT A GACTATAGC GGGGGCCG CGGGGCCG CCGGGTCCC A GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG CCCAGAACCC CCAGAACCC CCAGAACCAC CCAGAACCAC CCAGAACCAC CCAGAACCAC CCAGAACCAC CCAGAACCAC CCAGAACCAC CCAGAAACCAC CCAGAAACAC CCAGAAACAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAAACCAC CCAGAACACAC CCAGAACACAC CCAGAACAC CCAGAAACCAC CCAGAACACAC CCAGAACACAC CCAGAACACAC CCAGAACACAC CCAGAACCAC CCAGAACCAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACACAC CCACACAC CCACAC CCACACAC CCACAC CCACACAC CCACAC CCCACAC CCACAC C	ATTAGECTTE TOTAL T	GCTATATCCC GTGGTTGGTG ATACANACAA ATTAAATATG  41	CAGGCCAAT AAACCTTATA  51   TGTGGTGGAA CCGGAGCAG CGCGCCGGA CTTTAAGGGC ACAACGGGGA CTTTAAGGGC CAGGGAGCAG CAGGGAGCAG CTTAAGGGC ACAACGGGA CATTAAGGCC ACATAGCACT TCCCCAGCAG CAGGGAGCAG CACTTCCCGGCAG CACTTCCCGGCAG CACTTCCCGG	4020 4080 4140 4160 60 120 180 240 300 420 480 540 600 600 720
50 55	AGCATGTGAC CTTCTGCCT CTTCTGCCT TGTGTACAAA TAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1   GCGCTTGCGG TTTGCAGTTG GAAACTCAC CAGAACGCCC CAGGAGGCA CTGCTGTTGG AGAGCGCCC CATATCTCAG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CATAGTCCCA GAAGAGGT CTAAGTCCCA GAAGAGGT CTAAGTCCCA CAGAAGAGT CTAAGTCCCG CAGAAGAGTT CAAGAAGAGTT GAAGAAGATT	GGTTTTGTT ACAGGACAGC ATACTTATGT AAAAAAAAA  112 DNA Se d Accessic ence: 286. 11   AGGATTGCG7 CACATTGGAT GCCGCCGC GGCCTGAGG CGGCCTGAGG CGCCTGGGC TCTCAGCTG CACAACAAAA ACATCCTTTT GCACACGAG CCTCCTGAGG CTCCTGAGG CTCCTGAGG CTCCTGAGG CTCCTGAGG CTCCTGAGG CTCCTGAGA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  GUENCE  ### NM_14  1521  ### TUACGAGAC CCCAGAGACA CCCAGAGACA CCCAGAGACA GGGGCCCG GGGGCCCC GGGCCCC GGGGCCCC GGGGCCCC GGGGCCCC GGGGCCCC GGGCCCC GGGGCCCC GGGGCCC GGGCCCC GGGCCC GGGCCCC GGGCCCC GGGCCCC GGGCCCC GGGCCC GGGGCCC GGGCCC GGGGCCC G	ATTAGGCTTT TO THE TOTAL TH	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41 GTCACCAACC TGACGCTTGG GCCCATGGA GCCCATGGA GCCCATGGA GCCCATGGA GCCCATGGA GCCCATGGA GCCCATGGA GCCCATGGA GCCAGGACC TGATCTAGC ATGGACAGGA GGATTTGTGTCC ATGGACAGGA GGGAAAGAAG GGGAAAGAAG GGGAAAGAAG	CAGGCCAAT AAACCTTATA  51 TGTGGTGGAA CCGGAGCAG CGGGCCGGA CTTTAAGGC ACAACGGGGA CAGCAGG CAGCAGGAGCAG CAGCAGGAGCAG CAGCAGGAGCAG CTTAAGGC ACAACGGGAA CTGAAGGAGAGCAG CACTGAACAGGGAGCAG ACTGAACGGGAGCAG CTCATAGGACT TCAAGGACT TCAAGGACT TCAAGGCAG CACCTTCCCG ACGCACTCCGG ACGGACAGGAGCAG CACTTCCGG ACGGACAGG CACCTTCCGG ACGGACAGG CACCTTCCGG CACCTCCGGC CACCTTCCGG CACCTCCGGC CACCTCCGGC CACCTCCGGC CACCTCCGGCGCCGCCGCC CACCTCCGCGCCGCCGCCCGCC CACCTCCGCGCCCGCCCCCCCCCC	60 120 180 4140 4160
50 55 60	AGCATGTGAC CTTCTGCCCT CTTCTGCCCT CTGTGTACAAA ITAAAAAAAAA Seq ID NO: Nucleic Acic Coding seque 1   GCGCTTGCGG TTTGCAGTTG GAAACCCAC CAGAAACCCAC CAGAAACCCAC CAGAAACCCC CAGGAGCCA CTGCTGTTGCG AGAGCGCC CATATCTCAG CACTGGAATG CTAAGTCCCT GAAAGAATA CAAGAAGAATA CAAGAAAAAAAAAA	GGTTTTGTT ACAGGACAGC ATACTTATGT ANAAAAAAAA  112 DNA Se ence: 286. 11   AGGATTGGG CACATTGGA ATCTTGGG GGCCGGCG ATCTCTGGG GGCCTGAGG TCTCAGCTG TCTCAGCTG CACAACAAA AAGACGGTM ACCTCCTTTT GCACCACGAC CTCCTGAGGA CTCCTGAGGA CTCCTGAGGA	GTTTAGTTAG CCTAGTGTAG GUENCE on #: NM_14' .1521 21 1 TGACGAGAC CCCAAAAT A GACTTATAGAC A GAGTTCAG GGGGGCCG GGGGCCCG CGGGTCCC A GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGATCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGTCCAG GAGATCCAG GCGCGGAACAC GGGCCCGGTCC CCCAGAACAC GGGCCCGGTCG CCCAGAACCAC GGGCCCGGTCAG CCCCAGAACAC GGCCCGGATCAG CCCCAGAACCAC GGCCCGGAACCAC GGCCCGCGAGTCAG CCCCAGAACCAC GCCCAGAACCAC GCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCAGAACCAC GCCCCCAGAACCAC GCCCCCAGAACCAC GCCCCACAGCCC CCCCACAGCCC CCCCCACACC CCCCCC	ATTAGECTTE T TOTAL TATATATA T CCATGACCAA  31   T CITATTTATT C CCGCCCGAA A CACCGACGAT A GCCTTCCCTA A GAACCCTTG A AAAAGCACT C AAAAACCACT C TCCTACAAAACCACGT C TCCTGCAAAA C TCCTGCAAAAACCACGT A GTGTGTCAATA C TGCCGCACCAA	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTAAATATG  41	STATEGET CAGGAGGCAAG COGGAGGCAG COGGAGGAGCAG COGGAGGAG COGGAGGAGGAG COGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	4020 4080 4140 4160 120 180 240 300 360 420 540 660 720 780 840
50 55 60	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTACA CAGAACGCCC CGGGGAGCCA CTGCTGTTGG AGAGCGGCC CATATCTCAG CACTGGAATG CACTGAATG CACTGGAATG CACTGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGAATG CACTGA	GGTTTTGTT ALABARAAA  112 DNA Se d Accessic ence: 286. 11   AGGATTGGG GCCGGCCG ATCTTGGGC GGCCTGAGG TCTCAGCTG TCTCAGCTG CACAACAAA AAGACGGTAA ACTCCTTTC GCACCACACAA ACTCCTTTGCACTGG CTCCTGAGGA TCTCTGAGTAG ACTCCTTTTGACTAG TCACAACAAA AAGACGGTAA AAGACGGTAA AAGACGGTAA ACTCCTTTTTTACACTGG TCTCAGAGAA TTCACAAGAA TTCACAAGAA TTCACAAGAA TTCACAAGTA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  ATTTATGAG  TOAGAGAGAC CTGATTGGG CCCACAGAAAT A GACGTCCAG A GTCGCTCGG G GGGGCCGG CCCGGGTCCC A GTCGCTCGC CTGATTGGC CTGGGTCCAG CTGGTTCCAG CTGGGTCCAG CTGGTGCCGG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCAG CTGGGGTGCAG CTGGGGTGCAG CTGGGGTGGAG CTGGGGTGGAG CTGGGGTGGAG CTGGGGTGGAG CTGCGGTAGT CAGCGTAGT CAGCGT CAGCAGT CAGCGTAGT CAGCGT CAGCAGT CAGCT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCGT CAGCAGT CAGCAGT CAGCGT CAGCAGT CAG	ATTAGECTTT  A TAGGETTATA  CCATGACCAA  187.1  31  I CTTATTTATT  CCGCCCGGAA  CCACCGACGAT  A GCGTCCCTA  G AAAAGCACTT  G AAAAGCACTT  G ATCACCAAG  C CCCTCGAAAT  C TCGACACAG  C TCGTGAAAT  C TGCACAGG  G TCCTGCAAAT  C TGCACAGG  C TCGCACAG  C TCGCACAG  C TCCTGCAAAT  C TGCACAGG  C TCCTGCATTT  C TTGATTTTC  C TTGATTTTC  TTGATTTTTC  TTGATTTTTC  TTGATTTTTC  C TTGATTTTTC	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41   GTCACCANCC TGACGCCTGC TANATCAGCA GCCCAGGAC TGCTCGTTGT ANGACCTAGC GATTGTGTC ATGGACAGGG GGTATTCAGCA GGGAAGAGG GGTATTCAGC TGCACAAGG GCCACGAGC TGCTCGTTGT TGCACAAGG TCCACAAAGG TCCACAAAGG TCCACACAGG TCCACACAGG TCCACACAGG TCTACACAAGG TCTACACACG TCTACACAAGG TCTACACACG TCTACACACC TCTACACACAC	SI   TGGGGGGA CCTTTANGGCA CCGGGGGGA CCTTTANGGC CAGGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGACA CAGGAGCAG CAGGGACA CAGGAGCAG CAGGAGCAG CAGGAGCAG ACAGGGGACA TAGGACAC TAGGACAC TAGGGATG ATGGGATG TAGGGATG TAGGGATG TAGGGATG TAGGGATG TAGGGATG TGAGGATG TAGGGATG TAGGAATG TAGAATG	4020 4080 4140 4160 60 120 180 240 300 420 480 540 600 720 780 840 900
50 55 60	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTACA CAGAACGCCC CGGGGAGCCA CTGCTGTTGG AGAGCGGCC CATATCTCAG CACTGGAATG CACTGAATG CACTGGAATG CACTGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGGAATG CACTGAATG CACTGA	GGTTTTGTT ALABARAAA  112 DNA Se d Accessic ence: 286. 11   AGGATTGGG GCCGGCCG ATCTTGGGC GGCCTGAGG TCTCAGCTG TCTCAGCTG CACAACAAA AAGACGGTAA ACTCCTTTC GCACCACACAA ACTCCTTTGCACTGG CTCCTGAGGA TCTCTGAGTAG ACTCCTTTTGACTAG TCACAACAAA AAGACGGTAA AAGACGGTAA AAGACGGTAA ACTCCTTTTTTACACTGG TCTCAGAGAA TTCACAAGAA TTCACAAGAA TTCACAAGAA TTCACAAGTA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  ATTTATGAG  TOAGAGAGAC CTGATTGGG CCCACAGAAAT A GACGTCCAG A GTCGCTCGG G GGGGCCGG CCCGGGTCCC A GTCGCTCGC CTGATTGGC CTGGGTCCAG CTGGTTCCAG CTGGGTCCAG CTGGTGCCGG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCCAG CTGGGGTCAG CTGGGGTGCAG CTGGGGTGCAG CTGGGGTGGAG CTGGGGTGGAG CTGGGGTGGAG CTGGGGTGGAG CTGCGGTAGT CAGCGTAGT CAGCGT CAGCAGT CAGCGTAGT CAGCGT CAGCAGT CAGCT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCAGT CAGCGT CAGCGT CAGCAGT CAGCAGT CAGCGT CAGCAGT CAG	ATTAGGCTTT TO THE TOTAL TH	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41   GTCACCANCC TGACGCCTGC TANATCAGCA GCCCAGGAC TGCTCGTTGT ANGACCTAGC GATTGTGTC ATGGACAGGG GGTATTCAGCA GGGAAGAGG GGTATTCAGC TGCACAAGG GCCACGAGC TGCTCGTTGT TGCACAAGG TCCACAAAGG TCCACAAAGG TCCACACAGG TCCACACAGG TCCACACAGG TCTACACAAGG TCTACACACG TCTACACAAGG TCTACACACG TCTACACACC TCTACACACAC	SI   TGGGGGGA CCTTTANGGCA CCGGGGGGA CCTTTANGGC CAGGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGA CAGGGGACA CAGGAGCAG CAGGGACA CAGGAGCAG CAGGAGCAG CAGGAGCAG ACAGGGGACA TAGGACAC TAGGACAC TAGGGATG ATGGGATG TAGGGATG TAGGGATG TAGGGATG TAGGGATG TAGGGATG TGAGGATG TAGGGATG TAGGAATG TAGAATG	4020 4080 4140 4160 50 120 180 240 300 360 420 540 560 660 720 840 900 960
50 55 60 65	AGCATGTGAC / CTTCTGCCCT TGTGTACAAA / TAAAAAAAA / Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTTGCAGTTG TGAAAGTACA GAACCCCGCA TGAAACCCCAC CAGAACGCCC CAGGAGCCA CTGCTGTTGG AGAGCCCC CATATCTCAG CATGGAAT CTAAGGAG TTACATAGGAG TTACTATGGAG TTACTATGGAG TCATAGGAGG CTGAGAGGTG ATCATAGGAG CTGAGAGGTG CTGAGGGTG	GGTTTTGTT  ACAGGACAGC  ATACTTATGT  ANAAAAAAA  11 DNA Se  12 DNA Se  13	GTTTAGTTAG CCTATTGAA  ATTTATGAA  ATTTATGAA  ATTTATGAA  ATTTATGAA  ATTTATGAA  ATTTATGAA  AGACTAGTAGA CCCAAGAAA AGACTATAAG CGGGGCCCG CCGGGTCCC AGAGTCAC CGGGGCCCG CCGGGTCCC CGGGTCCC CGGGTCCC AGAGTCAG CGGGGCCGG CCGGGTCCC CGGGTCCC AGCGGTCCC CGGGGTCCC CGGGGTCCC CGGGGTCCC CGGGGTCCC CTCCACACC CTCACACC CTCACACACC CTCACACC CTCACACACC CTCACACC C	ATTAGGCTT  TOTAL  TOTAL	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41	SAGGACCAAT TACTTTCATG GGAAGCACT AAACCTTATA  51   TGTGTGGAA CCGGAGCAG CCGGAGCAG CCGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACATAGCACT TACAGCAT TACAGCAT TTGCAGTAGT	4020 4080 4140 4160 120 180 240 300 360 420 540 660 720 780 840 900 960 1020
50 55 60	AGCATGTGAC CTTCTGCCCT CTGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTCCAC CAGAACGCCC CGGGGGGCCA CTGCTGTTGCA AGACCGCCC CATATCTCAG CACTGGAATG CTAAGTCCCT GAAGAGGCT CTAAGTCCCT GAAGAGGTCCCT GAAGAAGGTCCCT GAAGAAGGTCCCT GAAGAAGAGTT AAGGTCGTGA TTACTGTGGA TTACTGTGA TTACTGA TTACTGTGA TTAC	GGTTTTGTT ALAAAAAAAA  112 DNA Se dd Accessic ence: 286. 11   AGGATTGGGT CACATTGGAT CACATTGGGC GGCCCGCGCCTTGGGCCTGAGC TCTCAGCTGG CACAACAAA AAGACGGTAA ACTCCTTTT GGCACCACACA CTCCTGAGCT TCACACTGGT TCACACTGGT TCACACTGGT TCACACTGGT TCACACTGGT TCACACTGGT TCACACTGAGT TCACACTGAGT TCACACTGT TCACACTGT AGAAAGTCC TTGGACACAA ACTTCTACTGT AGAAAGTCC TCGACACACA TCTCCAGCT TCGACACACA TCACACACT TCACACTC TCGACACACA TCACACTC TCACACT TCACACTC TCA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG  ATTTATGAG  TOAGAGAGAC CTGATTGGG CCCACAGAGAC AGCGTAGT AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG AGAGTCCAG CCAGAGACA CCAGAGACA CCAGAGACA CCAGAGACA CCAGAGCAG CCAGAGCAG CCAGAGCAG CCAGAGCAG CCAGCAGC CCAGCAGC CCAGCAGC CCAGCAGC CCAGCAGC CCAGCAGC CCAGCAGC CCACCAGC CCACCCAGC CCACCCAGC CCACCCAGC CCACCCAGC CCACCCAGC CCACCCAC	ATTAGGETTE A TAGGETTATA CCATGACCAA T187.1  31 T CITATITATT C CCGCCCGAA C CACCGACGAT A GCCTCCCTA A GCCTCCCTA C CAAGACCAT C CAAGACCAT C CAAGACCAT C TCAACACGAT C TCCATCAGACG C TCCTGAAAT C TGCACCAGT G TGCTCCATA G TGTGTCAT G TGCTCACAGT C TGCATCACCAGT C TCGATCACACGT C TCGATCACACGT C TCGATCACACGT C TTGATTTTCC C TTGATTTTCC C TTGATTTTCC C TTGATCACCACC C TCGAGACCACC C TCGAGACCACC C TTGATTTCTCC C TCGAGCACC C CCTGAGCACC C C C C C C C C C C C C C C C C C C	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTANATATG  I GTCACCAACC TGACGCCTGC TANATCAGCA GCCCAGGAC TGCTCGTTGT AAGACCTAGC GATTGTGTCC ATGGACAGGG GGATTGTGTCC TCACAAAGG GCCACGAGAC TCCACAAGG GCTACTTTGT TCCACAAAGG TCACACAAGG TCACACAAGG AGGACAATG AAGACAATG AAATGGACAATG AAATGGACA	CAGGCCAAT  TTGCTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGCAG CGCGCCGGA CTTTAAGGGCAC CAGGAGCAG ACAACGGGGA ACAACGGGGA CTTTAAGGACC TGCAGCAG ACATGGCACC TGAAGTGGAG CACTTCCGG AGGATGGTG TGAAGTGAG TTGCAAGGAT TTGCAAGTGT TTGCAAGTGT TTGCAGGATC TTGCAAGTGT TTGCAGGATC TTGCAAGTGT TTGCAAGTGT TGCAGGATC TTGCAAGTGT TGCAGGATC TTGCAAGTGT TGCAAGGATC TTGCAAGTGT TGCAAGGATC TCCTCAATGAG	4020 4080 4140 4160 50 120 180 240 300 360 420 540 560 660 720 840 900 960
50 55 60 65	AGCATGTGAC CTTCTGCCCT CTTCTGCCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTTGCAGTTG GAAACTCAC GAAACCCCGCA TGAAACTCAC CGGGAGCCA CTGCTGTTGG AGAGCGCCC CATATTCTCAG CATTGTCAGTCCT TGAAGGATT AAGGTCGTT AAGGTCGTT AAGGTCGTT ATCATGAGGAG TTACTTGTGAA CTTGTGGAGTA ATCGTGAGTG ATTGTTGTGAGTA ATCGTGAGTA ATCGTGAGTG ACCAGGCCAA	GGTTTTGTT  ACAGGACAGO  ATACTTATGT  AAAAAAAAA  I DNA Se  d Accessic  ence: 286.  II  AGGATTGCGG  CACATTGGAT  GCCGGCCGCTTG  GGCCTGGGC  TCTCAGCTG  CACACAAAA  AAGACGGTAA  ACCTCCTTT  GCACCACGAG  ACTCTGCAG  ATTGTACAC  TCACAGTTG  ATTGTACAC  TCACAGTTG  ATTGTACAC  TCACAGTTG  ACAGATTGCAG  TCACAGTTG  ACAGATTGCAG  TCACAGTTG  TCACAGAAAA  TCTTGCAGCA  TCTTGCAGCA  TCTTGCAGCA  TCACGTTCA	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA: ATTTATGAA CCCACAAAATCA CCCACAAAATCA CCCACAAAATCA AGACTATAAAG CGGGGGCCCG CGGGGCCCG CGGGGTCCC CGGAAACAC CCCACAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCCCACGT TCCTTACCT GCCCCACGT CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCACG CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCACGT CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCACG	ATTAGGETT  T CATTAGGETT  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  G CATGACCAA  G CATGACCAA  G ACACCAGAGA  G ATCACCAAC  C CATCAGAGAC  C TCTGACAAC  C TGCACCAGG  T TCCACCAGG  T T TCCACCAGG  T T TCCACCAGG  T T TCCACCAGG  T T T TCCACCAGG  T T T TCCACA	GTATATCCC GTGGTTGGTG ATACAACAA ATTAAATATG  I GTCACCAACC TGACGCCTGC TAAATCAGCA GCCCGATCTA CGGCCATGGA GCCCATGGA GCCCAGGACC GGTGATCAGC GGTGATTGGT GGTCAGAAGA GCTGGTTTGG AGAGCAATC AAGACCATC AAGACCATC AAATGAAAG AATGAAAT CAAAGCAATC AAAATGAAAT CAAAGCAATC CAGAGCATC CAGAGCAT	SAGGAGGCAAT TOCTTTCATG GGAGCCAT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC ACACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGAGCAG CACGGAGCAG CACTGGACAG TCCCCAGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAGG TGAGGGGACC TGCGAGGGCAC CCCCAATGAG CCCCAATGAG	4020 4080 4140 4160 120 180 240 300 360 420 540 660 720 780 840 900 960 1020
50 55 60 65	AGCATGTGAC CTTCTGCCCT CTTCTGCCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTTGCAGTTG GAAACTCAC GAAACCCCGCA TGAAACTCAC CGGGAGCCA CTGCTGTTGG AGAGCGCCC CATATTCTCAG CATTGTCAGTCCT TGAAGGATT AAGGTCGTT AAGGTCGTT AAGGTCGTT ATCATGAGGAG TTACTTGTGAA CTTGTGGAGTA ATCGTGAGTG ATTGTTGTGAGTA ATCGTGAGTA ATCGTGAGTG ACCAGGCCAA	GGTTTTGTT  ACAGGACAGO  ATACTTATGT  AAAAAAAAA  I DNA Se  d Accessic  ence: 286.  II  AGGATTGCGG  CACATTGGAT  GCCGGCCGCTTG  GGCCTGGGC  TCTCAGCTG  CACACAAAA  AAGACGGTAA  ACCTCCTTT  GCACCACGAG  ACTCTGCAG  ATTGTACAC  TCACAGTTG  ATTGTACAC  TCACAGTTG  ATTGTACAC  TCACAGTTG  ACAGATTGCAG  TCACAGTTG  ACAGATTGCAG  TCACAGTTG  TCACAGAAAA  TCTTGCAGCA  TCTTGCAGCA  TCTTGCAGCA  TCACGTTCA	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA: ATTTATGAA CCCACAAAATCA CCCACAAAATCA CCCACAAAATCA AGACTATAAAG CGGGGGCCCG CGGGGCCCG CGGGGTCCC CGGAAACAC CCCACAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCTGCAGTGA CCCCACGT TCCTTACCT GCCCCACGT CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCACG CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCACGT CCCCACGT CCCCCACGT CCCCCACGT CCCCACGT CCCCCACGT CCCCACGT CCCCACG	ATTAGGETT  T CATTAGGETT  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  T CATGACCAA  G CATGACCAA  G CATGACCAA  G ACACCAGAGA  G ATCACCAAC  C CATCAGAGAC  C TCTGACAAC  C TGCACCAGG  T TCCACCAGG  T T TCCACCAGG  T T TCCACCAGG  T T TCCACCAGG  T T T TCCACCAGG  T T T TCCACA	GTATATCCC GTGGTTGGTG ATACAACAA ATTAAATATG  I GTCACCAACC TGACGCCTGC TAAATCAGCA GCCCGATCTA CGGCCATGGA GCCCATGGA GCCCAGGACC GGTGATCAGC GGTGATTGGT GGTCAGAAGA GCTGGTTTGG AGAGCAATC AAGACCATC AAGACCATC AAATGAAAG AATGAAAT CAAAGCAATC AAAATGAAAT CAAAGCAATC CAGAGCATC CAGAGCAT	SAGGAGGCAAT TOCTTTCATG GGAGCCAT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CTTTAAGGGC ACACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGGAGCAG CACGGAGCAG CACGGAGCAG CACTGGACAG TCCCCAGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAG TGAAGTGGAG CACCTTCCAGG TGAGGGGACC TGCGAGGGCAC CCCCAATGAG CCCCAATGAG	4020 4080 4140 4160 60 120 180 240 300 360 420 480 660 660 780 840 960 1020 1080
50 55 60 65	AGCATGTGAC CTTCTGCCCT CTTGTGCAAA TAAAAAAAA  Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTGCAGTTG TGAAAGTACA GAACCCCGCA TGAAACCCAC CAGAACGCCC CGGGAGCCA CTGCTTGTGG AGAGCGCCC CATATCTCAG CATATCTCAG ATCATAGGAG TTACTGTGGA TTACTGTGGA CTGAGGTG ATCGTAGGTG ATCGTAGG	GGTTTTGTT ACAGGACAGC ATACTTATGT ANAAAAAAAA  11 DNA Se 11   AGGATTGCGT CACAGTGGAC ATCTCTGCG GGCCTGGGCTTTCTCAGCTGGCCTGGC	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG AG	ATTAGGCTT  TOTAL  TOTAL	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  41	SAGGCCAAT TOCTITICATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CCGGAGGCAG CCGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACAGGAGGCAG CACATAGCACT TAGCACT TAGCAGGACC TAGGAGCC TAGGAGCC TAGGAGCC TAGGAGCC TAGGAACC TAGCAACC TAGCAGACC TAGCAC TAGCAGACC TAGCACC TA	4020 4080 4140 4160 120 180 240 300 360 420 480 540 660 720 840 900 1020 1020 1040
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGCATGTGAC CTTCTGCCCT CTTCTGCCCT CTTCTTACAAA ITAAAAAAAA  Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTCAC CAGAACGCCC CGGGGGGCCA CTGCTGTTGG AGAACCCAC CATTTCCAG CACTGGAATG CTAAGTCCT GAAGAAGCTCCT GAAGAAGCTCCT GAAGAAGCTCCT GAAGAAGCTCCT GAAGAAGCTCCT GAAGAAGCTCCT GAAGAAGTT AAGTCGGTG ATCATAGGAG TTACTTGGA TTACTTGGA TTACTTGGA TTACTTGGA ATCGTAGGTT ACTGAGATT ACGAGAACTC ACGAGAACTC ACTGAGACTC	GGTTTTGTT ACAGGACAGC ATACTTATGT AAAAAAAAA  112 DNA Se d Accessic ence: 286. 11   AGGATTGCGT CACATTGGAT CACATTGGAT CACATTGGAT GGCCTGAGCT CGCCTGGCCT CGCCTGGCT CACACAAAAAAAAAA	GTTTAGTTAG CATAGTATAG CATAGTAGAG ATTTATGAG ATTTATGAG  ATTTATGAG  TGAGTAGAG CTGAGTAG CCACAAAAT AGACTATAG GGGGGCCG CCACAAAAT CTGATTCGC GGGGCCGG CCGGGTCCCAGCGC CCAGCAAACAC CTGATTCGCT GGG GGGGCCGGAACAC CTGAGTCAG CCAGCAAACAC CTGAGTCAG CCAGCAGGAGC CCAGCAGGAGC CCACCAGGAGCAG CCAGCAGGAGCAG CCAGCAGGAGCAG CAGCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAC CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAG CCACCAGGAGCAC CCACCAGGAGCAG CCACCAGGAGCAC CCACCAGGACCAC CCACCAGGACCAC CCACCAGGACCAC CCACCAGGACCAC CCACCCAGGACCAC CCACCAGGACCAC CCACCAGGACCAC CCACCAGGACCAC CCACCAGGACAC CCACCAGGACCAC CCACCAGGACCAC CCACCAGGACCAC CCACCACACAC CCACCACAC CCACCACAC CCACCA	ATTAGECTTE A TAGECTTE A ATGTGTATA CCATGACCAA  1087.1  31 1 T CTTATTTATT C CCGCCCGAA CCACCGACAA A CACCGACGAT A GCGTTCCCTA G AAAAGCACTT G AAAAGCACT C TCCACAGGT C TCCTGAAAT C TGCACCAGGT C TGCATGACCAA C TGCACCAGGT C TGCATGACT C TGCATGACT C TGCACCAGGT C TGCATGACT C TGCACCAGGT C TCGACCAGGT C TTGATTGTC C TTGATTGTC C TTGAGGCAC C CCCGGGGAGT C CCCGGGGAGT C CCCGGGGAGT C CCCGGGGAGT C CCTGAGCAC C CCCGGGGAGT C CTTGACCAGCT C CTTGACCAGCT C CTTGACCAGCT C CTTGACCAGCT C CTTGACGCAC C CCCGGGGAGT C C CTTGACGCAC C CCCGGGGAGT C C CTTGACACCT C C C CTTGACACCT C C C CTTGACACCT C C C C C C C C C C C C C C C C C C	41	SI   TOTOTTATA  SI   TOTOTTATA  AAACCTTATA  AAACCTTATA  AAACCTTATA  SI   TOTOGOGAA COGAGGAG COGCCCGGA CTTTAAGGGC CAGGAGCAG CACTTCCAGCAG CAGGAGCAG CACTTCCAG TOTOGGATC TOTOGAGACC TOTOGGACC TOTOGCACC	4020 4080 4140 4160 120 180 240 300 360 420 540 600 720 780 960 1020 1080 1140
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50 55 60 65	AGCATGTGAC TTGTGCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1   GCGCTTGCGG TTTGCAGTTG GAAACCCGCA TGAAACCCAC CAGAAGCCC CAGAAGCCC CAGAAGCCC CATATCTCAG CACTGGAGT TAAAGTCCCT GAAGAGAGT CTAAGTCCCT GAAGAGAGT TTACTGTGGG ATCATAGGAG CTTGAGGTG CTTAAGGCGCC CTGAGAGACCT GAAGACGTC GAAGACGTC GAAGACGTC GAAGACCCC ATCGTAGGTC GAAGACGTC GAAGACCCCCCC GCAGACCCCC ACTGAGGTC ACTGAGGTC ACTGAGGTC ACTGAGGTC ACTGAGGTC ACTGAGGTC ACTGAGGCCCCCTC GCAGCCGCCC GCAGCCCCC GCAGCCCC GCAGCCC GCAGCCCC GCAGCCC GCAGCC GCACC GCAGCC	GGTTTTGTT  ACAGGACAGC  ATACTTATGT  ANAAAAAAA  112 DNA Se  ence: 286. 11	GTTTAGTTAG CCTATTTGAA  GQUENCE IN #: NM_14' .1521 21 1 TGACGAGAC CCTAGTTGAC CCCAGGTCAC CGGGGCCCG GGGGGCCCG GGGGCCCG CGGGGTCCC A GACTATAGC CCAGGATCAC CCAGGTCAC CCAGGTCAC CCAGGTCAC CCAGGTCAC CCAGGTCCC CCAGGTCAC CCAGGTC	ATTAGGETT  TOTAL  TOTAL	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACA ATTANATATG  41	CAGGCCAAT TATACTTTATA  S1 I TOTGTTGTATA AACCTTATA  S1 I TOTGTGGAA CCGGAGCAG CGCGCCGGA CCTATAGCACT TACCCCGAGCAG CACTGGACAG CACTTCCGG CACGGAGCGAG CACTTCCGG CACGGAGCGAG CACTTCCGG CACGGAGCGAG CACTTCCGG CACGGAGCGA CACTTCCGG CACGGAGCAG CACTTCCGG CACGGAGCCA CACTGGACCG CACGGAGCCA CACTGGACCG CACGGAGCCA CACTGGACCG CACGGAGCCA CACTGGACCG CACGGAGCCA CACGGAGCCC CACGGAGCCA CACGGAGCA CACGGAGCA CACACCGGAGCA CACACCGGAGCA CACACCCGGAC CACACCCGAGCA CACCCCAC CACCCCCAC CACCCCAC CACCCCCAC CACCCCAC CACCCCCAC CACCCCCAC CACCCCCAC CACCCCCC	4020 4080 4140 4160 120 180 240 300 360 420 780 840 900 960 1020 1080 11200 1260 1380
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGCATGTGAC TTTTGCCCT TGTGTACAAA TAAAAAAAA  Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTCAC CAGAAGGCCC CAGGAGAGCAC CAGTAGTCCCT GAAAGTCCCT GAAAGTCCCT GAAGAGGTCCCT GAAGAGGTCCCT GAAGAGGTCCCT GAAGAGGTCCCT GAAGAGGTCCCT GAAGAGGTCCCT GAGGAGGGTACTGAGTAGTAC ACTGAGATG ATCATAGGAG TTACTTGGA CCTGAGGTG ATCATAGGAG TTACTGGATG ATCATAGGAG TTACTGGATG ATCATAGGAG TTACTGGATG ATCATAGGAG TTACTGGATG ATCATAGGAG TTACTGGATCCCT GAAGAGCTCC GAGAGAGCTCA GCAGAGCCCC CGAGAGGCCCC CCAGAGGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGGCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCAGAGCCCC CCACACC CCCC CCACAC CCCC CCACAC CCCC CCACAC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	GGTTTTGTT ACAGGACAGC ATACTTATGT ANAAAAAAAA  112 DNA Se dd Accessic ence: 286. 11   AGGATTGCGT CACATTGGAT GGCCGGCGCCG ATCTCTGGGC GGCCTGAGCT TCTCAGCTGG CACAACAAA AAGACGGTAA ACTCCTTTT GGACCACGA CTCCTGAGT GGACAGAA CTCCTGAGT TCACAGT TCACAGGT ACAGCAGAA CTCTTGAGCAGAA CTCTTGAGCAGAA AAGACGGTAA AAGACGTCT TGAGACAGAA AAGACGTCT TGAGACAGAT TGAGACAGT TGAGCACGAA AAGGTCTC TGAGCAGGACAAA AAGGTCTC TGAGCAGGACAAA AAGGTCTC TGAGCAGGACAGA CACAGGGACAA AAGGCACT TGAGCACGAC CACAGGACAGA CACAGGGACAA ACAGGGACAA ACAGGGACAC CTGAGCACGAC CTGAGCACGAC CCTGAGCACGAC CCTGAGCACGAC CCTGAGCACGAC CCTGAGCACGCACAC CCTGAGCACGAC CCTGAGCACGAC CCTGCCACA CTGTCCACA	GTTTAGTTAG CATAGTATAG CATAGTATAG CATAGTAGAG ATTTATGAG  ATTTATGAG  TOTAGTAGAG CTGAGTAG CCACAGTAG CCACAGTCAG CCACAGTCAG CGGGGCCGG CGGGGGCCGG CGGGGCCGG CGGGGCCGG CGGGCCGGG CGGGCCGGG CGGGCCGGG CGCGGGGCCCGCCCGCCCGCCCCGCCCCCC	ATTAGECTTT  TOTAL TATAGECTTT  TOTAL TATAGECTTT  TOTAL TATAGECTTT  TOTAL TATAGECTT  TOTAL TATAGECT  T	41	SI   TGGGGGGAAGCAA  SI   TGGGGGGAAGCAG  GGAAGCAG  GGGGGCGGA  CTTTANAGGGC CAGGGAGCAG CAGGAGCAG CACTTCCAGCAG CACTTCCAGGATC CTAAGGATC CTAAGGATC CTAAGGATC CTAAGGATC CTCAGGAGC CTAGGGACC CTGGGACCG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CTAAAGGGATC CTAAAGGCAG CTAAAGGGAC CTAAAGGCAG CTAAAGCTGAG CAGAACCGG CTAAACCGGGA CAAAACCGGGA AGGAACCGGA AGAGATTGCC	4020 4080 4140 4160 120 180 240 300 360 420 480 540 600 660 600 600 960 1020 1020 1140 1260 1320 1320 1340
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGCATGTGAC TTGTGCCT TGTGTACAAA TAAAAAAAA  Seq ID NO: Nucleic Acic Coding sequi 1   GCGCTTGCGG TTTGCAGTTG GAACCCAC CAGAACCCAC CAGAACCCAC CAGAACCCAC CAGAACCCAC CATATTCTCAG CACTGGAAT CTAAGTCCT TAAGTCCT TAAGTCCGT ATCATAGGAG TTACTTGGAG TTACTTGGAG TTACTTGGAG ATCATAGGAG CTGAGCGCT ATCATGAGCT ATCATGAGT ATCATGAGGCT ACGAGAGCCT ACGAGAGCCT ACGAGAGCCT ACGAGAGCCT AAGCCGCTCA ACCAGAAGCT AAGCAGAAGAG ACAGAGAGAG ACAGAGAGAG ACAGAGAGAG	GGTTTTGTT  ACAGGACAGO  ATACTTATGT  AAAAAAAAA  112 DNA Se  d ACCESSIC  ence: 286.  11    AGGATTGCGT  CACATTGGAT  GCCCGGCCGCT  GGCCTGGGC  CGGCCTGGGC  CTCTCGGCG  CACAACAAA  AAGACGGTAA  ACCTCCTTT  GCACCACGAGA  CTCTCGAGA  CTCTCGAGA  TCTTGCAGC  CAGGTGTCA  AAAGGTCTC  TGAGACAGT  TGAGGAAGT  ACAGGCAC  AAAGGTCTC  TGAGACAGT  TGAGGAAGT  TGAGGAAGT  ACGGGACC  TGAGACAGT  TGAGGAAGT  ACGGGACC  TGAGCAGT  TGAGGAAGT  ACGGGACC  TGAGCAGT  TGAGGAAGT  ACGGGACC  TGAGCAGT  TGAGGAAGT  ACGGGACC  TGAGGAAGT  ACGGGACC  TGAGGAAGT  TGAGGAAGT  ACGGGACC  TGAGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACGGGAAGT  ACAGGGAAGT  ACGGGAAGT  AC	GTTTAGTTAG CATAGTATAG CCTATTTGAA ATTTATGAA: ATTTATGAATTCGC CCCCAGAGTCA AGCTATTAAG AGCTATTAAG AGCTATTAAG CCCAGAGTCA AGGTCCCGGA AGTTGCCCGAA CCTGCGGGTCCC CCCCAGGTCA CCTGCAGGTGA CCTCACAGCC CCTCCAGGTGA AGAGGAGGAC CCTCCAGGTGA AGAGGAGGAC CCTCCAGGTGA CCTCTGATGG CCTCCAGGTGA CCTCTGATGG CCTCCAGGTGA CCTCTGATGG CCTCCAGGTGA CCTCTGATGG CCCTCTGATGG CCCTCTCTGGG CCCTCTCTGGG CCCTCTCTGGG CCCCCTGCTGGG CCCCTCTTGTACAC CCCTCTCTGGG CCCCTCTTGTACAC CCCTCTCTGGG CCCCTCTTGTACAC CCCTTGTTGACAC CCTTGTTGACAC CCCTTGTTGACAC CCTTGTTGACAC CCTTTGTACAC CCTTTGTACAC CCTTTGTACAC CCTTTGTACAC CCTTTGTACAC CCTTTGTACAC CCTTGTTGACAC CCTTTGTACAC CCTTTGTACAC CCTTTTTTTTTT	ATTAGACTTT  TOTAL TATATATATA  TOTAL TATATATA  TOTAL TATATATATA  TOTAL TATATATA  TOTAL TATATATA  TOTAL TATATATATA  TOTAL TATATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATATA  TOTAL TATATATA  TOTAL TATATATATA  TOTAL TATATATATATA  TOTAL TATATATATATATA  TOTAL TATATATATATATATATA  TOTAL TATATATATATATATATATATATATATATATATATA	GTATATCCC GTGGTTGGTG ATACAACA ATTAAATATG  I I GTCACCAACC GTGACCATCC TAAATCAGCA GCCCATCTA GCCCATCTA ATTGGCAGGACC TGCTCGTTGT AAGACCTAGC GGTGATCCACC GTGATCACC GGTGATCCACC GGTGATCCACC TCCACCAACG TCAGGACC TCAGGACC TTGGGCCT TAAAGGTGG AAGTGGCTCA TAAAGGTGG AAGTGGTCA ACGCTGGGAG TTCATGGACG TTCATGTATC	SAGGACTACT TOCATTCATG GGAAGCACA AAACCTTATA  S1   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CCGCGCGGA CACACGGGA CACACGGGACAC CACACGGGACAC AACACGGGACCA AACACGGGACCA AACACGGGAACG CACACCGGGCC AACACCGGGACCA AACACCGGACCA AAGGTAATCCC TAAACCCGGA CAAAACCGGGA CAAAACCGGGA CAAAACCGGGA CAAAAACCGGGA CAAAAACCGGGA AAGACCTGAC CAAAAACCGGGA CAAAAACCGGGA AAGAACCTGAC CAAAAACCGGGA AAGACCTGAC CAAAAACCGGGA AAGAACCTGAC CAAAAACCGGGA AAGAACCTGAC CAAAAACCGGGA AAGAACCTGAC CAAAAACCGGGA AAGAACCTGAC CAAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGA AAAAACCGGGAAAAACACGGAAAAACACGGAAAACACGGAAAACACGGGAAAAACACGGGAAAAACACGGGAAAAACACGGAAAAACACGGAAAAACAGGAAAAAA	4020 4080 4140 4160 120 180 240 300 360 420 480 540 660 720 1080 1020 1020 1140 1200 1380 1380 1340
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGCATGTGAC TTTTGCCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1 1 GGGCTTGCGG TTTGCAGTTG GAAAGCTACA GAACCCGCA TGAAAGCCCC CGGGGGGCCA CTGCTGTTGG AGACGGCC CATATCTCAG CATGGAATG CTAAGTCCCT GAAGAAGATT AAGGTCGTT AAGGTCGTT AAGGTCGTGAGATG CTTAAGTCCCT GAAGAAGATT CTAAGGAG TTACTGTGAGA TTACTGTGAGA CCTGAGCGCC CATATCTCAG CCTGAGCGCC CATATCTCAG CCTGAGCGCC CAGAGGCCAA GCAGAGCCTC ACGAGAGCTC GAGCGGCC CGAGATGCCT AACCAGAAGA	GGTTTTGTT AAAAAAAAA  112 DNA Se da Accessic ence: 286. 11 j AGGATTGCG CACATTGGA ACCTGGGC ATCTCTGGG GGCCGGCGTTGGGCCTGGG ATCTCTGGC GGCCTGGGC TCTCAGCTG TCTCAGCT TCTCAGCTG TCTCAGCT TCTCAGCT TGGACAGA TCTTGCAGC TCTGGACAGA TCTTGCAGC TGGACAGA TCTTGAGCACT TGAGCAGAT TGAGGACGT TGAGGACGT TGAGGACGT TGAGGACGC CTGTCCACA TTGAGGACC CCATGTCCACA	GTTTAGTTAG CCTATTTGAA  ATTTATGAA  CCTGGAGTCCA  AGAGTCCAG  CAGAAACAC  CTGGAGTCCA  CTGCTGCTT  TCTTTACCA  CTTGTTACA  CCTTGTACAC  CTTGTTACAC  CTTGTACAC  CTTGT	ATTAGGETTI  TOTAL TATAGATTATA  TOTAL TATATATATA  TOTAL CACAGAGATA  TOTAL CACAGAGAGATA  TOTAL CACAGAGAGATA  TOTAL CACAGAGAGATA  TOTAL CACAGAGAGAGA  TOTAL CACAGAGAGAGA  TOTAL CACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTANATATG  41	CAGGCCAAT AAACCTTATA  51   TGTGTGGAA CCGAGGCAG CCGGAGGCAG CTTTAAGGGC ACACGGGGA CTTTAAGGGC ACACGGGGA CTTTAAGGAC CTATAGCACT TCCCCAGCAG CAGGAGGCAG CAGGAGCCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGAGCAG CAGGA	60 120 180 300 360 360 420 420 420 420 420 420 420 420 420 42
50 55 60 65 70	AGCATGTGAC CTTCTGCCT CTTCTGCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAACTACAC CAGAAGGCCA CTGAAACTACAC CAGAAGGCCA CTGCTGTTGG AGAGCCGCC CATATCTCAG CACTGGAATG CTAAGTCCCT GAAGAAGATT AAGGTCGGTG ATCATAGGAG TTACTTGGAA CCTGAAGGAG ATCATAGGAG TTACTGTGGA CCTGAGGAGC ATCATAGGAG CTGAGGAGC ATCATAGGAG CTGAGGAGC ACGAGAACCTG ACGAGACCTA ACGAGAGCCAA GCAGAGCCCA ACGAGGACCTCA GCAGCAGAAGA GCAGAAGCTCT AAGCAGAAGA GCAGAAGACTCT CAGCAGAAGAC CCGAGAGACCTCA CCAGAATGCCT AAGCAGAAGA GCAGACACTCT CAGCAGAAGAC CCGAGAGACCTCT CAGCAGAAGAC CCGAGAGACCTCT CCGAGAGACCTCT CCGAGAGACCTCT CCTTTTTTCT CCTTTTTTTCT CCTTTTTTTCT CCTTTTTT	GGTTTTGTT  ACAGGACAGG  ATACTTATCT  ANAAAAAAAA  d Accessic  ence: 286.  11	GTTTAGTTAG CATAGTATAG CCTATTTGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG AG CCTAGTTGAG CCCAAGTCAG CCCAAGTCAG CCCAAGTCAG CCCAAGTCAG CCCAAGTCAG CCCAGGTCAG CCGGGTCCCGGAG CCGGGTCCCGGAG CCTGGGGTCAG CCGGGAGCAG CCTGGAGTGAG CCTGGAGTGAG CCTGGAGTGAG CCTGCGGAGCAG CCTGGAGTGAG CCTGGAGTGAG CCTGCGGAGCAG CCTGCGGAGCAG CCTGCGGAGCAG CCTGCGGGAGCAG CCTGCGGGAGCAG CCTGCGGGAGCAG CCTGCGGGAGCAG CCTGCGGGGAGAGAGAG CCTGCGGGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	ATTAGGETTA  T CCATGACCAA  A ATGTTATATAT  C CATGACCAA  A CACCAGGACAA  G CCTGGACACA  G CCTGGACACA  G AAAAGCCTAG  G AAAAGCCTAG  G AAAAGCCTAG  G AACCCTAG  G ATCACCCAAC  C CCCTGAGAG  C TCCTGCACAC  C TCGACCAC  C TCTGACTAC  C TATTATTATAT  C TGCACAGGT  C TGCACAGGT  C TGCACAGGT  C TTTGCAGAC  C TTTGCAGAC  C TTTGCAGAC  C TTTGCAGGT  C TTTGCAGAC  C TTTCAGGAG  C TTTCAGGAG  C TTTTCAGGAC  C TTTCAGGAC  C TTTTCAGGAC  C TTTTCAGGAC  C TTTCAGGAC  C TTTTCAGGAC  C TTTCAGGAC  C TTTCAGC  C TTTCAGGAC  C TTTCAGC  C	GTATATECCE GTGGTTGGTG ATACANACA ATTANATATG  I GTCACCAACC TGACGCTGC TANATCAGCA GCCCGATCTA GCCCAGGACC GTGGTTGGTTGGT GGCAAGGAC GTGGTTCAGC GGGAAGAAGC GTGGTTTGGT GCTCAGGTG AGACCAGC TGCACAAGG TGCACAGGAC TCACAAGGAC TCACAGGAC TCACAAGGAC TCACAAGGAC TCACAAGGAC TCACAAGGAC TCACAAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGATGC AAGTGGGTCA AAGTGGCAC TTAAAGTGGGT AAGTGGTCAAC TTAAAGTGGGT AAGTGGTCAAC TCAGAACT TCAGACT TC	SAGGACCAAT TOCCTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGGCAG CGCGCCGGA CCTTTAAGGGC ACAACGGGA CCGCCGCGGT TCCCCAGCAG ACAACGGGAGCAC TGAAGTGGAC TGAAGTGGAC ATCAGGCAT TGAGGGACCA AGGAGGACCA AGGAGGACCA TGGTGAACC TGGTGGAACC TGGTGGAACC TGGTGGAACC TGGTGGAACC TGGTGGAACC TCCAATGGG TCCAATGGG TCCAATGGG TCCAATGGG TCCAATGGACC TTGGTGGGACC TTGAGTGTACC TTGGTGGGACC TTGAGTGATC TTGACTCCTGG TTAAACCGGG TTAAACGGG TTAAA	4020 4080 4140 4160 120 180 240 300 360 420 480 540 600 660 600 600 960 1020 1020 1140 1260 1320 1320 1350 1440 1500 1500
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	AGCATGTGAC TTGTGCCT TGTGTACAAA TAAAAAAAA  Seq ID NO: Nucleic Acid Coding sequi 1   GCGCTTGCGG TTGCAGTTG GAAAGTACA GAACCCCGCA TGAAAGTACA CCGGGAGGCCA CTGCTGTTGG AGAGCGCCC CATATCTCAG CATTGTTGAGTAC ATCATAGGAG TTACTGTGAG TTACTGTGAGT ATCATAGGAG TTACTGTGAG ACTGGAGTA GCAGAGCCAA GCAGAAGCTG ACTGAGCCTCA GCAGGCGCCC CAGATGCCT AAGCCGTCA CCTGAGCGTC ACTGAGACTC CATGAGCCTCA CCAGATGCCT CAGAGCGCTCA GCAGCGGCCC CAGATGCCT CCTTTTTTC CCTTTATCCCC CATGACCTCC CCAGATGCCTCA CCAGAGAGCC CCAGATGCCT CCTTTTTTC CCTTTATCCCCT CCATGACCGGC CCAGATGCCTCA CCAGAGAGCTC CCTTTTTTC CCTTTATCCCCT CATGACCGGT CCATGACCGGTC CATGACCGGT CCATGACCGGT CCATGACCGGT CCATGACCGGT CCATGACCGGT CCTTTTTTC CATGACCGGT CCATGACCGGGT CCATGACCGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGT CCATGACCGGT CCATGACCGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGGT CCATGACCGGT CCATGACCG	GGTTTTGTT  ACAGGACAGO  ATACTTATGT  AAAAAAAAAA  I DNA Se  A ACCESSIC  GGCCGGCGCGCG  CGGCCGCTTGGGC  CCCCTGGGC  CTCCTGGGC  CTCTGGGC  CTCCTGGGC  CTCCTGGGC  CTCCTGGGC  CTCCTGGGC  CTCCTGGGC  CTCCTGGGC  CTCCTGGGC  CAGGTCT  CAGGTC	GTTTAGTTAG CCTATTGAA ATTTATGAA ATTTATGAA ATTTATGAA ATTTATGAA ATTTATGAA ATTTATGAA ATTTATGAA ATTTATGAA AGACTATTAGA CCACAAAAT AGACTATAAAG CGAGGACCG CCAGAAACA AGACTAGAG CTGAGGACCA CCACAGAAACA CTGCAGGAGAC CCACAGAACA CTGCAGGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACAGAGAC CCACCAGGAC CCACAGGAC CCACCAGGAC CCACCAGGAC CCACCAGGAC CCACCAGGAC CCACCAGGAC CCACAGGAC CCACCAGGAC CCACCAGC CCACCAGGAC CCACCAGC CCACCAC CCACCAC CCACCAC CCACCAC CCACCA	ATTAGACTTT  TOTAL TATATTATT  TOTAL CACCAGA  TOTAL CACCAG  TOTAL CACCAGA  TOTAL C	GCTATATCCC GTGGTTGGTG ATACANACAA ATTANATATG  I GTCACCAACC TGACCCCT TANATCAGCA GCCCAGTCTA CGGCACTGGAGC GCTGGTTCGTTGT ATGACGCAG GTGATTCAGCA GGCAAGAAG GTGATTCAGC GGAAGAAG GTGATTCAGC GGAAGAAG TCCCAAAAG TCCACAAAG TCCACAAAG TCCACAAAG TCAGCAAAG AGGCATCA AGGACATC AAGACCTAC AAGACTAC AAGACTAC AAGACTAC AAGACTAC AAGACTAC AAGACATC CAGCAAATG TGGTGCCCT TCAGCAAAG ACGCTAGGAAG ACGCTAGGAAG ACGCTAGAAAG ACGCTAGGAAG ACGCTAGGAAG ACGCTAGGAAG ACGCTAGAAG ACGCTAG	CAGGCCAAT TOCTITICATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGCAG CCGGAGCAG CCGGAGCAG CACAGGGAGCAG CAGGAGCAG CACAGGGAGCAG CACAGGAGCAG CACAGGACTAGCG CACAGGAGCAG CACAGGACAG CACAGGAC CACAGGAC CACAGGAC CACAGGAC CACAGGAC CA	4020 4080 4140 4160 120 180 240 300 360 420 480 540 660 720 1080 1020 1020 1140 1320 1380 1440 1560 1560 1680
50 55 60 65 70	AGCATGTGAC TTTTTGCCTT TGTTTACANA TANANANANA Seq ID NO: Nucleic Acic Coding seque 1 1 GCGCTTGCGG TTTGCAGTTG GAAAGTACA GAACCCGCA TGAAAGTACA CAGCAGCCC CGGGGAGCCA CTGCTTTTGG AGAGCGCC CATATCTCAG CACTGGAATG CTAAGTCCT GAAGAAGATT AAGGTCGTT ATCATAGGAG TTACTGTGGA GCAGAGCGCT ATCATAGGAG TTACTGTGAGACT GAGAAGCTG ACTGAGACT GCAGAGCGCC CGAGATGCCT CAGAGCGCC CGAGATGCCT CAGCAGGGCC CGAGATGCCT CAGCAGAGCGCC CCAGATGCCT CAGCAGAGCGCC CCAGATGCCT CAGCAGAGCCC CCAGATGCCT CATGACCGGCC CCAGATGCCT CATGACCGGCC CCAGATCCCT CATGACCGGCC CCAGATGCCT CCATGACCGTCT ACTGAGACTC CCAGACTCC CCAGATGCCT CCATGACCGGCC CCAGATCCCT CATGACCGGCC CCAGATCCCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTTTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTATTTCT CATGACCGTTTTTCT TTTTTCT TTTTTCT TTTTCT TTTTCT TTTTTCT TTTTCT TTTTTCT TTTTCT TTTTCT TTTTCT TTTTCT TTTTTCT TTTTCT TTTTCT TTTTTCT TTTTTT	GGTTTTGTT ALABARAAAA  112 DNA Se dence: 286.  11 j AGGATTGCG CACATTGGAG ATCTTGGGC GGCCGGCGCG ATCTCTGGC GGCCTGAGC TCTCAGCTG GCCTGGCT TCTCAGCTG TCTCAGCTG TCTCTGAG ACTCCTTT GCACCACAA ACTCCTTT GCACCACAGA TCTTGCAG TCTGAGAG TCTTGCAG TGAGAGAG TCTGGAGAG TCTGAGAGA TCTTGCAG CAGACAAA ACTCCTTTGAG AGAAGTCC TGGACAGA TCTGAGAGA TCTGAGAGAA TCTGAGAGAA TCTGCACAC TGAGAGAAA CCTGCTGAGAGAA AGGAGAG CTGCACAC CCATGCACA ACTGCACAC CCATGCACA ACTGCACAC ACTGCACAC ACTGCACAC ACTGCACAC CCATGCACAC ACTGCACAC CCATGCACAC CTGCACAC CTGCACC CTCC CT	GTTTAGTTAG CCTATTTGAA CTTTATGAA CTTT	ATTAGGCTTI  TOTAL TATAGATT  TOTAL TATATATA  TOTAL TATATATAT  TOTAL TATATATAT  TOTAL TATATATATA  TOTAL CACAGAGAT  TOTAL	GCTATATCCC GTGGTTGGTG GTGGTTGGTG ATACANACAA ATTANATATG  41    GTCACCAACC TGACGCTGGC GCCATGGA GCCCAGGAC TGCTCAGTGG AAGACCTAGG GGGAAGAACG GGGAAGAACG GTGCTCAGGTGG TCCACAAAG CTGCAGGAC TCGCAGGAC TGCTCAGGTGC ATAGACAAG CTGCTAGGTG AAAAGGTGG AAAAGGTGG AAAAGGTGGAAAGAC ACGCTGGGAG TCAGGTATC AAAAGGTGG AAATGAAATG	CAGGCCAAT TACTTCATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGAGGCAG GCGGGCGGA CTTTAAGGGC ACAACGGGA CTTTAAGGGC ACACGGGA CTTTAAGGGC CGGGGGGGCG CGGGGGGGGC CGGGGGGGG CGGGGGG	60 120 180 240 300 360 600 660 780 960 1020 1080 1140 1260 1320 1360 1560 1560 1560 1620 1640
50 55 60 65 70	AGCATGTGAC TTTTGCCCT TGTGTACAAA TAAAAAAAA  Seq ID NO: Nucleic Acid Coding seque 1   GGGCTTGCGG TTTGCAGTTG GAAAGTACA CAGAAGGCCC CGGGGAGCA CTGCTGTTGC AGGAGCCC CATATTCTCAG CACTGGAATG ATCATAGGAG TTTACTGGAATG ATCATAGGAG TTACTGGAATG ATCATAGGAG TTACTGGAATG ATCATAGGAG CTGAGAGCCA AGGAGAGCTA AGGTCGGTG ATCATAGGAG CTGAGGAGC ATCATAGGAG CCGAGAGCCTA ACGAGAGCCTA ACGAGAGCCTC ACGAGAGCCTC ACGAGAGCCTC ACGAGAGCCTC CGAGAGGCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCTC CGAGAGCCT CCTTTTTTCC CATGACCGGT TAACTTTTCA GGAAATGTCT	GGTTTTGTT ACAGGACAGG ATACTTATCT ANAAAAAAAA  d Accessic ence: 286.  11    GAGTTGCGG CCACATTGGAT GGCCGGCCCG ATCTTGCGG CGGCCTGGGC TCTCAGCTGG CCCCTTGGAC ATTGAAAAAAA AAGTCCT TGAGAAAGT CAGGAAGT ACGGAAGT TCAGGAAGT TCAGATT TCAGGAACAT TCAGAACAT TCAGGAACAT TCAGGAACAT TCAGGAACAT TCAGAACAT TCAGGAACT TCAGGAACAT TCAGGAACAT TCAGGAACT TCAGGAACT TCAGGAACT TCAGAACT TCAGAACT	GTTTAGTTAG CATAGTATAG CCTATTTGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG ATTTATGAG CAGAGAGAC CCCAAGTCAG CCTGAGTCAG CCCTGCTGG CCCACCAGGT CCCTTGACT CCCTTGAGTGAG CCCTGCTGG CCCCTGCTGG CCCCCTGCTGG CCCCCCG CCCTGCTGG CCCCCCG CCCTGCTGG CCCCCCG CCCTGCTGG CCCCCCCG CCCCCCG CCCCCCCG CCCCCCCC	ATTAGGETT  G TGTGTCACTC  A ATGTGTATA  T CCATGACCAA   187.1  31    T CTTATTTATT  T CCGCCCGAA  G CCTGGACACA  G CCTGGACACA  G AAAGGCCTG  G AAAGGCCTG  G AAAGCCTTG  G ATCACCCAAC  C CCTTGGAGG  C TCTGCACAC  C TGCACCAGG  C TCTGGACAC  C TGGACGCT  C TTGCACAC  C TTGGAGGCT  C TTGCAGGCT  C CTTGGAGGCT  C TTGCAGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  C CTTGGAGGCT  T CTTGGAGGCT  T TTGCAGACT  T TTGCAGACT  T TTTGAGGCT  T TTGGAGGT  T TTTGAGGCT  T CTGGTAGGT  T CTGGTAGGT  T CTGGTAGGT  T CTGGAGGT  T CTGGAGGT  T CTGGAGGT  T CCAGTCAGT  T CTAGTCAGGT  T CTAGTCAGGT  T CTAGTCAGT  T CTAGTCAGT  T CTAGTCAGT  T CTAGTCAGT  T TATAGCTGAA  T ATTTGAGGT  T ATTTGAGGT  T TTTAGGGT  T TTTAGGGT  T TTTAGGGT  T TTTAGGGT  T TTTAGGGT  T TTTAGGT  T TTTAGGT  T TTTAGGGT  T TTTAGGGT  T TTTAGGT  T TT	GCTATATCCC GTGGTTGGTG ATACANACA ATTANATATG  I GTCACCAACC TGACGCCTGC TANATCAGCA GCCCGATCTA GCCCAGGAC GTGGTTGGTCG GATGGACGGC GATTGTACC GAGACTAGCA GCCCAGGAC GTGATTCAGC GGGAAGAAGC GTGGTTTGG GCCAGGAAGAAGC TGCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGGAC TCACAGATGC TCACAGATGC TCACAGATGC TCACAGATGC TCACAGATGC TCACAGATGC TTAAAGGTGG TTAAAGTGGC TTAAAGTGGT TTAAAGTGGT TTAAAGTGGT TTAAAGTGGT TTAAAGTGGT TTAAAGTGC TTAAAGTGGT TTAAATTT TTAGTTTTGGT TTAAATTT TTAGTTTTGGT TTAAATTT TTTGGTTTTGGT TTAAATTT TTTGGTTTTGGT TTAAATTT TTTGGTTTTGGT TTAAATTT TTTGGTTTTGGT TTAAATTT TTTGGTTTTGGT TTAAATTT TTTGGTTTTGGT TTTGGTTTGGT TTTGGT TTTGGTTTGGT TTTGGT T	SAGGACCAAT TOCCTTATA  S1   TGTGGTGGAA CCGGAGGCAG CGCGGCGGA CGCGCGGA CGCGCGGGC TCCCCAGCAG ACAACGGGA CGCGCGGTC TCCCCAGCAG ACAACGGAGCAC TGAAGTGGAA TCATAGGACT TGAAGTGGAA ACTTCCGA ACAACGGAACGA TCCTAATGAG TCCCAATGAC TGGTGGAACCG AAGAACCGGA AAGAACCGG TAAAACCGGG TAAAACCGGG TAAAACCGGG TAAAACCGG TAAAAACCGG TAAAACCGG TAAAACGG TAAAACCGG TAAAAACGG TAAAAACGG TAAAAACGG TAAAAACGG TAAAAACGG TAAAAACGG TAAAAACGG TAAAAACGG	4020 4080 4140 4160 120 180 240 300 360 420 480 540 900 960 1020 1020 1320 1320 1340 1560 1560 1560 1680 1760 1880
50 55 60 65 70	AGCATGTGAC TTTTTGCCCT TGTGTACAAA TAAAAAAAAA  Seq ID NO: Nucleic Acic Coding seque 1   GCGCTTGCGG TTTGCAGTTG GAACCCCGCA TGAAACCCAC CAGAAGCCCC CAGAAGCCCC CATATCTCAG CACTGGAGT TAAGTCCCT GAAGAGAC CTGAGAGGCC CTTATACTGAG CTTAAGTCCCT GAAGACAC CTGAGAGCCA ATCGTGAGT ATCGTGAGT ATCGTGAGT ATCGTGAGT ATCGTGAGT CCTGAGGT CCTGAGGT CCTGAGCCCC CAGAATGCCT CCTGAGCCCC CAGAATGCCT CCTGAGCCCC CCAGATGCCT ACCTGAGCCCC CCAGATGCCT CCTTTTTCC CCTTTTTCC CATGACCGGT TAACTTTTCA GCAGACCGC CCAGATGCCT CCTTTTTCC CTTTACCCGGT TAACTTTTCA GGAAATGTCT CTTTCACCGGT TTTCACAGCA TTTCACAGCA TTTCACAGCG TTTCACACCGT TTTCACACCA TTTCACAGCA TTCACACAG TTCACACAG TTTCACAGCA TTCACACAG TTCACACAC	GGTTTTGTT ACAGGACAGC GTCAAAGGTC ATACTTATGT AAAAAAAAAA	GTTTAGTTAG CCTATTGAA  GQUENCE IN #: NM_14' .1521 21 1 TOACGAGAC CCTCATTAGAC CCCAAGTCA CCCAAGTCA CCCAAGTCA CCCAGGTCCC CCCAGGTCA CCGGGGCCCG CCGGGGGCCG CCGGGGCCCG CCGCGGGG CCGCGGGGCCCG CCGCGGGGCCCG CCCCGCGGG ACGGCCCAGGCCCC CCCCGCGGG ACCCCGGCCCAGGCCC CCCCGCGGG ACCCCGGCCCCAGGCCCCCCCC	ATTAGGCTTI  TOTAL TATAGATT  TOTAL TATATATA  TOTAL TATATATAT  TOTAL TATATATAT  TOTAL TATATATATA  TOTAL CACAGAGAT  TOTAL	GCTATATCCC GTGGTTGGTG ATACANACA ATTANATATG  41	CAGGCCAAT TOCTITICATG GGAAGCACT AAACCTTATA  51   TGTGGTGGAA CCGGAGCAG CCGGAGCAG CCGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACAGGAGCAG CACATAGCACT TAGAACT CACAGGAGCAG CACATAGCACT CACAGGAGCAG CACATAGCACT TAGAACT CACAGGAGCAG CACATAGCACT CACAGGAGCCAG CACATAGCACT CACAGGAGCCAG CACATCCT CACAGGACCAG CACATCCT CACAGGACCAG CACAATCCT CACAGGACCAT CACAGACCAT CACAGGACCAT CACAGGACC	4020 4080 4140 4160 120 180 240 300 360 420 480 540 660 720 1020 1020 1030 1240 1240 1350 1350 1350 1350 1460 1560 1560 1680 1740 1860 1860

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	TOGGESCARGA AGRAGAGTE CECTGTAAGA TGTCACTGTC TGGGTTCCAG CCCTCCTCA	2400
		2460
10	ACCTTACAAG TATATGAGTA TTATTTATAG GTAGTTGTTT ACATATGAGT CGGGACCAAA	2520
	- GAGAACTGGA TCCACGTGAA GTCCTGTGTG TGGCTGGTCC CTACCTGGGC AGTCTCATTT	2580
	GCACCCATAG CCCCCATCTA TGGACAGGCT GGGACAGAGG CAGATGGGTT AGATCACACA	2640
	TAACAATAGG GTCTATGTCA TATCCCAAGT GAACTTGAGC CCTGTTTGGG CTCAGGAGAT	2700
1.5	AGAAGACAAA ATCTGTCTCC CACGTCTGCC ATCGCATCAA GGGGGAAGAG TAGATGGTGC	2760
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	ATCTGTCACC CTGAGCCCAT GAGCTGCCTT TTAGGGTACA GATTGCCTAC TTGAGGACCT TGGCCGCTCT GTAAGCATCT GACTCATCTC AGAAATGTCA ATTCTTAAAC ACTGTGGCAA	2940
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	GATCACACAT TCAGACTGTT GTGTCTGTGG AGTTTTAGGA GTGGGGGGTG ACCTTTCTGG	3240
	TOTTIGGACT TOCATOCTCT COCACTICCA TOTGGCATCC CACGCGTTGT CCCCTGCACT	3300
	TCTGGAAGGC ACAGGGTGCT GCTGCCTCCT GGTCTTTGCC TTTGCTGGGC CTTCTGTGCA	3360
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	ACAGAGGCCT TCCTAGAAGA TGCATCTAGA GTGTCAGCCT TATCAGTGTT TAAGATTTGT	3480
	CTTTTATTTT TAATTITTTT GAGACAGAAT CTCACTCTCT CGCCCAGGCT GGAGTGCAAC	3540 3600
	GGTACGATCT TGGCTCAGTG CAACCTCCGC CTCCTGGGTT CAAGCGATTC TCGTGCCTCA GCCTCCGGAG TAGCTGGGAT TGCAGGCACC CGCCACCACG CCTGGCTAAT TTTTGTATTT	3660
30	TTAGTAGAGA CGGGGTTTCA CCATGTTGGT CAGGCTGGTC TCGAACTCCT GACCTCAGGT	3720
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	CTATTCTTT AAAGTAAGCT TCCTGACGAC ATGAAATAAT TGGGGGTTTT GTTGTTTAGT	3840
	TACATTAGGC TTTGCTATAT CCCCAGGCCA AATAGCATGT GACACAGGAC AGCCATAGTA	3900
	TAGTGTGTCA CTCGTGGTTG GTGTCCTTTC ATGCTTCTGC CCTGTCAAAG GTCCCTATTT	3960
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40	Coding sequence: 1572565 1 11 21 31 41 51	
	CCGAGGAGCG CTCGGGCTGT CTGCGGACCC TGCCGCGTGC AGGGGTCGCG GCCGGCTGGA	60
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	GGGGTCCTGC TGAGTGTGCC TGGGCCTCCA GTCTTGTCCC TGGAGGCCTC TGAGGAAGTG	240
	GAGCTTGAGC CCTGCCTGGC TCCCAGCCTG GAGCAGCAAG AGCAGGAGCT GACAGTAGCC	300
	CTTGGGCAGC CTGTGCGGCT GTGCTGTGGG CGGGCTGAGC GTGGTGGCCA CTGGTACAAG	360
50	GAGGCAGTC GCCTGGCACC TGCTGGCCGT GTACGGGGCT GGAGGGGCCG CCTAGAGATT	420 480
50	GCCAGCTTCC TACCTGAGGA TGCTGGCCGC TACCTCTGCC TGGCACGAGG CTCCATGATC GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG	540
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	TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC	660
	AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA	720
55	CAGGCCTTTC ATGGGGAGAA CCGCATTGGA GGCATTCGGC TGCGCCATCA GCACTGGAGT	780
	CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CGCGGCACAT ACACCTGCCT GGTAGAGAAC	840
	GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGG	900
	CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACAGCCG TGGTGGGCAG CGACGTGGAG	960
<i>c</i> 0	CTGCTGTGCA AGGTGTACAG CGATGCCCAG CCCCACATCC AGTGGCTGAA GCACATCGTC	1020
60	ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA	1080 1140
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65	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGCGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGGG	1200
65	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGCGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGG CTGTATCGAG GGCAGGGGT CCACGGCCGG CACCCCCGCC CGCCCCCCAC TGTGCAGAAG	1200 1260 1320
65	ACGGGGCGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG GGCCCGAGGC CAGGTATACG GACATCATCC TGTAGGGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGGG CTGTATCGAG GGCAGGCGCT CCACGGCCGC CACCCCCCCC CGCCCCCAC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTGGAGT CAGGCTCTTC CGGCAAGTCA	1200 1260 1320 1380
65	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGGG CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCGCC CGCCCGCAC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTGGAGT CAGGCTCTTC CGGCAAGTCAGCTCATCCC TGGTACGAGG CGTCGCTCTC TCCTCCAGCG GCCCCGCCTT GCTGCGGGC CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCCGGA CAGGCTGGTG	1200 1260 1320 1380 1440 1500
	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGCGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGG CTGTATCGAG GGCAGGGGCT CCACGGCCGG CACCCCCGCC CGCCCGCCAC TGTGCAGAAG CTCTCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTGGAGT CAGGCTCTTC CCTGCAGGA AGCTCATCCC TGGTACGAGG GTGCGTCTC TCCTCCAGGG GCCCGGCTT CCTGCCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCGA GGCCTGCTTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGC	1200 1260 1320 1380 1440 1500 1560
65 70	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG GGCCCGAGGC CAGGTATACG GACATCATCC TGTACAGGTC GGGCTCCCTG GCCTGGCTG TGCTCCTGCT GCTGCCGGC CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCGCCAC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGGCAAGTCA AGGTCATCCC TGGTACGAGG GTGGCTTCT TCCCTCCAGGG GCCCGGCCTT GCTGCCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GCCCAGGTAG TACGTGCAGA GGCCTTGGG ATGGACCCTG CCCGGCCTGA CCAAGGCCAGC ACTGTGCCCG TCAAGATCCT CAAAGACAAC	1200 1260 1320 1380 1440 1500 1560 1620
	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCTG GTGCCCGGC CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCCC CGCCCGCCAC TGTGCAGAAG CTCTCCCCGGT TCCCTCTGGC CCGACAGTTC TCCTCCAGGG GCCCGGCTT CCCTCCAGGAGC CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCCGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GGCCAGGTTG TACCTGCAGA GGCCTTTGGC ATGGACCCTG CCCGGCCTGA CCAAGCCAGC ACTGTGGCCG TCAAGATCGT CAAAGACACA GCCTCTGACA AGGACCTGGC CGACCTGGTC TCGGAGATGG AGGTGATCAA GCTGTATCAC	1200 1260 1320 1380 1440 1500 1560 1620 1680
	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGCGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTCGT GCTGGCCGG CTGTATCGAG GGCAGGCGCT CCAGGGCCGG CACCCCCGCC CGCCCACCAC TGTGCAGGAG CTCTCCCCGT TCCTCTGGC CCGACAGTTC TCCTCCAGCG GCCCCGCCTA CGGCAAGTCA AGCTCATCCC TGGTACGAGG GTGCGTTCT TCCTCCAGCG GCCCCGCCTT GCTCCGCCGG CTCGTGAGGTC TAGATCTAAC TCTGCACCCA CTATGGGAGT TCCCCCCGGG CAGGCTGGTG CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GGCCAGGTAG TACGTGCAG GGCCTTTGGC ATGGACCCTG CCCAGGCCTGA CCAGGCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC CCCTCTGACA AGGACCTGGC CGACCTGGTC TCCGAGATGG AGGTGATGAA GCTGATCGGC CGACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGCC CCTGTACGTG	1200 1260 1320 1380 1440 1500 1560 1620 1680 1740
	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGGCAGCAG GGCCCGAGGC CAGGTATACG GACATCATCC TGTACGGCTG GGGCTCCCTG GCCTTGGGTG TGCTCCTGCT GCTGCCGGC CTGTATCGAG GGCAGGCGCT CCACGGCCGC CACCCCCCC CGCCCCCCA TGTGCAGAAG CTCTCCCCGCT TCCTCTGGC CCGACAGTTC TCCCTCGAGG GCCCGGCCTT CCTCGAGGAG AGGCTATCCC TGGTACGAGG GGTGGTTCT TCCTCCAGGG GCCCCGCCTT GCTGGCGGGC CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCCGA GGGCTGCTTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGG ATGGACCCTG CCCGGCCTGA CCAGGCCAG ACTGTGGCG TCAAGATGGC CAGGAAGACAAC GCCTCTGACA AGGACCTGGC CGACCTGGT TCGGACATG AGGTGATGAA GGTGATCGC CGACACAGAA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGC CCTGTACCGG ATGGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAATTCC TCGGGCCCC GGCCCCCCA	1200 1260 1320 1380 1440 1500 1560 1680 1740 1800
70	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGCCAGCAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGCCGGG CTGTATCCAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCCCCC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCCAGCG GCCCCGCCTT CCCTCCAGCA AGCTCATCCC TGGTACGAGG CGTGCGTCT TCCTCCAGCG GCCCCGCCTT GCTGCCGGGC CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGCTGGTG CTTGGGAAGC CCCTAGGCCGA GGGCTGCTTT GGCCAGGTTA TACCTGCAGA GGCCTTTGGC ATGGACCTG CCCGGCCTGA CCAAGCCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC GCCTCTGACA AGGACTGGC CGACCTGGTC TCGGAAGTGG AGGTGATGAA GCTGTATCGGC CGACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGCC CCTGTACCTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGGTTCC TGCGGGCCCG CCGCCCCCAG GGCCCCCACC TCAGCCCCGA CGGTACCTG AGCAGTTGC GGCCCCCCC GCCCCCCCAG	1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1860
	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGAG CGCCCGAGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGGCCGG CTGTATCGAG GGCAGGCGCT CCAGGGCCGG CACCCCCGCC CGCCCCACA TGTGCAGAAG CTCTCCCGCT TCCTCTCGGC CGGACAGTTC TCCTCCAGGG GCCCCGCCAC TGTGCAGAGAG CTCGTGAGTC TAGATCTACC TCTGACCCA CTATGGGAGT TCCCCCCGGG CTCGTGAGTC TAGATCTACC TCTGACCCA CTATGGGAGT TCCCCCCGGG CAGGCTGCT CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGC ATGGACCCTG CCCAGCCTGA CCAGGCCAGC ACTGTGGCCG TCAAGATCCT CAAAGACAAC GCCTCTGACA AGGACCTGGC CGACCTGGTC TCGGAGATGC AGGAGTGAGA GCCTTTACGTG CCGACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGCC CTTGACGTG ATGGTGGACT GCGCCCCCAA GGGAAACCTG CGGGAGTTCC TCGGGGCCCC GGCCCCCCGT CCGGCTCTCC TCAGCCCCCGA CGGTCCTCGG AGCAGTAGGG GGCCCCCCCTC CTTCCCAGTC CTGGTCTCCT GCGCCTACCA GGTGGCCCGA GGCATCAGAT ATCTGGAGTC CCGGAAGTGT	1200 1260 1320 1380 1440 1500 1660 1620 1680 1740 1860 1920 1980
70	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGG GCCCCAGGGC CAGGTATACG GACATCATCC TGTACOGGTC GGGCTCCCTG GCCTTGGGTG TGCTCCTGCTG GCTGCCCGG CTGTATCGAG GGCAGGCGCT CCACGGCCGC CACCCCCCC CGCCCCCCAC TGTGCAGAG CTCTCCCCGT TCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGGCAGTCA AGGTCATCCC TGGTACGAGG GGTGCTTCT TCCTCCAGGG GCCCCGCCTT GCTGGCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCCGA GGGCTGCTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGG ATGGACCCTG CCCGGCCTGA CCAGGCCAG ACTGTGGCG TCAAGATGAC ACGCTTTGGC CGCACACAGA ACATCATCAA CCTGCTTGGT TCGGACCC GCAGAGCGGC CCTGTACCTG ATGGTGGAGT GGCCGCCAA GGGAAACCTG CGGAAGTTCC TGGGGCCC CCTGTACCTG GGCCCCGAC TCAGGCCGA GGGAAACCTG CGGAAGTTCC TGGGGCCC GCCCCCCA GGCCCCCAC TCAGCCCGA GGTCCTCGG AGCAGTGAG GGCGCTCTC CTCCCAGTC CTGTTCTCT CGGCCCCAA GGTCCTCGG AGCAGTCAGT ATCTGGAGTC CCGCAATGTG ATCACCGGG ACCTGGCTGC CGGCAATTGC TGGTGCCCC AGGAAGGTC CCCGGAAGTTC ATCGTCCCGG ACCTGGCCCAA GGTCCTCGG AGCACTCAGT ATCTGGAGTC CCGGAAGTTC CTGGTCTCCT CGGCCCTACCA GGTGCCCGA GGCATCCAGT ATCTGGAGTC CCGGAAGTT	1200 1260 1320 1380 1440 1500 1660 1620 1680 1740 1800 1860 1920 1980
70	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGG GGCCCCAGGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCTG TGTGCCGGG CTGTATCCAG GGCAGGCGCT CCACGGCCGG CACCCCCCC CGCCCCCC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGT CAGGCTCTTC AGCTCATCCC TGGTACGAGG CGTGCGTCT TCCTCCAGCG GCCCCGCCTT GCTGGCGGGC CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCCAG CGACCTGGTC TCAGGAGTG TACGTGCAGA GGCCTTTGGC ATGGACCTG CCCGGCCTGA CCAAGCCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC GCCTCTGACA AGGACTGGC CGACCTGGTC TCGGAGATGG AGGTGATGA GCTGATCGGC CACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGC CCTGTACGTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAGTTCC TGCGGCCCC GCGCCCCCCA GGCCCCCAACC TCAGCCCCGA CGGTACCCCG AGCAGTGAGG GGCCTCTC CTTCCCCAGTC CTGGTCTCCT GCGCCTACCA GGGAACCTG CTGGTGACTG AGCAGTAGAT ACTTCAGAGTC CTGGTCTCCT GCGCCTACCA GGGAACCCGA CGCATCACT ATCTGGAGTC CCGGAGTTG ATCCACCGG ACCTGGCTGC CCGCAATGTG CTGGTGACTT AGGACAATGT GATGAAGATT GCTGACTTTG GGCTGCCCC CGGCGTCCC CACATTGACT ACTATAAAGAA AACCAGCAACA	1200 1260 1320 1380 1440 1500 1660 1620 1680 1740 1860 1920 1980
70 75	ACGGTGCTGC CAGAGGAGGA CCCCACATGA ACGGCAGCAG CGCCCGAGGC CAGGTATACCA GACATCATCC TGTACGGTC GGGCTCCCTG CCCTTGGCTG TGCTCCTGCT GCTGGCGGG CTGTATCGAG GGCAGGCGCT CCAGGGCCGG CACCCCCGCC CGCCCACCAC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGG CGCCCCGCCAC TGTGCAGAAG ACGTCATCCC TGGTACGAGG CGTGCGTCT TCCTCCAGCG GCCCCGCCAC TGTGCAGGAG CTCGTGAGTC TAGATCTACC TCTGGACCCA CTATGGGAGT TCCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGC ATGGACCCTG CCCAGCCTGA CCAAGCCAGC ACTGTGGCCG TAAAGACACA CGCCTCTGACA AGGACCTGGC CGACCTGGTC TCGGAGATGG AGGTGATGAA GGTGATCAGC CCGCACAAAGA ACATCATCAA CCTGCTTGGT GTCTGACCC AGGAAGGGC CCTGTACCTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAATTCC TGCGGGCCCC GGCCCCCCCA CGGCCCCACC TCAGCCCCGA CGGCCCCCGA GGCATCAGT ATCTGGAGT CCGGAAGTGT ATCCACCGGG ACTGGCTGC CGCAATGTG CTGGTACCAT ACTTGGAGT CCGGAAGTGT ATCCACCGGG ACTGGCCCG CGCGATCAC CACATTGACT ACTATAAGAA AACCAGCAGG GCCCCCCCC CTGTGAAGTG GGCTGCCCC CGCACTTGT TTGACCCGGT GTCACACAC GCCCCCCCC CTGTGAAGTG GATGGCCCCC AGGACTCTTT TTGACCCGGT GTCACACAC	1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1860 1920 1920 2040
70	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGCCAGCAG CGCCCCAGGGC CAGGTATACCA GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGCTG TGCTCCTGCT GCTGCCCGGG CTGTATCCAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCCCCAC TGTGCAGAAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGCCAGGCC AGCTCATCCC TGGTACGAGG CGTGCGTCT TCCTCCAGCG GCCCCGCCTT GCTCGCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCGGCCTGA CCAAGCCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC AGCTCTGACA AGGACTGGC CAACCCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC CGCTCTGACA AGGACTGGC CAACCCAGC ACTGTGGCCG TCAGGAGGGC CCTGTACGTG CGACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAGGGCC CCTGTACGTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAGTTC TGCGGGCCCC CGGCCCCCCA GGCCCCCACC TCAGCCCCGA CGGTCCTCG AGCAGTGAG GGCCTCTC CTTCCCAGTC CTGGTCTCCT GCGCCTACCA GGGCACCCGA GGCATGCAGT ATCTGGAGT CCGGAAGTGT ATCCACCGGG ACCTGGCCCC CGGCATCCAC TATGGAGTC CCGGAAGTGT ATCCACCGGG ACCTGGCCCC CGGCGTCCCC CACATTGACT ACTATAAGAA AACCAGCAAC GCCCCCTCC CTGTGAAGTG GAGGGCCC GAGGCCTTT TCACCCGGT GTACACACC CAGAGTGAGT TGTGGTCTTT TGGAGGAGCCC TATGACGGG ACTGCACCT CCGGAGTGT TTCCCCGGT GGAGGAGCTC TTCTCACCCCT CCGCGGCCCCC CCCTATCCTCG GGCAGCCCC CGGCGTCCCC CACATTGACT ACTATAAGAA AACCAGCAAC CCCTATCCTG GCACCCCGG GGAGGAGCTC TTCTCACCCCT CCGGGGGCC CCCGATCCCT TGCGGAGGGC CTTCTCCCGGT GGAGGAGCT TTCTCCCCCT CCGGGGGCC CCCGATCCCC TGCGGAGGCC CGGCGCCCCC CACGCCCTCC TCCCCGGGGGCC CCCGATCCCC TTCCCCGGT GGAGGAGCTC TTCTCCCCCT CCCGGAGGG ACACCCCC CCCTATCCCTG GGAGGAGCTC TTCTCCCCTC TCCCGGAGGG ACACCCCC CCCTATCCCTG CGCCCCC CGGCGCCCC CCCCTATCCCCTC TCCCGGAGGG ACACCCCC CCCTATCCCTG TGCGGCCCC CGGCGCCCCC CACGCCCCCC TTCCCCACTCC CCCTATCCCTG TGCGGGCCC CGGCGCCCCC TTCTCCCCCTC TCCCGGGGGCC CCCCCCCC	1200 1260 1320 1380 1440 1500 1660 1740 1860 1920 1980 2040 2160 2220
70 75	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGG GCCCCAGGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGGTG TGCTCCTGCTG GCTGCCGGG CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCCCCA TGTGCAGAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGGCAAGTCA AGGTCATCCC TGGTACGAGG GGTGGTTCT TCCTCCAGGG GCCCCGCCTT GCTGCCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCCGA GGGCTGCTTT GCCCAGGTAGT TACGTGCAGGA GGCCTTGGG ATGGACCCTG CCCGGCTGA CCAAGCCAGG ACTGTGGCCG TCAAGATCAC CAAGACACA GCCTCTGACA AGGACTGGC CCACCTGGT TCGGAGATGG AGGTGATGAA GCCCTGACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGC CTGTACGTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAATTCC TCGCGGCCC GGCCCCCCA GGCCCCGACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCGACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCCACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCCCACC TCAGGCCCGA CGTCCTCGA AGCAGTGAG GGCACCCCCA ATCGTGCTCT GGGCCCCCACA GGGAATGTG CTGGTACTGG ATCCACCGGG ACCTGGCCCCC CGCGTCCAC ACATGACT ACTGGAGTC CGGAAGTGT ATCCACCGGG ACCTGGCCCCC CGCGTCCAC CACATTGACT ACTATAAGAA AACCAGCACC CGCGCCCCCC CTGGAATGTG CTGGTACTTG TGGCCGGGG TGTCCCCCAC CAGAGTGAC TGTGGACTGC CGCGATCCC CACATTGACT ACTATAAGAA AACCAGCAC CAGAGTGAC TGTGGACCTG GAGGCGCTCC CAGAGCTTT TTGACCCGGGGGGACCC CACATACCTG CATCCCCGG GGAGGCGT TTCTCCCCTGC TGGGGGGGCCCC CCCTATCCTG GATCCCCGG GGAGGCGT TTCTCCCCTGC TGGCAGGGG ACTTCGACC CCCTATCCTG GATCCCCGGG GGAGGCGT TTCTCCCCCCC CCCCACCCCC CCCACAGCCTG TACGGGGGA ACTTCGAGG ACCCGACCCC CACATTGCCC CCCACAGCTG TACCGGCTGA CCTCACGGGGACACTCC CCCTATCCTG GATCCCCGGGGGGGGT TTCTCCCCCTGCCCCCCAC	1200 1260 1320 1380 1440 1560 1620 1680 1740 1860 1920 1980 2040 2160 2280 2280 2340
70 75	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACGCCAGCAG GCCCCAGGGC CAGGTATACCA GACATCATCC TGTACOGGTC GGGCTCCCTG GCCTTGGGTG TGCTCCTGCT GCTGCCCGGG CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCCCAC TGTGCAGAAG CTCTCCCCGT TCCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGGCAAGTCA AGCTCATCCC TGGTACGAGG GGTGGTTCT TCCCTCGAGG GCCCGGCCTT GCTGCCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAGC CCCTAGGCCGA GGGCTGCTTT GGCCAGGTTG TCCCCCGGGA CAGGCTGGTG ATGGACCCTG CCCGGCCTGA CCAGGCCGA CATGTGGCG TCAAGATGAC CAGGCAGACAGA ACATCATCAA CAGCCTGCT TCGGACCCA AGGAAGGGC CCCTGTAGGTG CCGACACAGA ACATCATCAA CCTGCTTGGT GTCTGCACC AGGAAGGGC CCTGTAGGTG GGCCCCGAC TCAGGCCCGA GGGAAACCTG CGGGAATCTC TCGGGGCCC CAGCCCCCA GGCCCCGACC TCAGGCCCA GGGAAACCTG CGGGAATCTC TCGGGGCCC CCCCCCCA GCCCCCGACC TCAGCCCCA GGGAACCTG TCGGTGCTC CTCCGCGCCCCCCCCCC	1200 1260 1320 1380 1440 1500 1620 1680 1740 1860 1980 2040 2100 2220 2280 2340 2400
70 75	ACGGTGCTGC CAGAGGAGGA CCCCACATGG ACCGCAGGG GCCCCAGGGC CAGGTATACG GACATCATCC TGTACGGTC GGGCTCCCTG GCCTTGGGTG TGCTCCTGCTG GCTGCCGGG CTGTATCGAG GGCAGGCGCT CCACGGCCGG CACCCCCGC CGCCCCCCA TGTGCAGAG CTCTCCCCGCT TCCCTCTGGC CCGACAGTTC TCCCTCGAGGT CAGGCTCTTC CGGCAAGTCA AGGTCATCCC TGGTACGAGG GGTGGTTCT TCCTCCAGGG GCCCCGCCTT GCTGCCGGG CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG CTTGGGAAGC CCCTAGGCCGA GGGCTGCTTT GCCCAGGTAGT TACGTGCAGGA GGCCTTGGG ATGGACCCTG CCCGGCTGA CCAAGCCAGG ACTGTGGCCG TCAAGATCAC CAAGACACA GCCTCTGACA AGGACTGGC CCACCTGGT TCGGAGATGG AGGTGATGAA GCCCTGACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGC CTGTACGTG ATCGTGGAGT GCGCCCCCAA GGGAAACCTG CGGGAATTCC TCGCGGCCC GGCCCCCCA GGCCCCGACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCGACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCCACC TCAGGCCCGA GGTCCTCGA AGCAGTGAG GGCCCCCCCA GGCCCCCCACC TCAGGCCCGA CGTCCTCGA AGCAGTGAG GGCACCCCCA ATCGTGCTCT GGGCCCCCACA GGGAATGTG CTGGTACTGG ATCCACCGGG ACCTGGCCCCC CGCGTCCAC ACATGACT ACTGGAGTC CGGAAGTGT ATCCACCGGG ACCTGGCCCCC CGCGTCCAC CACATTGACT ACTATAAGAA AACCAGCACC CGCGCCCCCC CTGGAATGTG CTGGTACTTG TGGCCGGGG TGTCCCCCAC CAGAGTGAC TGTGGACTGC CGCGATCCC CACATTGACT ACTATAAGAA AACCAGCAC CAGAGTGAC TGTGGACCTG GAGGCGCTCC CAGAGCTTT TTGACCCGGGGGGACCC CACATACCTG CATCCCCGG GGAGGCGT TTCTCCCCTGC TGGGGGGGCCCC CCCTATCCTG GATCCCCGG GGAGGCGT TTCTCCCCTGC TGGCAGGGG ACTTCGACC CCCTATCCTG GATCCCCGGG GGAGGCGT TTCTCCCCCCC CCCCACCCCC CCCACAGCCTG TACGGGGGA ACTTCGAGG ACCCGACCCC CACATTGCCC CCCACAGCTG TACCGGCTGA CCTCACGGGGACACTCC CCCTATCCTG GATCCCCGGGGGGGGT TTCTCCCCCTGCCCCCCAC	1200 1260 1320 1380 1500 1560 1680 1740 1860 1920 1980 2040 2160 2220 2340 2460

	TTGGGATCCA GCTCCTTCCC CTTCGGGTCT GGGGTGCAGA CATGAGCAAG GCTCAAGGCT	2580
	GTGCAGGCAC ATAGGCTGGT GGCCTTGGGC CTTGGGGCTC AGCCACAGCC TGACACAGTG	2640
	CTCGACCTTG ATAGCATGGG GCCCCTGGCC CAGAGTTGCT GTGCCGTGTC CAAGGGCCGT	2700
5	GCCCTTGCCC TTGGAGCTGC CGTGCCTGTG TCCTGATGGC CCAAATGTCA GGGTTCTGCT	2760 2820
)	CGGCTTCTTG GACCATGGCG CTTAGTCCCC ATCCCGGGTT TGGCTGAGCC TGGCTGGAGA GCTGCTATGC TAAACCTCCT GCCTCCCAAT ACCAGCAGGA GGTTCTGGGC CTCTGAACCC	2880
	CCTTTCCCCA CACCTCCCCC TGCTGCTGCT GCCCCAGCGT CTTGACGGGA GCATTGGCCC	2940
	CTGAGCCCAG AGAAGCTGGA AGCCTGCCGA AAACAGGAGC AAATGGCGTT TTATAAATTA	3000
	TTTTTTTGAA ATAAA	3015
10		
	Seq ID NO: 114 DNA Sequence	
	Nucleic Acid Accession #: NM_022963.1	
	Coding sequence: 1572445 1 11 21 31 41 51	
15		
	CCCAGGAGGG CTCGGGCTGT CTGCGGGACCC TGCCGCGTGC AGGGGTCGCG GCCGGCTGGA	60
	GCTGGGAGTG AGGCGGCGGA GGAGCCAGGT GAGGAGGAGC CAGGAAGGCA GTTGGTGGGA	120
	AGTCCAGCTT GGGTCCCTGA GAGCTGTGAG AAGGAGATGC GGCTGCTGCT GGCCCTGTTG	180
20	GGGGTCCTGC TGAGTGTGCC TGGGCCTCCA GTCTTGTCCC TGGAGGCCTC TGAGGAAGTG	240 300
20	GAGCTTGAGC CCTGCCTGGC TCCCAGCCTG GAGCAGCAAG AGCAGGAGCT GACAGTAGCC CTTGGGCAGC CTGTGCGGCT GTGCTGTGGG CGGGCTGAGC GTGGTGGCCA CTGGTACAAG	360
	GAGGGCAGTC GCCTGGCACC TGCTGGCCGT GTACGGGGCT GGAGGGGCCG CCTAGAGATT	420
	GCCAGCTTCC TACCTGAGGA TGCTGGCCGC TACCTCTGCC TGGCACGAGG CTCCATGATC	480
	GTCCTGCAGA ATCTCACCTT GATTACAGGT GACTCCTTGA CCTCCAGCAA CGATGATGAG	540
25	GACCCCAAGT CCCATAGGGA CCTCTCGAAT AGGCACAGTT ACCCCCAGCA AGCACCCTAC	600
	TGGACACACC CCCAGCGCAT GGAGAAGAAA CTGCATGCAG TACCTGCGGG GAACACCGTC	660 720
	AAGTTCCGCT GTCCAGCTGC AGGCAACCCC ACGCCCACCA TCCGCTGGCT TAAGGATGGA CAGGCCTTTC ATGGGGAGAA CCGCATTGGA GGCATTCGGC TGCGCCATCA GCACTGGAGT	780
	CTCGTGATGG AGAGCGTGGT GCCCTCGGAC CGCGGCACAT ACACCTGCCT GGTAGAGAAC	840
30	GCTGTGGGCA GCATCCGCTA TAACTACCTG CTAGATGTGC TGGAGCGGTC CCCGCACCGG	900
-	CCCATCCTGC AGGCCGGGCT CCCGGCCAAC ACCACAGCCG TGGTGGGCAG CGACGTGGAG	960
	CTGCTGTGCA AGGTGTACAG CGATGCCCAG CCCCACATCC AGTGGCTGAA GCACATCGTC	1020
	ATCAACGGCA GCAGCTTCGG AGCCGACGGT TTCCCCTATG TGCAAGTCCT AAAGACTGCA	1080
26	GACATCAATA GCTCAGAGGT GGAGGTCCTG TACCTGCGGA ACGTGTCAGC CGAGGACGCA	1140
35	GGCGAGTACA CCTGCCTCGC AGGCAATTCC ATCGGCCTCT CCTACCAGTC TGCCTGGCTC	1200 1260
	ACGGTGCTGC CAGGTACTGG GCGCATCCCC CACCTCACAT GTGACAGCCT GACTCCAGCA GGCAGAACCA AGTCTCCCAC TTTGCAGTTC TCCCTGGAGT CAGGCTCTTC CGGCAAGTCA	1320
	AGCTCATCCC TGGTACGAGG CGTGCGTCTC TCCTCCAGCG GCCCCGCCTT GCTCGCCGGC	1380
	CTCGTGAGTC TAGATCTACC TCTCGACCCA CTATGGGAGT TCCCCCGGGA CAGGCTGGTG	1440
40	CTTGGGAAGC CCCTAGGCGA GGGCTGCTTT GGCCAGGTAG TACGTGCAGA GGCCTTTGGC	1500
	ATGGACCCTG CCCGGCCTGA CCAAGCCAGC ACTGTGGCCG TCAAGATGCT CAAAGACAAC	1560
	GCCTCTGACA AGGACCTGGC CGACCTGGTC TCGGAGATGG AGGTGATGAA GCTGATCGGC	1620
	CGACACAAGA ACATCATCAA CCTGCTTGGT GTCTGCACCC AGGAAGGGCC CCTGTACGTG	1680
45	ATCGTGGAGT GCGCCGCCAA GGGAAACCTG CGGGAGTTCC TGCGGGCCCG GCGCCCCCCA	1740 1800
43	GGCCCCGACC TCAGCCCCGA CGGTCCTCGG AGCAGTGAGG GGCCGCTCTC CTTCCCAGTC CTGGTCTCCT GCGCCTACCA GGTGGCCCGA GGCATGCAGT ATCTGGAGTC CCGGAAGTGT	1860
	ATCCACCGGG ACCTGGCTGC CCGCAATGTG CTGGTGACTG AGGACAATGT GATGAAGATT	1920
	GCTGACTTTG GGCTGGCCCG CGGCGTCCAC CACATTGACT ACTATAAGAA AACCAGCAAC	1980
	GGCCGCCTGC CTGTGAAGTG GATGGCGCCC GAGGCCTTGT TTGACCGGGT GTACACACAC	2040
50	CAGAGTGACG TGTGGTCTTT TGGGATCCTG CTATGGGAGA TCTTCACCCT CGGGGGCTCC	2100
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	GTGCAGGCAC ATAGGCTGGT GGCCTTGGGC CTTGGGGCTC AGCCACAGCC TGACACAGTG	2520
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۷0	GCCCTTGCCC TTGGAGCTGC CGTGCCTGTG TCCTGATGGC CCAAATGTCA GGGTTCTGCT	2640
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	CCTTTCCCCA CACCTCCCC TGCTGCTGCT GCCCCAGCGT CTTGACGGGA GCATTGGCCC	2820
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, 0	ATGAGGGGAC TTGGGACTTG CCTGGCGACT TTGGCCGGAC TTTTGCTAAC TGCGGCGGGC	60
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45	ACCTGTGTCC CCCCCTGCTG GGATTCTCTT	11   GGCCCTTCCC CCCAGCGCCG CCCACTCTCC TCTCTTTCTC	21   CTCGGCTTTG CTCCACCCAG TGCTGCTCGG TTCTGGCCCA	CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC	TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG	120 180 240
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	ACCTGTGTCC CCCCTGCTG GGATTCTCT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGACGA TGAGGACGA TGAGGACGA TGAGGACGCA CAGTCCCCA CCGCCACTT CCTCCAGCCC	11	21   CTCGGCTTTG CTCCACCCAG TGCTGCTCGG TGCTGCCCA TGGGTTCCGG CCTCCCTGGA CTGGGAGCCC GGCTCCGAGT CTGACGGCCA AACTGCTCCA AACTGCTCCA CAGGACGAG GTGCAGAAGG GTGCAGAAGG	CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC AGCTGCCGGT GATCCACCCC CCTGCTACGC GCTGCCCCAA CAGTGTGTAG GCACAGAGAA ACACCACCCCC	I TCCTGCCTCC CCCCCTTCTG ACAGCTTGTC AATGGGCTG CTGAGCCTGA CGCAGCTCTG GTGCAGTCCA ACCCTGCCCT CCAAATGTGT CGCGTTGCCGC GAGTCAGGAGCAGAGCA	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGC GTCTTGAGGC CCGTCCTGCA GGTTATCGTG CCAGGCACCT GACCCAGCCA GGCTGCAGCC GCTTACGCCA ACCCTGTGTC	120 180 240 300 360 420 480 540 600 660 720 780
50	ACCTGRETCE CCCCTGCTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGGACGA TGAAGGAGGA TGAAGGAGGA ACATTGCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC	11   GGCCCTTCCC CCCAGCGCCG CCCACTCTCC TCCTTTCTTCTC TCCTGCTAGC CTGGGGGCCT TCTCACCTTC GTACCCAGTG CGCGGGAG CCTGAATGGC CGCGAGCCGG CGCCAGAGCCGG CCCGGGGGACCCG CCCGGGGGACCCG	21   CTCGGCTTTG CTCCACCAG TGCTCTCGG TCTGGCCA TGGGTTCCCG CCTCCTGGA CTGGGAGCCC GCTCCAGT CTGACGGCA CTAACAGT AACTGCTCCA CAGGACGGG CTCACACAGT CTCACACAGT CTCCCCACT CTCCCCCCC CTCCCCCCCCCC	I CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC GATCACACCC CCTGCTAGGC GCTGCCCCAA CAGTGTGTAA ACCACTGCG GAGGACAGAA ACCACTGCG GAGGACCAA ATGGGACCCAA ATGGGACCAA ACCAA ATGGGACCCAA ATGGGACCCAA ATGGGACCCAA ATGGGACCCAA ATGGGACCCAA ACCAA ATGGGACCCAA ACCAA AC	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCGGTGCCG GAGTCAGGAC	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGG GTCTTGAGGC CCGTCCTGCA GGCACCT GACCCAGCCA GGCTGCAGCC GCTTACGCC ACCCTGTGTC CAGCACCT CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA	120 180 240 300 360 420 480 540 600 660 720 780 840
50	ACCTGRGTCC GCATTCTCTT CTGGAGTTCA CTCCTGGAG TGGTGCTGTA AGGAGGAGG ACATTCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAAGTGCAG	II   GGCCTTCCC CCAGGGCCG CCCAGCGCGG CCCACTCTC TCTTCTTCT CCTGGTAGC CTGGGGGCT TCTCACCTTC GTACCAGTG CTGCAGGGAG CCTCAATGGC GGCAAGCGGG CTGCATCGTC GGCCAGAGG CCCGGGGAC CCTGGGTGGTG CCTGGCTGGTG	21   CTCGGCTTTG   CTCCACCAG   GGTGCTGGGCCA   TGGGTTCCGG   CTGGGAGCCC   GGCTCCGAGT   CTGACAGGCA   CTAAGCAAGT   AACTAGCAGGCA   CTGACAGGGGCA   CTGACAGGGGGG   CTGACAGGAGGGGG   CTGACAGGAGGGGG   CTGACAGAAGG   CTGACAGAA	I CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAG GATCACCCC CCTGCTACGC GCTGCCCAA CAGTGTGTA GCACAGGACAGAAA ACACTGCGC GAGGCACCA ATGGACCGAGAGACAGAAA ATGGACCGGAGAGGACAGAGAA ATGGACCGGAGGACGGACAGAGAA ATGGACCGGAGGACCGGAGGACTGGGACAGGACTGGGACAGGACAGAGAA ATGGACCCT AAGGACCCT AAGGGACCCT AAGGGACCCGAGCTGGGACGAGGACTGGGACAGGACA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT CGCCGTGTGT CGCGTGTGGT CGCGTGTGGCGC CGAGGAATGT	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGC GTCTTGAGGC CGTTCTGCGG GGTATCGTG GCCAGCACCT GACCCAGCCA GCCTTACGCA ACCCTGTGTC CAGCACCAGCA ACCCTGTGTC CAGCACCAGCA ACCCTGTGTC CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA CAGCACCAGCA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	ACCTGRETCE CCCCCTGCTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA AGATGCCCA TGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAGTGCCAC GGTGGTTTCT	11	21   CTCGGCTTTG CTCCACCCAG TGCTGCTCGG TTCTGGCCA TGGGTTCCGG CCTCCTGGAG CTGGGAGCC GGCTCGAGT CTGACGGCA ACTAGCAGC GTGCAAGAGC TTGCAACG TTCTCCCA ACGAAGAGC CTCGCAAGCC CTCGCAAGCC CTCGCAAGCC CTCGCAACG CTCGCATCC CTCGCAACG CTCGCATC	I CCTGGACAGC CAGGCCTGAG GTCTGAGGC CAGCCCCAG GAGCCCCAA CAGTGTGTGA ACCACTGCCCAA ATGGACACCA ATGGACACCA TCATTTTTT	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC AATGCCCTGA CCGAGCTCTG CCCAGCTCTG GTGCAGTCCA ACCCTGCCCT CCAAATGTGT CGCGTGCTGC GAGTAGGAG GGAGGAATGT CAACAGGT CAACAGGT CAACAGGT CAACAGGT CAACAGGT CACCACAGTT CACCACAGTT CACCACAGTT	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GTCTTGAGGC CCGTCCTGCA GGTTATCGTG CACCAGCA GGCTGCAGCA GCTGCAGCA GCTGCAGCA GCTGCAGCA GCTGCAGCA GCTGCAGCA CACCTGGTAG CACCAGGA CACCTGGTAT CAGCACCAGA CACTGGGTAT GGCCTAATCA	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	ACCTGRETCE CCCCTGCTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGGACGA TGAAGGAGGAC ACATTCCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAAGTGCAG GGTGGTTTCA	11   GGCCCTTCCC CCCAGCGCCG CCCAGCGCCG CCCACTCTC TCTCTTTCTC TCTGCTAGC CTGCGGGGGCC TCTCACCTTC GTACCCAGTGG CCGCGAGCCGG CCGCAGCCGG CCCGCAGCCGG CCCGGGGACC CTGCATCGTC CTCAGGGACC AGGAGAGAAGAAGAAGAAGAAAGAAAGAAAG	21 CTCGGCTTTG CTCCACCAG TGCTGTCGCCA TGGGTTCCGG CTCCCTGGA CTGGGAGCCC GGCTCCGAGT CTGAAGGAGC CTAAGCAAGT AACTGCTCA AACTGCTCAA AACTGCTCAA AACTGCTCAA CTGCAGAAGGCG CTCTCACGC CTCTCCCACCG CCCAAGGGGCG CCCAAGGGGGCG CCCAAGGGGGG	I CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC CCTGCTAGGC CCTGCTAGGC GATCCACAC GAGGACAGAA ACCACTGCAGGACAGAGAA ACCACTGCG GAGCACCAGAGCACAC CAGTTGTTGCATTG CAGTG GACAGGACACA ACCATTGCAGTG CAGGACAGAA ACCACTGCG CAGGCACCAGACACTTCATTGTTTA CATGTCATGT	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT GCCGTGTGT GCCGTGTGT GCCGTGTGT GCAGTAGGAC CCACAGTTC CACAGTTCACAGTC GAGGAGTCCCC GAGTCAGGAC CCTCCACAGTT GGTGATCGTC	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGG GTCTTGAGGC CCGTCCTGCA GGCACCT GACCCAGCCA GCCTGCTACGCA ACCCTGTGTC CAGGCACCT CAGCACCAGCA CACTGGGTAT GGCTTAATCA TCCCTCCAGC TCCCTCCAGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	ACCTGRGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA TGAAGGAGGC ACATTGCCCA TGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAAGTGCAG GGTGGTTTCT TATGTGTGAA GGAAAAGACA	II   GGCCCTTCCC CCAGCGCCGC CCCACTCTCC TCTCTTCTC TCTGSTAGC CTGGGGGCT TCTCACCTTC GTACCAGTG GGCGGGGG CCTCAATGGC GGCAGAGCGGG CTGCATGGC GGCCAGAGG CCCGGGGAGC CCCGGGGACC CTCAGGGAGC CTCAGGGAGC CCGGGAGC CTCAGGGAGC CTCAGGGAGC CTCAGGGAGC GGGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	21   CTCGGCTTIG   CTCCACCAG   GGTGCTGGG   TCTGGCCA   TGGGTTCCGG   CTCGCTGGA   CTGGGAGCCC   GGCTCCGAGT   CTGAGCAGGC   CTAAGCAAGT   AACTAGCAGG   CTGGAGAAGG   CTGGAGAAGG   CTCGTCATCG   CCCAAGGGGC   CTCGTCATCG   CCCAAGGGGCA   CGTGAGAAGG   CTCGTCATCG   CGTGAGGGCAG   CGTGAGGGCAG   CGTGAGGGCAG   CGTGAGGGCAG   CGTGAGGGCAG   CGTGAGGGCAG   CGTGAGGCCAG   CGTGAGGCCAG   CGTGAGGCCAG   CGTGAGGCCAG   CTCGGCATCG   CGTGAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCATCG   CGTGAGGCCAG   CTCGGCAGGCCAG   CTCGGCCAG   CTCGGCAGGCCAG   CTCGGCCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAG   CTCGGCAGGCCAGCAGCAG   CTCGGCAGGCCAGCAGCAGCAGCAG   CTCGGCAGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	I CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAG GATCACCCC CCTGCTACGC GCTGCCCAA CAGTGTGGA GGACAGAGAA ACCACTGCGC GAGGCACCGA TGGACCGAGTGTGAGACCA TGGACCAA CAGTGTGGACCA ATGGACCA ATGGACCA CAGTGGACCA CAGTGGACCA CAGTCATTAGTCAA ACACTACTACACACACACACACACACACACACACA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG CTGAGACCTGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT CGCCGTGCCGC GGAGCAGGAC GGAGGAATGT CAGCAGGAC GGAGGAATGT CAGCAGGAC GGAGGATCAGGAC GGAGGATGT CAGCAGGTC CCCACAGTT GGTGATCCTGCGC GGTGCTGCGCG GGTGCTGCGG	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGG GTCTTGAGGC CCGTCCTGCA GGCTACCGC GCTTACGCG GCTTACGCG GCTTACGCA ACCCTGTGTC ACCCAGCCA ACCCTGTGTC GCCCACCAGCA ACCCTGTGTC GCCCACCAGCA ACCCTGTGTC GCCCACCAGCA ACCCTGTGTC GCCCACCCGG CACTGCTCCGG CACCCCGGCTACCCAGC CCCTCCCGG GCCCCCCCGG GCCCCCCCGG GCCCCCCCGG GCCCCCC	120 180 240 300 360 420 480 660 720 840 900 960 1020 1080
50	ACCTGRETCE CCCCTGCTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA AGATGCCCA TGGGCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC TGGGTTTCT TATGTGTAA ACGTCACCA	11	21   CTCGGCTTTG   CTCCACCCAG   GGGTCCCAG   TGGTGCCCA   TGGGTTCCG   CCTCCTGGA   CTGGGAGCCC   GGCTCCGAGT   CTGACGAGCA   CTAACCAGT   AACTGCTCCA   AACTGCTCCA   CTGGAAGAGCG   CTCGTCATCCC   CCCAGGGGGG   CCCAGGGGGGG   CCCAGGGGGGGGGC   CCCAGGGGGGGGGGGCCAG   GGGGAGCCAG   GAGGAGACAA	CCTGGACAGC CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC CAGCCGCAGC GATCCACCC GCTGCCCCAA CAGTGTGTAGC GGACAGAGAA ACCACTGCCC GAGGCACCCAA ATGGGACCCA ATGGGACCCCA ATGGGACCCC CAGCTGGGCC CAGTCTGTTAGC CAGTCTGTTAGC CAGTCTGTAGC CAGTCTGCAC CAGT	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGCGCTTG CTGAGCCTGA CCCAGCTCTG CTGAGCTGAC CCCAGCTCTG CTGAGCTCCA ACCCTGCCCT CCCAATGTGT CGCGTGTGT CGCGTGCTGC CGAGTACGAC GGAGCACTC CTCCACAGTT GGTGATCGT GGCCTGCCCC CTCCACAGTT GGCCTGATCGC CTCCACAGTT GGCCCTGCCCC CTCCACAGTT CGGCCCTGCCCC CACAGGGAGC CACGGGAGC CACGGGAGC CACGGGAGC CACGGGAGC CACGGGAGC CACGGGAGC CACGGGAGC CACGGGAGGACC CACGGGAGGACC CACGGGAGGACC CACGGGAGGACC CACGGGAGGACC CACGGGAGGACG CACGGAGGACG CACGGGAGGACG CACGGGAGGACG CACGGGAGGACG CACGGGAGGACG CACGGAGACC CACGGGAGC CACGGGAGC CACGGGAGC CACGGAGC CACGCAC CACGGAGC CACGCAC CA	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC CTGTTCAGGC CCGTCCTGCA GGTTATCGTG CCAGGCACGCA GGCTGCAGCC GCTTACGCC ACCCTGCAGCC ACCCTGCAGCC ACCCTGGTAT CAGCACAGA CACTGGGTAT TCGCCTAATCA TCCGTCCAGC ACCCTCCCGG AGCCCTCCCGG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	ACTGRICC CCCCCGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGGGACGA AGATTGCCCA TGGGCCTGC AGACTGCCC CCAGCCC CCAGGCC CCAGGTTTCA GGAACTGCCC CCAGGTTTCT TATGTTGAA AGGAAAGACA ACTGCCACC AGAAAGACA ACTCACCA ACGACCACC AGAACACA ACGACCACC	11   GGCCCTTCCC CCCAGCGCCG CCCAGCGCCGC CCCAGCGCCGC TCTCTTTCTC TCCTGCTAGC CTGCGGGGCCT TCTCACCTTC GTACCCAGTGG CTCCAATGGC CGCAGCCGG GCCAGAGC CCTGCATCGTC GGCCAGAGC CCTGGCTGGTG CCCAGGGACC CTGCCTGGTG CTCAGGGACG CTGGCAGAG GGAGCAGAA GGAGCAGAA GGAGCAGAA AGAACTGCCGTA AGAACTGCCAGAA	21   CTCGGCTTTG   CTCCACCAGE   TGCTGCTCGGCTTTG   TGCTGCTCGGCTTTGGCCCA   TGGGTTCCCGG   CTGCCTGGA   CTGGGAGCCC   GGCTCCGAGT   AACTGCTCCA   AACTGCTCCA   ACGAAGGGGG   CTCGTGATCG   CCAGGGGGCG   CTGTGATCG   CCAGGGGGCCA   GGGGAGACAA   CCCCGAGGCCC   CGGGAGCCCA	CCTGGACAGC CAGGCCTGAG CAGGCCTGAG GTTCTGAGGC CAGCCGCAGC GATCACCCC CCTGCTAGGC GCTGCCCCAA CAGTGTGTAG GGACAGAGAA ACCACTGCG GAGGCACCGA CAGTGTGTGA CAGTCTGTGT CAGTGTGTGA CAGTCTGTGT CAGTCTTTGTTAG CAGTCATTGA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGCTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGTGTGT CGCCGGAGCATCGCAC CGCACGGTACGCAC CGCACGGAGCGCGCGCGCGCGCGCGCGCGCGCG	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGGAGG GTCTTGAGGC CCGTCCTGCA GGCTAGCAGCC GCTTACGCC GCTTACGCA ACCCTGGTC ACCCAGCCA ACCCTGTGTC CAGCACCAGCA ACCCTGTGTC CAGCACCAGCA CACTGGGTAT GGCTTAATCA GCCTAATCA CCCTCCAGC AGCCCCAACC CCGCCCAACC CCGCCAACC CCGCCAACC CCGCCAAACC CTGCCTAATCA AGCCCAAACC CCGCCTCAGAAG CCCCAAACC CTGCTGAAAG	120 180 240 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	ACCTGRGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA TGAAGGAGGC ACATTGCCCA TGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAAGTGCAG GGTGGTTTCT TATGTGTGAA ACGTCACCAC ACGTCACCAC ACGCTGACCACA ACGTCACCAC	II   GGCCCTTCCC CCCAGCGCCG CCCACTCTCC TCTCTTCTC TCTGSTAGC CTGGGGGCC TCTCACCTTC GTACCAGTG GGCGGAG CCTCAATGGC GGCAGAGCGGG CTGCATCGTC GGCCAGAGG CCGGGGAGC CTCAGGGGGG CTCAGGGGAG CCTGGGTGGG CTCAGGGGAG GGAGCAGAG GGAGCAGAG GGAGCAGAG CGTGGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGAGCAGGAG CGTGGCAGGAA CCTGGGCGGAA	21   CTCGGCTTTG   CTCCACCAGE   GGTGCTGGCCA   TGGGTTCCGG   CTCGGGGCCC   GGTTCCGGGCC   GGTCCGAGT   CTGGGGGCC   CTAGCAAGT   AACTGCTCCA   AACTAGGGCG   CTGGCAGAGGCG   CTCGTCATCG   CTCGTCATCG   CTCGTCATCG   GGTGAGACAA   GGTGAGGCCA   GAGGAGCAA   GAGGAGCAA   CCCCGACGCC   CCCCCGCACGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCGCGCGCC   CCCCCCGCGCCC   CCCCCCCGCCCC   CCCCCCCGCCCC   CCCCCCCCCC	CCTGGACAGC CAGGCCTGAG GTTCTGAGGG CAGCCGCAGC AGCTGCCGCA AGCTGCCCCAA CAGTGTGTGA GCTGCCCAA ACCACTGCGC ATGGGACA ATGGGACCT ATGTGTTTA ATGTATCAA CAGTCATTGT ATGTATCACAC CAGGGCCT CAGGGACCCAA ATGGGACCT ATGTGTCGAGC TCATTGTTTG ATGTATCAAA CAGTCATTGT CAGGACCCT CAGGAGAGAACAC CAGGAGACCCA CAGGAGACCCC CAGGAGATACCT CCCGGAGGCTT CCCGGAGGCT CCCCGAGGGCT CCCCGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCGGAGGCCT CCGGAGGCCT CAGGCCTCAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCCGGAGGCCT CAGGCCTCAGGCCT CCCGGAGGCCT CCCGGAGGCCT CCGGAGGCCT CCCGGAGGCCT CCCGGAGGCT CCCGGAGGCCT CCCGGAGGCCT CCGGAGGCCT CCGGAGGCT CCGGAGGCCT CCGGAGGCT CCGGAGGCT CCGGAGGCCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGGCT CCGGAGCCCAA CCGGAGCCCAA CCGGAGCCCAA CCGGAGCCCAA CCGGAGCCCAA CCGCGAGCCCAA CCGCGAGGCCT CCGGAGGCCT CCGGAGGCCT CCGGAGCCCAA CCGCGAGCCCAA CCGCGAGCCCAA CCGCGAGCCCAA CCGCGAGCCCAA CCGCGAGCCCAA CCGCGAGCCCAA CCGCAA CCGCAA CCGCAA CCGCAA CCGCAA CCGCAA CCGCAA CCCCCAA CCCCCC	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGGCTGG CTGAGACCGAC CCCAGCTCTGG GTGCAGTCTGC CCCAAATGTGT CGCCGTGCTGC CGAGGAACGAC CCCAGCTCTGC CGCGTGCTGC CGCGTGCTGC CGCGTGCTGC CGCGGGAGGATGT CAGGGGAATGT CAGCAGCTCC CTCCACAGTT GGTGATCGT CGCGGGAGG CGCCTGCAG CGCGGGAGG CGCGGGAGG CGGGGAGGACG CGGGGGAGG	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGAGG GTCTTGAGGC CCTCCTGCA GCTACCAGCCA ACCCTGTGTC GCCCAGCCACCA ACCCTGTGTC GCCCAGCCACCA ACCCTGTGTC GGCTGACCAGCA CACTGGCTAT GGCCTAATCA CCCTTCCGG GCCCCTCCGG GCCCCTCCGG CCCCTGCAGC CCCTGCAGCACCC CCCTGCAGCACCC CTGCTCCAGC CCCCTGCGGTAT CGCCTAAACC CCTGCTGAAAGC CCCCTGCAGCACCCCGG CCCCTGCAGCACCCCGGCTGCGGCTG	120 180 240 300 360 420 660 660 720 780 840 900 1020 1080 1140
50	ACTGRGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGGACGA AGATTGCCCA AGGACGACTTCCA CCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCA AGGTCACA AGGTCACACA AGGTCACCA AGGTCACCA AGGCTCCCC GCTCCAGCCC CCAGGTCCCA AGGCTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCCAGGTCCCC CCCAGGTCCCC CCCAGGTCCCC CCCGTCCT CCCCGTCCT CCCCGTCCT CCCCCGTCCT CCCCCTCCTCCT CCCCCTCCTCCT CCCCCTCCT	II   GGCCCTTCCC CCCAGGGCCGC CCCAGGGCCGC CCCAGGGCCCG TCTCTTTCTC TCCTGCTAGC CTGGGGGGCC TCTCACCTTC GTACCCAGTG CTGCAGGGGCC CTGCATGGC GGCCAGAGC CCTGGCTGGGG CCCGGGGACC CTGGCTGGGG CCCGGGGACC CTGGCGGGAC CCTGGCGGAC CCTGCCGGGAC CCTGCCCGG AGAAGAAAG GGAGGCAGAA CGTGCCGGAA CCTCCAGTGC TTCCCATGCG TTCCCATGC TTCCCATGCG TTCCCATGCG TTCCCATGCG TTCCCATGCG TTCCCATGCC TTCCCATGCG TTCCCATGC TTCCCATGCC TTCCCATGC TTCCCATGC TTCCCATGC TTCCCATGC TTCCCATGC TTCCATGC TTCA	21   CTCGGCTTTG   CTCCACCAGE   TGCTGCTCGGCTTTG   TGCTGGCCA   TGGGTTCCGG   CTCCCTGGA   CTGGGAGCCC   GGCTCCGAGT   AACTGCTCCA   AACGAAGG   GTGCAGAAGG   CTAGCAGAGG   CTGCAGAGG   CTGTGATCG   CCAGGGGGG   CCAGGAGGCCA   CCAGGAGGCCA   CCAGGAGGCCA   CCAGGAGGGGAGGGGGAGGGAGGGAGGGGGGGGGGGGG	CCTGGACAGC CAGGCCTGAG CAGGCCTGAG CAGCCGCAGC CAGCCGCAGC CAGCCGCAGC CAGCCGCAGC CAGCCCCAA CAGTGTGTACACC CAGCCCCAA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTCATGCC CAGCCCCTAC CAGCCTCCCC CAGCCCTCCCC CAGCCCCTCCCCCCCCCC	TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT GCCGTGTGT GCCGTGTGT GCCGTGTGT GCGCTGTGT GCGCTGTGT GCGCTGTGT GGCGTGCCG GAGTCAGGAC GGAGGAATGT GTGATCGTCA GGCGGAGG GGGGGCTCCC GGGGGCTCCC GGGGGGCTCCC GGGGGGCTCCC CTGGGGGACGG CTGGGGGACGG CTGGGGGACGG CTGGGGGACGC CTGGGGTAGG CTGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGGGGGACGC CTGGTGGGGACGC CTGGGGGTAGG CTGGGGTAGG CTGGGGTAGG CTGGGGTAGG CTGGTGGGGTAGG CTGGGGGTAGG CTGGGGGACGC CTGGGGGACGC CTGGGGGACGC CTGGGGGACGC CTGGTGGGTAGG CTGGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACCC CTGGGGACCC CTGGGACCC CTGGGACCC CTGGGGACCC CTGGGACCC CTGGGGACCC CTGGGACCC CTGGCC CTGCC CTCC CTC CTCC CTCC CTCC CTCC CTCC CTCC	CCCCCAGGA CAGCCCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGCA CACCAGGA CACCAGA CACCAGGA CACCAGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGA CACCAGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGGA CACCAGA CACCAGGA CACCAGA CACCAG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1200 1260
50 55 60	ACTGRGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGGACGA AGATTGCCCA AGGACGACTTCCA CCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCA AGGTCACA AGGTCACACA AGGTCACCA AGGTCACCA AGGCTCCCC GCTCCAGCCC CCAGGTCCCA AGGCTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCAGGTCCCC CCCAGGTCCCC CCCAGGTCCCC CCCAGGTCCCC CCCGTCCT CCCCGTCCT CCCCGTCCT CCCCCGTCCT CCCCCTCCTCCT CCCCCTCCTCCT CCCCCTCCT	II   GGCCCTTCCC CCCAGGGCCGC CCCAGGGCCGC CCCAGGGCCCG TCTCTTTCTC TCCTGCTAGC CTGGGGGGCC TCTCACCTTC GTACCCAGTG CTGCAGGGGCC CTGCATGGC GGCCAGAGC CCTGGCTGGGG CCCGGGGACC CTGGCTGGGG CCCGGGGACC CTGGCGGGAC CCTGGCGGAC CCTGCCGGGAC CCTGCCCGG AGAAGAAAG GGAGGCAGAA CGTGCCGGAA CCTCCAGTGC TTCCCATGCG TTCCCATGC TTCCCATGCG TTCCCATGCG TTCCCATGCG TTCCCATGCG TTCCCATGCC TTCCCATGCG TTCCCATGC TTCCCATGCC TTCCCATGC TTCCCATGC TTCCCATGC TTCCCATGC TTCCCATGC TTCCATGC TTCA	21   CTCGGCTTTG   CTCCACCAGE   TGCTGCTCGGCTTTG   TGCTGCCCA   TGGGTTCCCGG   CTCCCTGGA   CTGGGAGCCC   GGCTCCGAGT   CTGACGGGA   CTAAGCAAGT   AACTGCTCCA   ACGAAGGGG   GTGCAGAAGG   CTCGTGATCG   CCAGGGGGGAG   CCAGGAGGCCA   CCAGGAGGCCA   CCACGGAGGCCA   CCACGGAGCCCA   CCACGGAGGCCA   CCACGGAGCCCA   CCCACGGAGCCCA   CCACGGAGCCCA	CCTGGACAGC CAGGCCTGAG CAGGCCTGAG CAGCCGCAGC CAGCCGCAGC CAGCCGCAGC CAGCCGCAGC CAGCCCCAA CAGTGTGTACACC CAGCCCCAA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTGTGTACA CAGTCATGCC CAGCCCCTAC CAGCCTCCCC CAGCCCTCCCC CAGCCCCTCCCCCCCCCC	TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC AATGGCGTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT GCCGTGTGT GCCGTGTGT GCCGTGTGT GCGCTGTGT GCGCTGTGT GCGCTGTGT GGCGTGCCG GAGTCAGGAC GGAGGAATGT GTGATCGTCA GGCGGAGG GGGGGCTCCC GGGGGCTCCC GGGGGGCTCCC GGGGGGCTCCC CTGGGGGACGG CTGGGGGACGG CTGGGGGACGG CTGGGGGACGC CTGGGGTAGG CTGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGGGGGACGC CTGGTGGGGACGC CTGGGGGTAGG CTGGGGTAGG CTGGGGTAGG CTGGGGTAGG CTGGTGGGGTAGG CTGGGGGTAGG CTGGGGGACGC CTGGGGGACGC CTGGGGGACGC CTGGGGGACGC CTGGTGGGTAGG CTGGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACGC CTGGGGACCC CTGGGGACCC CTGGGACCC CTGGGACCC CTGGGGACCC CTGGGACCC CTGGGGACCC CTGGGACCC CTGGCC CTGCC CTCC CTC CTCC CTCC CTCC CTCC CTCC CTCC	CGCAGGGCCC CTGCCAGACA ACACCGAGGC AGTTCCTCTG GGCATGAGG GTCTTGAGGC CCTCCTGCA GCTACCAGCCA ACCCTGTGTC GCCCAGCCACCA ACCCTGTGTC GCCCAGCCACCA ACCCTGTGTC GGCTGACCAGCA CACTGGCTAT GGCCTAATCA CCCTTCCGG GCCCCTCCGG GCCCCTCCGG CCCCTGCAGC CCCTGCAGCACCC CCCTGCAGCACCC CTGCTCCAGC CCCCTGCGGTAT CGCCTAAACC CCTGCTGAAAGC CCCCTGCAGCACCCCGG CCCCTGCAGCACCCCGGCTGCGGCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1220
50 55 60	ACCTGRETCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGAGA TGAAGGAGGC ACATTGCCCA TGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCAC AGGCCACTT TATGTGAA ACGTCACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC CCACGTGCCAC CCCACGTGCCAC CCCCCGGGCCAC CCCCCGGGCCAC CCCCCGGGCCAC CCCCCTGGGCCCCCCCCCC	II  GGCCCTTCCC CCAGCGCCG CCCACTCTCC CCCAGCGCCC CCCACTCTCC TCTCTTTCTC TCTCACTC CTGGCAGC CTGGCAGCG CTCAGCGCAG CCTCAATGGC CTGCAGCGC CTGCAGCGCAG CCCGGGACC CTGCATGGC AAGAAAAA GGTGCCGGT AAGACTCTGCA CCTCCAGTGC TCCAGTGC TCCAGTGC TCCAGTGC TCCTCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CTCCAGTGC CCTCCAGTGC CTCCAGTGC CCTCCAGTGC CCTCCAGTGC CCTCCAGTGC CCTCCAGTGC CCTCCAGTGC CCTCCAGTGC CCTCCAGTCC CCTCCAGTGC CCTCCAGTCC CCCCCCAGAC CCCCCCAGAC CCCCCCAGAC CCCCCCAGAC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCAGCC CCCCCCCC	21   CTCGGCTTTG   CTCGGCTTTG   CTCGCCAG   TGCTGCTCGG   CTCTCTGGGCA   TGGGTCCAG   GGTCCGAGT   CTAGCGGCA   ACTAGCAGCA   CTCTCCCG   CTCGCAAGCCG   CTCGTCATCG   CTCGTCATCG   CCAAGGGGT   CCACGGAGC   CCCGACGGGG   CCCGACGGGG   CCCGACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CCTGGACAGC CAGGCTGAG GTTCTGAGGC CAGCCCAGGC GTTCTGAGGC CAGCCCCAGC GCTGCCCCAA CAGTGTGTAGC GGACAGGAA ACCACTGCC GAGGCTCGGA ATGGACCC ATGGGACCCT ATGGACCCT ATGGACCCT ATGGACCCC AGGTCTGTACC CAGCTGGGCC CCTGCGGGCCCT CCTGGGGCCCT CCTGGGGCCCT CCTGGGGCCCT CTGCGGCCCT CCTGGGGCCCT CTGCGGCCCT CTGCGGCCCT CTGCGGCCCT CTGCGGCCCT CTGCGGCCCT CCTGGGGCCCT CCCCTGGGGCCT CCCCTCGGGCCCT CCCCTCGGGCCCT CCCCCTCGGGCCCT CCCCCCCC	I TCCTGCCTCC CCCCCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGC CCCAGCTCTG GTGCAGTCCA ACCCTGCCCT CCCAATGTGT CGCGTGCTGC GAGTACGAC GAGTACGAC GAGTACGAC GGAGCACCC GCACAGTTCGC GCACAGTTCGC CTCCACAGTT GGTGATCGTC GCCTGCACG CTCACAGTTCTCC GCCTCCACAGTT CTCACAGCTCC GTGACGACCC GGAGCACCC GGAGCACCC GGAGCACCC GCAGGACCC GCACGCAC	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GCTTTCAGGC CCGTTCCTGCA GGTTATCGTG CCAGGCACGCA GGTTATCGTG ACCCAGCA GGCTGCAGCC CGTTACGCCA ACCCTGGCTA CGCTAATCA CCCTTGGCTA TCGCCTAACC CGCTCCGGCTG AGCCCACGC CGCTGGAACC CTGCGCTG GCCTGGGACG CGCTGGGACG CGCTCGGCTG CGCTGGGACG CGCTGGACC CGCTGGACC CGCTGGACC CGCTGGACC CGCTGGACC CACACCCAGC CACACCCAGC	120 180 240 300 360 420 480 540 660 720 840 900 1020 1140 1260 1320 1380 1440
50 55 60	ACTGRICC CCCCCGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGAGGG ACATTGCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC CCAAGTGCAG GGTGGTTTCT TATGTGTAA AGGTAACACAC ACGTCACCAC ACGTCCCCC GCTCCCCCCAGGCC CCCCCCGGGCCA CCCCCCCGGCC CCCCCCGGGCCA CCCCCCCAGGCCCC CCCCCCAGGCCC CCCCCCAGG	11   GGCCCTTCCC CCCAGGGCCGC CCCAGGGCCGC CCCAGGGCCCG TCTCTTTCTC TCCTGCTAGC CTGGGGGGC TCTCACCTTC GTACCCAGTG CTGCAGGGGCC CTGCATGGC CGCAGAGCCGG CCCCAGGGACC CTGCCTGGTGGC CTCAGGGACC CTGCCTGGTG CCCAGGGACC CTGCCCAGGAC CCTCAGGACC CTGCCCAGGAC CCTCAGGAC CCTGCCCGGAAA CCTCCAGGGAC CCTCCAGGGAC CCTCCAGGGAC CCTCCAGGGAC CCTCCAGGGAC CCCAGGAC CCAGCCCAGAA	21  CTCGGCTTTG  CTCCACCAG  TGCTGCTCGG  TCTGGCCA  TGGGTTCCGG  CTGGGAGCCC  GGCTCCGAGT  CAGGAGGCC  CAGGAGGGGG  CTAACCAAGT  AACTGCTCCA  AACTGCTCCA  ACGAAGGGGG  CTGCAGAGG  CTGCAGAGG  CTGCAGAGG  CCAGGAGGCC  CCAGGCC  CCAGGCCATG	CCTGGACAGC CCTGGACAGC CAGGCCTGAG CAGCCCAGC CAGCCCAGC CAGCCCCAGC CAGCCCCAA CAGTGGTACACC CAGCCCCAA CAGTGGTACAC CAGTGGTACAC CAGTGGTACAC CAGTGGTACAC CAGTGGTACAC CAGTGGTACAC CAGTGTACAC CAGCTGCAGAA ACCACTCCCC CAGAGCAC ACCCCCATT AATGAATACCA CAGTCATTGA ACAGCATACCC CCCGAGGCT CGCCCCCCCC CCCCCAGCCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCACCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCACCC CCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCCAGCC CCCCCAGCC CCCCCCAGCC CCCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCCAGCC CCCCCAGCC CCCCAGCC CCCCACACC CCCCACC CCCCCC	TCCTGCCTCC CCCCTCTGTG ACAGCTTGTC AATGGCGTG CTGAGCCTGA CAGAACCGAC CCCAGCTCTGG GTGCAGTCCCA ACCCTGCCCT CCAAATGTGT CGCCGTGTGT CGCCGGAGC CGGGGGGCTCCC CGGGGGGGGGTCCG CTCCACGTT CTCCACGTTCGGGGTAGG CCTGCGGGGGGTCCG CTGCGGGGGGTCGGGGGGTGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGTGTGGGGTAGG CTGGGGGTAGG CTGGGGGTAGG CTGGGGGGGGTAGG CTGGGGGGGGGTAGG CTGGGGGGGGGG	COCCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGCA ACACCAGCAC ACACCACACCAC ACACCACACC ACACCACACC ACACCAC	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560
50 55 60 65	ACCTGRETCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA TGAGGAGGC ACATTGCCCA TGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC CCAGTGCAG ACGTGTTCT TATGTGTGAA ACGTCACCAC ACGTGTCCA ACGTCTCCCACGCC AGGCTTCCC CCACGTGCCA GCTTCCTCCACGCC AGGCTTCCCACGCC AGGCTTCCCACGCC ACGCTCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACCCCACGCCCACCCACCCCACGCCCACCCCACCCCACCCACCCACCCACCA	II   GGCCCTTCCC CCAGCGCCG CCCACTCTCC CCCAGCGCCG CCCACTCTCC TCTTCTTCTC TCTGSTAGC CTGGGGGCCT CTGCAGGGCCG CTGCAGGGGCCT GTACCCAGTG GCCAGAGGGCCG CTGAATGGC GGGCAGAGG CCTGAATGGC CTGGGGGGAG CCTGAGGGGAG CCTGAGGGGAG CCTGGGGGAG CCTGGGGGAG CCTGGCGGGAG CCTGGCAGGG CCTGCGGGGAG CCTGCAGGGG CCTGCCAGGG CCTGCAGGGGAA CCTGCGGAA CCTGCGGAA CCTGCGGAA CCTGCGGAA CCTGCAGGG TCCTAGGGAG CCAGCAGAG CCAGCAGAG CCAGCAGAG CAGCACAGAC CAGCACAGGCC CAGCACAGGCC CGGCCAGAG	21 CTCGGCTTTG CTCCACCAG GTGTGCTGG TGCTGCTGG TGCTGCTGG CTCGGGGCCC GGCTCCGGG CTGGGGCCC GGCTCCGGG CTAGCAGGC CTAGCAAGT AACTGCTCCA ACGAGGGGG CTGGGAGAGG CTGGGAGAGG CTGGGAGAGG CTGGGAGAGG CTCGGAGG CCCGAGGC GGGGGAGGG AGGAGGGGG AGGAGGGGG AGGAGGGGG GGGGGG	CCTGGACAGC CAGGCTGAG GTTCTGAGGC CAGCCCAGG GTTCTGAGGC CAGCCCCAA CAGTTCACCCCA CAGTTGTGAA ACCACCCC GAGGCACCAA ATGGACCCT ATGGACCCT ATTATTTTT ATGTATTAT ATGATTAT CAGTCATT CAGGACCCT CAGGCCCT CCTGGGCCCT CCTGGGGCCT TCCCCCTAGGCCCT CCTGAGGCCT CCCCAGGCCT CTCCCCCTCAGGCCT CTCCCCCTCAAGCCC CCTCAAGCCC CCCCAAGCT CCCCAAGCCC CCCAAGCCC CCCAACCC CCCAAGCCC CCCAAGCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAAGCCC CCCAACCC CCCAACC CCCAACCC CCCAACC CCCAACCC CCCAACCC CCCAACCC CCCCAACCC CCCAACCC CCCAACCC CCCAACCC	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG CAATGCCTTGA CCGAGCTCTG CTGAGCCTGA CCCAGCTCTG CTGCAGTCCA ACCCTGCCCT CCAATGTGT CGCGTGCTGC CGCGGGGGGCCCC CGCGCGGGGGGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGGC GGCTGGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGCAGGAGG	120 180 240 300 360 420 480 540 660 720 720 780 840 960 1020 1140 1250 1320 1340 1550 1550
50 55 60	ACCTGRETCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGAGA AGGAGAGAGA AGGAGCACTA TGGCCTGCG AGAACTGCCC AGAACTGCCC AGAACTGCAC AGGCACTT TATGTGAAA AGGTCACCAC ACTGACCCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGCCAC ACTCCAC ACTGCCAC ACTGCCAC ACTGCCAC ACTCCAC ACTCC	II	21  CTCGGCTTTG  CTCCACCCAG  TGCTGCTCGG  TGCTGCTCGG  CCTCCTGGAGCC  GGCTCGAGT  CTAAGCAGT  AACTGCTCCA  AACTGCTCCA  AACTGCTCCA  ACGAAGGCC  CTCGGAGAGCC  CTAGGAGAGCC  GGTCAAGGCC  GGTCAAGGCC  CTCGTCATCC  ACCAAGGGTI  GGTGAGGCCAG  GGGGACTGG  GGGGACTGG  GGGGCCAGT  GCCACGGGC  CCGGGGCCCAGT  GGGGCCCAGT  GGGGCCCAGT  GGGGCCCAGT  GGGCCCACT  ACCACACCC  CCACACCC  ACCACACCC  ACCACACC  ACCACACC  ACCACACCC  ACCACACC  ACCACC	CCTGGACAGC CCTGGACAGC CAGGCCTGAG CAGCCCAGGC CAGCCCAGGC CAGCCCAGC CAGCCCCAA CAGTTCACACC CAGCCCCAA CAGTTGTGAA ACCACCCC CAGCCCCAA ATGGACCCC CAGCTGGGAC ATGGACCCC CAGCTCATCC CAGCCCCACCCC CCTGAGCCC CCTCACACCC CCTCACACCC CCTCACACCCC CCTCACACCC CCTCACACC CCTCACACCC CCTCACACC C	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	COCCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGGACA ACACCAGCA ACACCAGCAC ACACCACACCAC ACACCACACC ACACCACACC ACACCAC	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65	ACCTGRETCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGAGA AGGAGAGAGA AGGAGCACTA TGGCCTGCG AGAACTGCCC AGAACTGCCC AGAACTGCAC AGGCACTT TATGTGAAA AGGTCACCAC ACTGACCCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGACCAC ACTGCCAC ACTCCAC ACTGCCAC ACTGCCAC ACTGCCAC ACTCCAC ACTCC	II	21 CTCGGCTTTG CTCCACCAG GTGTGCTGG TGCTGCTGG TGCTGCTGG CTCGGGGCCC GGCTCCGGG CTGGGGCCC GGCTCCGGG CTAGCAGGC CTAGCAAGT AACTGCTCCA ACGAGGGGG CTGGGAGAGG CTGGGAGAGG CTGGGAGAGG CTGGGAGAGG CTCGGAGG CCCGAGGC GGGGGAGGG AGGAGGGGG AGGAGGGGG AGGAGGGGG GGGGGG	CCTGGACAGC CCTGGACAGC CAGGCCTGAG CAGCCCAGGC CAGCCCAGGC CAGCCCAGC CAGCCCCAA CAGTTCACACC CAGCCCCAA CAGTTGTGAA ACCACCCC CAGCCCCAA ATGGACCCC CAGCTGGGAC ATGGACCCC CAGCTCATCC CAGCCCCACCCC CCTGAGCCC CCTCACACCC CCTCACACCC CCTCACACCCC CCTCACACCC CCTCACACC CCTCACACCC CCTCACACC C	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGGC GGCTGGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGCAGGAGG	120 180 240 300 360 420 480 540 660 720 720 780 840 960 1020 1140 1250 1320 1340 1550 1550
50 55 60 65	ACCTGRETCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAG TGGTGCTGTA AGGAGGACGA TGAGGAGGG ACATTCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGGAGCTGCA GCTGGTGTTCT TATGTGGAA ACGTCACCAC ACTGACCCAC AGCTGTCCA ACTGCCCCAAGG CCTCCTGGGG CCTCCTGGGG GGCCTCAGCA CAGTGTGTCA ACTGTGCACAC ACTCCCAAGA CTCCCCAAGA CCTCCTGGGG GGCCTCAGCA CAGTGTGTCT AATATCTTGT AATATCTTGT	II   GGCCCTTCCC CCAGCGCCG CCCAGCGCCG CCCACTCTCC TCTTCTTCTC TCTGTTAGC CTGGGGGCT TCTCACCTTC GTACCAGTG GCCCAGGGCCG CCTCAATGGC GCCAGGGGCC GCCAGGGGCC CTGGCTGGT CTCACGGGAG CCTGGGGAG CCTGGGGAG CCTGGGGAG CCTGGGGAG CCTGGGGAG CCTGGCCGGG AAGAAGAAAA CGTGGCCAGG CCTGGCAGG CCTGGCAGG CCTGGCAGG CCTGGCAGG CCTGGCAGG TTCCCATGG TTCCTCATGG TTCCTCAGGAG TTCTATTGTG TTCTCCTCAJ	21   CTCGGCTTIG   CTCGGCTTIG   CTCCACCAG   GGTGCTGGG   CTGGGAGCCC   GGTTCCGGG   CTGGGAGCCC   GGTCCGAGT   AACTGTCCA   AACTGTCCA   CAGGAGGGGG   GTGCAGAAGG   CTGGCATCG   CCAGGGGGC   CTGGTCATCG   CCAGGGGGG   GGGGAGGGG   GGGGAGGGG   GGGGAGGGG   CCAGGGGCCAGGGG   CCAGGGGCCAGGGC   CCAGCGACCC   CCACCGAGCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   CCACCACCCC   AAAAAAAAAA	CCTGGACAGC CCTGGACAGC CAGGCCTGAG CAGCCCAGGC CAGCCCAGGC CAGCCCAGC CAGCCCCAA CAGTTCACACC CAGCCCCAA CAGTTGTGAA ACCACCCC CAGCCCCAA ATGGACCCC CAGCTGGGAC ATGGACCCC CAGCTCATCC CAGCCCCACCCC CCTGAGCCC CCTCACACCC CCTCACACCC CCTCACACCCC CCTCACACCC CCTCACACC CCTCACACCC CCTCACACC C	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGGC GGCTGGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGCAGGAGG	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65	ACTGGGTCC CCCCTGGTG CCCCTGGTG GGATTCTCTT CTGGAGTTCA TGGTGCTGTA AGGAGACGA ACATTGCCCA TGGGCCTGGG CAGGCCACTT CCTCCAGCCC AGAACTGCAG AGACTGGTTTCT TATGTGTGAA AGGTACCCAC AGGCTACTT CCCCCAGGG GCTTCCTCCAGCCC CCCCCCGGGG CCTCCCCCAGGG CCTCCCCCAGGG CCTCCCCCAGGG CCTCCCCCAGGG CCTCCTGGGG CCCCCTGGGG CCCCCTGGGG CCCCCTGTCT AATATCTTGT  Seq ID NO:	11 GGCCCTTCCC CCAGGCGCG CCAGGCGCG CCAGGCGCG TCTCTCTTTCT TCTGTTAGC TCTGCTAGC CTGGGGGGG CTGCCCGGGGGGC CTGCATGGC CGGGGGGCC CTGCATGGC CCGGGGGAC CTGCAGGGGG CCTGGCTGGT TCTCAGGGAGC CTGGCGGAA GGAGCAGAG GGTGCCGG AGGCCGG AGGCCGG TTTCCCTGGGGAC CTGGCGAAA CCTCGCGGAAA CCTCCAGGGC TTCTAGGGAC TTCCCTGGGGAC TTCCCTGGGGAC TTCCCTGGGGAC TTTAGTGGA TCTATTGTG TTCTCCTCAGG	21  CTCGGCTTTG CTCCACCAG TGCGGTTCCGG TTCTGGCCA TGGGTTCCCG TCTGGAGCCC GGCTCCGAG CTGAGCAGCC GGCTCCGAG CTGAGCAGC CTAAGCAAGT AACTGCTCA ACGAGCGCA CTAAGCAGC CTCGAGCGCA CTCGAGCGCA CCACGGAGCC CCACGCAGCC CCACCGAGCC CCACCGAGCC CCACCGAGCC CCACCGAGCC CCACCGAGCC CCACCGCACC CCACCGAGCC CCACCGAGCC CCACCCAC	CCTGGACAGC CAGGCTGAG GTATCACCC CAGCCCAGG GTATCACCC CCTGCACAG GATCACCCC CCTGCACAG GATCACCC CCTGCACAG CAGTGTGTACA CAGTGTGTACA CAGTGTGTAC CAGGCCCCAC ATGGGACCCA ATGGGACCCT CATGCT ATGTATCAC CAGTCATCC CAGCCCCAC CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CAAAAAAAAAA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGGC GGCTGGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGCAGGAGG	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65 70	ACCTGRETCE CCCCTGGTG CGGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGCACA AGGAGCACA ACATTCCCA AGGACTACA CCCCAAGTCCA AGGACTACA ACGTCACCA ACGTCCTCACA ACGTCACCA ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCA	11   GGCCCTTCCC CCAGGGCCG CCAGGGCCGG CCCAGCTCTC TCTCTTTCTC TCTGCTAGC CTGGGGGCG TCTCACCTTC GTACCCAGTG CTGCAGGGCC GCCAGGGCCG GCCAGGGCCGGG CCTCATGGC GGCCAGAGG CCTCAGTGGG CCCGGGAAG CCTCAGGAAA GGAGAAAA GGAGACAGAA CCTCCAGTGC TTCCCAGTGC TTCCCAGTGC TTCCCAGTGC TTCCCAGGAAC CCTGAGCAAA CCTCCAGGAC TTCCCATGCG TTCCTAGGAC CTTCAGGAGC TTCCTAGGAC TTCCTAGGAC TTCCTAGGAC TTCCTATGGG TTCTTAGTGGAT TTCTTATTGGT TTCTCTCAJ  118 DNA SG Lid Accessic	21  CTCGGCTTTG CTCCACCAG TCTGGCCCA TGGGTTCCGG TTCTGGCCCA TGGGTTCCGG CCTCCCTGGA CTGGGAGCCC GGCTCCGAGT CAGGAGGGG CTAAGCAAGT AACTGCTCCA ACTGGAGGGGG CTGGAGGGG CTGGAGGGG CTGGTGATGC CCAGGGGGGG CCAGGGGGGGG	CCTGGACAGC CAGGCTGAG GTATCACCC CAGCCCAGG GTATCACCC CCTGCACAG GATCACCCC CCTGCACAG GATCACCC CCTGCACAG CAGTGTGTACA CAGTGTGTACA CAGTGTGTAC CAGGCCCCAC ATGGGACCCA ATGGGACCCT CATGCT ATGTATCAC CAGTCATCC CAGCCCCAC CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CAAAAAAAAAA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGG GGCATGGAG GGTTATCGTG CCAGGCACGAG GGTTATCGTG ACCCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GCTGCAGCA GCCTGCAGCA GCCTGCAGC CACCTGGCAGCC ACCCTGGCAGCC ACCCTGGCAGCC ACCCTGGCAGC ACCCTGGAACC CGCGTGCAGC ACCCCGGGAGC CGCGCTGGAGC CGCGCTGGAGC CGCGCTGGAGC CGCGCTGGAGC CCCTGGGACG CCCCGGCCTGAACC CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGACG CCCTGGGGACG CCCTGGGACG CCCTGGACG CCCTGGGACG CCCTGGACG CCCTGGAC CCCTGGAC CCCTGGAC CCCTGGAC CCCTGCAC CCCTGCAC CCCTGCAC CCCTGCAC CCCCTGCAC CCCCCCC	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65	ACTGGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCTGGAGA TGGTGCTGTA AGGAGAGA TGAAGGAGGA TGAAGGAGGA GAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGGAGCACTT CCTCCAGCCC AGAACTGCCC AGGAGTCACACA CCTAAGTCACACA ACTGACCCAA ACTGACCCAA ACTGACCCAA CCTCCCAGGG CCTCCTGGGC GGCCTCAGCA CAGTGTGTCT AATATCTTGT AATATCTTGT Seq ID NO: Nucleic AC Coding sec	II   GGCCCTTCCC CCAGCGCCG CCCAGCGCCGC CCCACTCTCC TCCTGCTAGC CCTGCTGCT CTGCTGCT CTGCTGCT GTACCCAGTG CTGCAGGGCC CTGCAGGGCC GCCAGGGCCGG CCCAGGGCCGG CCCAGGGCCGG CCCGGGGAC CCTGGCTGGT CTCACGGGAG CCTGGCGGGA CCTGGCGGGA CCTGGCGGGA CCTGGCGGGA CCTGGCGGGA CCTGGCAGGC CTGCCAGTGC TCCATGGC TTCCCATGGC TTCCTCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGGC TTCCTCCATGC TTCCTCC TTCCTCCATGC TTCCTCCATGC TTCCTCCATGC TTCCTCCATGC TTCCTCCATGC	21   CTCGGCTTTG   CTCCACCAG   GTGCTGCTGGG   CTCGGCTGGG   CTGGGAGCCC   GGCTCCGAGT   CTGGGAGCCC   GGCTCCGAGT   AACTGCTCCA   CAGGAGGGGG   GTGCAGAAGG   CTGGCAGAGG   CTGGCAGAGG   CTGGCAGAGG   CTGGCAGAGG   CTGGCAGAGG   CTGGCAGGGC   CTGGCATCG   CCAGGGGCG   CGGGAGGGG   AGGAGAGGG   AGGAGAGGT   ACCACCGAGCC   CCAGCGAGCC   CAGGAGAGGT   CCACCGAGCCC   CAGGAGAGGT   CCACCGAGCCC   CAGGAGAGGT   CCACCGAGCCC   CAGGAGAGGT   CCACCACCGCC   CAGGAGAGGT   CCACCACCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCTGGACAGC CAGGCTGAG GTATCAGGC CAGCCTAGG GTATCACCCC GAGCCCCAA CAGTTCACCCCAA CAGTTGTGAA ACCACCCC GAGCCCCAA ATGGACACCA ATGGACCCAA ATGGACCCT ATGTATTTC ATGTATTTC ATGTATTCATC CAGCCCCCCC CTGGGGCCT CCCGAGGCT CCCCAGCCCC CTGCCCCCCCCCC	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTG ACAGCTTGTG AATGCCTTGA CAGAACCGAC CCCAGCTCTG GTGCAGTCCA ACCCTGCCCT CCCAATGTGT CGCCGTGTGT CGCGTGCTGC CGCAGCTCTG CGCGTGCTGC CAGCTGCCGC CAGCTGCCGC CAGCTGCCGC CAGCGGAGCACCC CAGCGGGACC CAGCGGACCTGCAC CAGCGGACC CAGCGGACCTGCAC CAGCGGACCTGCAC CAGCGGACCTGCAC CACGGGACCTGCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGGACCTCCAC CACGGCACCTCAC CACGGCACCTCAC CACGCCAC CACCCAC C	CGCAGGGCCC CTGCCAGACA ACACCAGGG AGTTCCTCTG GGCATGGAGC GCTTTGAGGC CGTTCTGCA GGTTATCGTG CCAGCACA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA CACCTCTCGG AGCCCTCAGG AGCCCTCAGG CCCTGGGAGC GCTGTGAAACC GTGCTGAAACC GCTGTGAAACC GCCTGGGAG GCCTGGGAG CCCTGGGGCTG GCTGGGAGC TGGCTTAGC TGGGTTGCTG GGTTGCTG GGAGGTTGCTG GGAGGATGTA	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65 70	ACCTGRETCE CCCCTGGTG CGGATTCTCTT CTGGAGTTCA CTCCTGGAGA AGGAGCACA AGGAGCACA ACATTCCCA AGGACTACA CCCCAAGTCCA AGGACTACA ACGTCACCA ACGTCCTCACA ACGTCACCA ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCA ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCAC ACCTCACCA	11   GGCCCTTCCC CCAGGGCCG CCAGGGCCGG CCCAGCTCTC TCTCTTTCTC TCTGCTAGC CTGGGGGCG TCTCACCTTC GTACCCAGTG CTGCAGGGCC GCCAGGGCCG GCCAGGGCCGGG CCTCATGGC GGCCAGAGG CCTCAGTGGG CCCGGGAAG CCTCAGGAAA GGAGAAAA GGAGACAGAA CCTCCAGTGC TTCCCAGTGC TTCCCAGTGC TTCCCAGTGC TTCCCAGGAAC CCTGAGCAAA CCTCCAGGAC TTCCCATGCG TTCCTAGGAC CTTCAGGAGC TTCCTAGGAC TTCCTAGGAC TTCCTAGGAC TTCCTATGGG TTCTTAGTGGAT TTCTTATTGGT TTCTCTCAJ  118 DNA SG Lid Accessic	21  CTCGGCTTTG CTCCACCAG TCTGGCCCA TGGGTTCCGG TTCTGGCCCA TGGGTTCCGG CCTCCCTGGA CTGGGAGCCC GGCTCCGAGT CAGGAGGGG CTAAGCAAGT AACTGCTCCA ACTGGAGGGGG CTGGAGGGG CTGGAGGGG CTGGTGATGC CCAGGGGGGG CCAGGGGGGGG	CCTGGACAGC CAGGCTGAG GTATCACCC CAGCCCAGG GTATCACCC CCTGCACAG GATCACCCC CCTGCACAG GATCACCC CCTGCACAG CAGTGTGTACA CAGTGTGTACA CAGTGTGTAC CAGGCCCCAC ATGGGACCCA ATGGGACCCT CATGCT ATGTATCAC CAGTCATCC CAGCCCCAC CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTGCGCCCT CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CCTCACAGCC CAAAAAAAAAA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTGTGTC ACAGCTGCCC CCCAGCTCTTG GCCGTGTGT CGCGTGTGT CGCGTGCTGC GAGTCCAA ACCCTGCCCT GGAGCAACGAC GAGCAACGAC CCCACAGTTGT GGCGTGCTGC GGGGAGCAACGAC GGAGCAACGC CTCCACAGTTGT GGTGATCGTC GGTGATCGTC GGTGATCGTC GGTGATCGTC GTGAACGAC CTCACAGGTT GGTGATCGTC GTGAGCAACGC CTCACAGGTC GGGGGGACGC GGGGGGACGC GGGGGGTAGG CTGACAGACCC GTGGGGTAGG CTGACAGACCC GGGGGGTAGG CTGACGGTAGG CTGACGGTAGG CTGACGGTAGG CTGAGGCCG GGGGGGTAGG CTGAGGCTAGG CTGAGGCTGCG GGGGGGTAGG CTGCGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGGCTGCC GGGGGGTAGG CTGAGCTGAC GGGGGGTGGC CTCACAGACCC GGGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC GGGGGTGGC CTCACAGCCC GTGGGGTGGG	CGCAGGGCCC GGCAGGGCAGGAGA ACACCAGGG AGTTCTCTGGG GGCATGGAG GGTTATCGTG CCAGGCACGAG GGTTATCGTG ACCCAGCA GGCTGCAGCA GGCTGCAGCA GGCTGCAGCA GCTGCAGCA GCCTGCAGCA GCCTGCAGC CACCTGGCAGCC ACCCTGGCAGCC ACCCTGGCAGCC ACCCTGGCAGC ACCCTGGAACC CGCGTGCAGC ACCCCGGGAGC CGCGCTGGAGC CGCGCTGGAGC CGCGCTGGAGC CGCGCTGGAGC CCCTGGGACG CCCCGGCCTGAACC CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGGACG CCCTGGGACG CCCTGGGGACG CCCTGGGACG CCCTGGACG CCCTGGGACG CCCTGGACG CCCTGGAC CCCTGGAC CCCTGGAC CCCTGGAC CCCTGCAC CCCTGCAC CCCTGCAC CCCTGCAC CCCCTGCAC CCCCCCC	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65 70	ACCTGGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGAGGA AGGAGGAGGA TGAAGGAGGC CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGACTGCAC ACTGGCCTGCG AGGCTACTCACCAC ACTGACCCAC ACTGACCCAC ACTGACCCAC ACGCTGTTCCT CCACGTGCCA CCCCCACGTGCCA CCCCCACGGCC CACGTGCCA CCCCACGTGCCA CCCCACGTGCCA CCCCCACGGCC CACGTGCCA CCCCACGGCC CACGGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC C	11   GGCCCTTCCC CCAGGCCCG CCAGGCCCG CCAGCCCG CCAGCCCG TCTCTTTCTC TCTGCTAGC CTGGGGGGG CTGCACCAGCCGG CGCAGCCGG CCGCAGGCCGG CCGCAGGCCGG CCGCAGGCCGG CCGGGGACC CTGCTCGTG CCGGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCCAGAC CTGCCAGAC CTGCCAGAC CTTCAGGGAC CTTCAGGGAC CTTCCAGGGC CTCTAGGGAC CTTCCAGGGC CTCTAGGGAC CTCCAGGC CTCTAGGGAC CTCCAGGCC CTGCCAGAC CTCCCAGGCCC CTCTAGGGAC CTCCCAGGCCC CTCTAGGGAC CTCCCAGGCCC CTCCCAGCC CTCCCAGCC CTCCCCAGCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	21   CTCGGCTTTG   CTCCACCAGE   TGCTGCTCGG   TCTGGCCCA   TGGGTTCCGG   TCTGGCCCA   TGGGTTCCCGG   CTCCCTGGA   CTGGCGCAC   CAGGAGGCG   CTAGCGGCA   CAGGAGGCG   CTCGCTCCAC   CCAGGGGCCC   CCACGGGGCC   CCACGGGGCC   CCACGGGGCC   CCACGGGCC   CCACGGGGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGCC   CCCCGGCC   CCCCGGCC   CCCCGGCC   CCCCGGCCC   CCCCGCACGCC   CCCCGGCCC   CCCCGCACGCC   CCCCGCACGCC   CCCCGCACGCC   CCCCCGCC   CCCCCGCC   CCCCCGCC   CCCCCGCC   CCCCCCCC   CCCCCCCC   CCCCCCCC   CCCCCCCC	CCTGGACAGC CAGGCTGAG GAGCCCCAG GAGCCCCAG GATCACCC GAGCCCCAA CAGTCGTACCC GAGCCCCAA ACAGTGTGTAA ACACTGCCC GAGCTGGAGA ATGGGACCCA ATGGGACCCA ATGGGACCCA ATGGGACCCC CAGCTCATCC GAGCTCGAGC TCATTGTTC AAGATACCA CCCGAGCCT CCTGGGGCCT CCTGGGGCCT TGCCCCTCGG	I TCCTGCCTCC CCCCCTCTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTGAC CCCAGCTCTG CCCAGCTCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCGAGCTGCCG CGGAGCACCG CGGAGCACCG CCCACAGGT CCTCCACAGTT CGCGGAGGACG CCTCCACAGTT CGCGGAGGACG CCTCCACAGTT CTCACAGCTG CCCGCAGGAGGACG CCGGCAGGAGGACG CCGGCAGGAGGACG CCGGCAGGAGGACG CCGCAGGAGGACG CCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GCTTTCAGGC CCGTCCTGCA GGCTAGCAGC GGCTGCAGCC GGCTGCAGCC GGCTGCAGCC ACCCTGCAA ACCCTGTCC CAGCACCAGA CACTGGCTAT CCCAGCACAGA CACTGGCTAT CGCCAAACC CGCTCCGGCTG GCCCCCGGCTG CCCCTGGGCTG CCCCTGGGCTG CCCCTGGGTATCA CCCTGTGATACC CGCTGTGAAAG CCCCTGGGCTG GGCCCTCCGG CTGGCTGCTG CCCTGGGCTG CCCTGGGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGCTG CCCTGGGTGGCTG CCCTGGG	120 180 240 300 360 420 480 540 600 660 720 960 1020 1140 1200 1140 1320 1380 1440 1500 1560 1660
50 55 60 65 70	ACCTGGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGAGGA AGGAGGAGGA TGAAGGAGGC CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGACTGCAC ACTGGCCTGCG AGGCTACTCACCAC ACTGACCCAC ACTGACCCAC ACTGACCCAC ACGCTGTTCCT CCACGTGCCA CCCCCACGTGCCA CCCCCACGGCC CACGTGCCA CCCCACGTGCCA CCCCACGTGCCA CCCCCACGGCC CACGTGCCA CCCCACGGCC CACGGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC CACGCC C	11   GGCCCTTCCC CCAGGCCCG CCAGGCCCG CCAGCCCG CCAGCCCG TCTCTTTCTC TCTGCTAGC CTGGGGGGG CTGCACCAGCCGG CGCAGCCGG CCGCAGGCCGG CCGCAGGCCGG CCGCAGGCCGG CCGGGGACC CTGCTCGTG CCGGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCTGGTG CTCAGGGAC CTGCCAGAC CTGCCAGAC CTGCCAGAC CTTCAGGGAC CTTCAGGGAC CTTCCAGGGC CTCTAGGGAC CTTCCAGGGC CTCTAGGGAC CTCCAGGC CTCTAGGGAC CTCCAGGCC CTGCCAGAC CTCCCAGGCCC CTCTAGGGAC CTCCCAGGCCC CTCTAGGGAC CTCCCAGGCCC CTCCCAGCC CTCCCAGCC CTCCCCAGCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	21   CTCGGCTTTG   CTCCACCAGE   TGCTGCTCGG   TCTGGCCCA   TGGGTTCCGG   TCTGGCCCA   TGGGTTCCCGG   CTCCCTGGA   CTGGCGCAC   CAGGAGGCG   CTAGCGGCA   CAGGAGGCG   CTCGCTCCAC   CCAGGGGCCC   CCACGGGGCC   CCACGGGGCC   CCACGGGGCC   CCACGGGCC   CCACGGGGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGACGCC   CCCCGGCC   CCCCGGCC   CCCCGGCC   CCCCGGCC   CCCCGGCCC   CCCCGCACGCC   CCCCGGCCC   CCCCGCACGCC   CCCCGCACGCC   CCCCGCACGCC   CCCCCGCC   CCCCCGCC   CCCCCGCC   CCCCCGCC   CCCCCCCC   CCCCCCCC   CCCCCCCC   CCCCCCCC	CCTGGACAGC CAGGCTGAG GAGCCCCAG GAGCCCCAG GATCACCC GAGCCCCAA CAGTCGTACCC GAGCCCCAA ACAGTGTGTAA ACACTGCCC GAGCTGGAGA ATGGGACCCA ATGGGACCCA ATGGGACCCA ATGGGACCCC CAGCTCATCC GAGCTCGAGC TCATTGTTC AAGATACCA CCCGAGCCT CCTGGGGCCT CCTGGGGCCT TGCCCCTCGG	I TCCTGCCTCC CCCCCTCTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTGAC CCCAGCTCTG CCCAGCTCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCCAGCTGCTG CCGAGCTGCCG CGGAGCACCG CGGAGCACCG CCCACAGGT CCTCCACAGTT CGCGGAGGACG CCTCCACAGTT CGCGGAGGACG CCTCCACAGTT CTCACAGCTG CCCGCAGGAGGACG CCGGCAGGAGGACG CCGGCAGGAGGACG CCGGCAGGAGGACG CCGCAGGAGGACG CCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GCTTTCAGGC CCGTCCTGCA GGCTAGCAGC GGCTGCAGCC GGCTGCAGCC GGCTGCAGCC ACCCTGCAA ACCCTGTCC CAGCACCAGA CACTGGCTAT CCCAGCACAGA CACTGGCTAT CGCCAAACC CGCTCCGGCTG GCCCCCGGCTG CCCCTGGGCTG CCCCTGGGCTG CCCCTGGGTATCA CCCTGTGATACC CGCTGTGAAAG CCCCTGGGCTG GGCCCTCCGG CTGGCTGCTG CCCTGGGCTG CCCTGGGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGTGCTG CCCTGGGCTG CCCTGGGTGGCTG CCCTGGG	120 180 240 300 360 420 480 540 600 660 720 780 840 1020 1140 1200 1140 1500 1620 1680 1724
50 55 60 65 70	ACCTGRICCE CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGAGGA TGAAGGAGGA TGAAGGAGGA TGAAGGAGGA CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC	III   GGCCCTTCCC CCAGGGCCGG CCCAGCGCGG CCCACTCTCC TCTTCTTCTC TCTGTTAGC CTGGGGGGGCT TCTCACCTTC GTACCCAGTG CTGCAGGGGGC CTCAATGGC GGCAGAGG CCTGATGGG CCCGGGGAC CCTGGGGAG CCTGGGTGGT CTCAGGGAG CCTGGGTGGT CTCAGGGAG CCTGGCCGGA CCTGGCCGGG CCTGGCCGGGAC CCTGGCCAGGG CCTGGCCAGGG CCTGCCAGTGC CTTCCCAGTGC CTCCAGTGG TTCCTCAGGGAG CTTCCCAGTGG TTCCTCAGGGAG TTCCTAGGGAG TTCCTATTGGT TTCTCCTCA  1 118 DNA St cid Accessic quence: 42. 11   CCAGGACCAGG ACTCTGAGGTA TCCTAGGGAG CCTGGGGAAG CTCTGAGGAC CTTCCTAGGGAC CTTCCTCAGGGAC CTTCCTCAGGGAC CTTCCTCAGGGAC CTTCCTCAGGGAC CTTCCTCAGGGAC CTTCCTCAGGGAC CTTCCTCAGGTAC CTTCCTCAGGTAC CCTGGGGACCAGG CCTGGGGACCAGG CCTGGGGACCAGG CCTGGGACCAGG CCTGGGACCAGG CCTGGAGCCAGG CCTGGAGCAGG CCTGGGAACAGG CCTGGGGAACAGG CCTGGGAACAGG CCTGGAGCAGG CCTGGGACAGG CCTGGGCCAGG CCTGGGCAGG CCTGGGACAGG CCTGGGAGAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGGAACAGG CCTGGAGCAGG CCTGGAGC CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGAGCAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGCGAG CCTGGGCAGG CCTGGGACAGG CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGAGC CCTGGGACAGG CCTGGCCGGAG CCTGGGCCGGAGG CCTGGCCGGAG CCTGGCCGGAG CCTGGCCGGAG CCTGGCCGGAGG CCTGGCCGGAG CCTGGCCGGAG CCTGGCCGG CTGGCCGGAG CCTGGGCCGGAG CCTGGGCCGG CTGGCCGGAG CCTGGGCCGGAG CCTGGGCCGGAG CCTGGGCCGGAGG	21   CTCGGCTTIG   CTCCACCAG   GGTGCTCGG   TCTGGCCA   TGGGTTCCGG   CTGGGAGCCC   GGCTCCGAGT   AACTGCTCA   GGGGAGGGG   GTGCAGAAGG   CTCGCATCG   CTGGCAGGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCAGGCC   CTGGCACGCC   CTGGCACGCC   CTGGCACGCC   CTGGCACGCC   CTGGCACGCC   CTGGCACGCCC   CTGGCACGCCC   CTGGCACGCCC   CTGGCACGCCCCC   CTGGCACGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COTGGACAGE CAGGCCTGAG GTTCTGAGGG CAGCCCCAG GTTCTGAGGG CAGCCCCAA CAGTTCGTACG GCTGCCCAA ACCACCCCAG ATGGACACCA ATGGGACCCT ATTATTCTTT ATTATTCTTT CAGGACCCCAC CAGGCCCCCCCCCC	TCCTGCCTCC CCCCTCTCTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG CCCAGCTCTG CCCAGCTCTG CCCAGCTCTG CCCAGTGTGT CCCAGTGTGT CCCAGTGCTGC CCCACAGGTTGT CGCCTGCTGC CCCACAGGTTGT CAGCAGGACGACCC CCCACAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	CGCAGGGCCC GGCAGGGCA GGCACGAGG GGCATGGAG GGCATGGAG GGCATGGAG GGTTATCGTG GACCAGCA GGTGCAGCA GGTGCAGCA GGTGCAGCA GGCTGCAGCA GGCTGCAGCA GCTGCAGCA GCCTGCAGCA GCCTGCAGCA GCCTGCAGCA GCCTGCAGCA GCCTGCAGC ACCCTGCAGC GCCCTCGGG AGCCCAACC GCCCTCGGG AGCCCAACC GCCTGCAGC GCCCTCGGGACG GCCCTCGGGACG TGCCTCAGC GCCTTGCAGC GCCTTGGCTG TGCTGAAACC TGGGTAATA TCTTTGATGCTG GGGTTGGCTG TGGGTTGGCTG TGGGTTGCTG TGGTTGCTG TGGTTGCT TGGTT TGGTTGCT TGGTT TGGT TGGTT TGGTT TGGTT TGGTT TGGT T	120 180 240 300 360 420 480 660 660 720 780 840 900 960 1140 1220 1380 1440 1550 1620 1680 1724
50 55 60 65 70	ACCTGGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGACGA TGAGGAGGC ACATTGCCCA AGGACTGCG CAGGCCACTT CCTCCAGCC AGAACTGCCC AGAACTGCCC CCAAGTGCAG ACGTGCTGTT TATGTGTGAA ACGTCACCAC ACGTGCTTCC CCACGTGCCA AGGCTTCCGTCCA CCTCCCAGAG CCTCCTGGGC GGCCTCAGCA CCTCCTGGGC GGCCTCAGCA CAGTTGCTCA CCACGTGCCA CCTCCTGGGC CAGGCCTCAGCA CCTCCTGGGC CCCACTGGCC AATATCTTGT  Seq ID NO: Nucleic Ac Coding sec 1   CAGGCACCAC CCCACTGGCC AGATTGGC CCCACTGGCC AGGCACCAC AGGCTCCTGGGC AGAATTCAT CCCCACTGGCC AGGCACCAC CCCCACTGGGC AGAAATTCAA	11   GGCCCTTCCC CCAGGCCCG CCAGGCCCG CCAGCCCG CCAGCCCG TCTCTTTCTC TCTGTTAGC TCTGCTAGC CTGGGGGAG CCTCAATGGC CGGGAGCCGG CCGCAGGCCGG CCGCAGGCCGG CCGGGAGCCGG CCGGGAGCCGG CCGGGAGAC CTGCTGGTG TCTCAGGAGC CTGGCGAAA CGAGCCAGAG CGGGACAGAG CTGCTGGCAAA CGAGCCAGAG TTCCTAGGGAC TCCTTAGGGAC TTCCTAGGGAC TCCTTAGGGAC TCCTTAGGGAC TCCTTAGGGAC TCCTTGAGGAC CCGGCCAGAC CGGCCCAGAC CGACCCAGAC CGACCCAGAC CGCCCAGAC TCCTAGGGAC TCCTTAGTGGAT TCCTTAGTGAT TCCTTGCTAA TCAGGACCAGG TCCTGAGGTT TCATTGCTAA TCAGGATAAA	21   CTCGGCTTTG   CTCCACCAGE   TGCTGTTCGCCCA   TGGGTTCCCG   GCTCCCAGGAGCCC   GGCTCCAGGT   CTGACGGGCA   CTAGGAGGCG   CTAGCAGGCC   CTGACGGGCA   CTAGCAGGCC   CTGACGGGCA   CCACGGGGCC   CCACGGGCCC   CCACGGGGCC   CCCCGGGGCC   CCCCGGGGCC   CCCCGGGGCC   CCCCGGGGCC   CCCCGGGGCC   CCCCGGGCC   CCCCGGGGCC   CCCCGGG	CCTGGACAGC CAGGCCTGAG CAGGCCTGAG GTTCTGAGGG CAGCCCCAG GTTCTGAGGG GTACCACCCC GCTGCCCAA CAGTGTGTAGA ACACTGCGC GAGGCACCAA ATGGGACCCA ATGGGACCCA ATGGGACCCA ATGGGACCCA ATGGGACCCA CAGTTAGTA CAGTATGTA ACAGTATGTA CAGTATTGA CAGTATTGA CAGTATTGA CAGTATTGA CAGTATTGA CAGTATTGA CAGCCCACGCT CCTGGGGCCTT CCTGGGGCCTT TGCCCCTCGG CAAAAAAAAAA	I TCCTGCCTCC CCCCCTCTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTTGTG ACAGCTGCCC CCCAGCTCTTG GCGTGTGTC CCCAGTGTGT CGCGTGTGTC CGCGTGCTGC GGAGCAACCC GAGTCAGAC GGAGGAATGT GGAGGACGC GCTCCACAGTT GGTGATGTG GCTGCACG GTGATGTG GCTGCACG GTGATGTG GCTGCACG GTGATGTG GCTGCACG GTGATGTG GCTGCACGT GTGATGTG GCTGCACGT GTGATGTG GAGGGACG GGGGGACG GGGGGACG GGGGGTAGG GGGGGTAGG GGGGGTTGC GGGGGCTGC GGGGGCTGC GGGGGTTGC GGGGGCTGC GGGGGCTGC GGGGGCTGC GGGGGCTGC GGGGGCTGC GGGGGCT GGGGGCT GGGGGCC GTTTTTTGCC GGGGGC TGTTTTACGG TTGCCCGCC TTTTTTCCC CCTTGCCGGC CCCCCCTT TGTCCCCGCC CCTCCCCCCCTT TGTCCCCGCC CCCCCCTT CCCCCCCC	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GCTTTAGGC CCGTCCTGCA GGCTGCAGCA GGCCCAGCA CACCAGCA CACCAGCA GGCCCTCCGG GGCCCCCGG GGCCCCCGG GGCCCCCGG GGCCCTCCGG TGGCTGAAAC CCTGGGATG GGCTGAAAC CCTGGGTAAT CCCTTGCA GGAGGATGTA CCCTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGAGGATGTA  51   CCCTGGGTG ATTGAATTCC GGAGGATGTA  52 A CATGCCTTCC ATCATCTTTG A CATGCCTTCC ATCATCTTTG TACCCTTCC TACCTTTCC TACCTTTCC TACCTTTCC TACCTTTCC TACCTTTCC TTGCATCTTTTG TACCCTTTCC TTGCATCTTTC TTGCATCTTC TTGCATCTTC TTGCATCTTTC TTGCATCTTC TTGCATCTTTC TTGCATCTTC TTGCATCT TTGCATCTTC TTGCATCT TTG	120 180 240 300 360 420 480 540 900 960 1020 1140 1200 1320 1380 1440 1500 1562 1620 1680 1724
50 55 60 65 70	ACTGGGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGAGGA ACATTGCCCA TGGGCCTGCG CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGACTCCAGC CCCAAGTGCAG CGTGCTTCT TATGTGTGAA AGGTAACACAC ACTGACCAC ACTGACCAC CCCCAGAG CCTCCTGGGCA CCTCCTGGGCA CATGTCCTCT AATATCTTGT AATATCTTGT  Seq 1D NO: Nucleic AC Coding seq 1   CAGGCACCAC CCCACATGGG TGCTCGGGGT AGAATTCAT CCCCACATGGG TGCTCGGGGGT AGAATTCAT TGATCGGGGT AGAATTCAT TGATCGGGGT AGAATTCAT TGATCGGCGGT AGAATTCAC CCCACATGGG AGAATTCAC TGATCACCT TGATCACCCT TGATCACCCT TGATCACCCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCT TGATCACCCT TGATCACCT TGATCACC TGATCACCT TGATCACCC TGATCACCA	11   GGCCCTTCCC CCAGGGCCGG CCCAGGGCCGG CCCAGCTCTC TCTCTTTCTC TCTGCTAGC CTGGGGGGC TCTCACCTTC GTACCCAGTG CTGCAGGGCCG GCCAGGGCCGG CCCGGGGACC CCGGCCAGGG CCCAGGGACC CCGCCAGGAC CCTGGCGGAC CCTGGCGGAC CCTGCCTGGG TCCAGGGAC CCTGCCAGTG TCCAGTGGC TTCCAGGAC CCTGCAGGAC CCTCCAGTGC TTCCAGGAC CCTGCAGGAC TTCCCATGGC TTCCATGGG TTCCTCATGGG TTCCTCAGGAC CCTGCAGGAC CCTGCAGGAC CCTCAGGAC CCTGCAGGAC CCTCCAGTGC TTCCTCATGGG TTCCTCATGGG TTCCTCAGGAC CCTGCAGGACC CTTCCCAGTGC TTCCTCAGGAC CCTGCAGGACCAG CCTGCAGGACCAG CCTGCAGGACCAG CCTGCAGGACCAG CCTGCCTGAGGAC CCTGCTGAGGAC CCTCCTCAGGAC CCTGCTGAGGAC CCTCTCAGGAC CCTGCTGAGGAC CCTCTCAGGAC CCTGCTAG CCAGGACCAGG CCAGCAG CCAGGACCAG CCAGGACCAG CCAGGACCAG CCAGGACCAG CCAGGACCAGG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGCAG CCAGC CCAGC CCAGGACCAGG CCAGC CCAGC CCAGC CCAGC CCAGGACCAG CCAGGACCAG CCAGC CCAGC CCAGC CCAGC CCAGC CCAGC CC	21    CTCGGCTTTG   CTCCACCAG   GTCTGGCCCA   TGGGTTCCGG   CTCTGGCCCA   CTGGGAGCCC   GGCTCCGAGT   CTGAGCAGCC   CTGAGCAGCC   CTGAGCGGCA   CTAAGCAAGG   CTGGGAGCGG   CTGGTATCG   ACGAAGGGG   CTGCAGGGCC   CTGTGATCG   CCAGGGGGCCA   CCAGGAGCCCA   CCAGGAGCCCA   CCACGGAGCC   CCAGGAGCCCAC   CCAGGAGCCCAC   CCAGGAGCCCAC   CCAGGAGCCCACCCCCCCCCCCCCCCCCCCCCCCCCCC	CCTGGACAGC CAGGCCTGAG GTCTGAGGC CAGCCCCAGC GTCTGCAGGC GTCTCACGC GAGCCCCAA CAGTGTGTAGA GGAGACAGAA ACACTGCCC GAGCTCGCAGC TCATTGTTG ATGGAGCCC AGAGCACAGA ATGGACCCA ATGGACCCC CCTGGAGCCT CCTGGAGCCT CCTGAGCCCCAGCCC CCTGGAGCCT CCTGAGCCCCAGCCC CCTGAGAGAA ACAAAAAAAAAA	TCCTGCCTCC CCCCTCTG ACAGCTTGTC AATGGCCTG CTGAGCCTGA CAGACCGAC CCCAGCTCTG GAGACCGAC CCCAGCTCTG CGCCTGTGT CGCCTGTGT CGCCTGTGT CGCCTGTGT CGCCTGTGT CGCGTGCTGC GAGTCAGAC CTCCACAGTT CGCGGGAGC CGAGCGACC CTCCACAGTT CGCGGGAGC CGCGGGAGC CGCGGGAGC CTCCACAGTT CTCACAGCTC CTCACAGACCT CTCACAGCCG CTCACAGCT CTCACAGCCG CTCACAGCT CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACAGCCG CTCACCGCG CTCACCGCGC CAATGGACC CTCATGCCGCA AGGCCCCCT CCCATGCCGCA AGGCCCCCC CCCATGCCCGCA AGGCCCCCC CCCATGCCCGA AGGCCCCCC CCCCCCCCCC	CCCTGGGTG CGGGGGGGG CTGCCAGGCA ACACCGAGGC CCTGCCAGGCA ACACCGAGGC GCTTACGCG GCTATCGTG GACCCAGCA ACACCGAGC CCTTCCCAGC CCTTCCCAGC CCTTCCCAGC CCTTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCTCCAGC CCCTCGGCTG CCCCCCGGGTG CCCCCCGGGTG CCCCCCGGCTG CCCCCCGGCTG CCCCCCGGCTG CCCCCCGGCTG CCCCCCGGCTG CCGGCTGAG CCCCAGC CCGGCTGAG CCCCAGC CCGGCTGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGGTGGAG CCCCAGC CCGGCTGGAG CCCCAGC CCGGCTGAG CCCCAGC CCGGCTGGAG CCCCAGC CCCCCAGC CCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCAGC CCCCCAGC CCCCCCAGC CCCCCAGC CCCCCCAGC CCCCCCCC	120 180 240 300 360 420 480 660 660 720 780 840 1080 1140 1200 1320 1380 1440 1500 1620 1620 1620 1620 1620 1620 1620 16
50 55 60 65 70	ACCTGRGTCC CCCCTGGTG GGATTCTCTT CTGGAGTTCA CTCCTGGAGA TGGTGCTGTA AGGAGGAGA TGAAGGAGAGA TGAAGGAGAGA TGAAGGAGAGA CAGGCCACTT CCTCCAGCCC AGAACTGCCC AGAACTGCCC AGAACTGCCC AGTGGTTTCT TATGTGTGAA ACGTCACCAC ACTGACCCAC GCTTCCGTGCG CCTCCTGGGC GGCCTCAGCA CACTGTCCT AATATCTTGT  Nucleic A CCCACTGCC 1	II  GGCCCTTCCC CCAGGGCCGG CCCAGCGCGG CCCACTCTCC TCTTCTTCTC TCTGTTAGC CTGGGGGGCT TCTCACCTTC GTACCAGTGG CCTGGGGGGG CCTCAATGGC GGCCAGAGG CCTGGGTGGT CTCACGGGAG CCTGGGTGGT CTCAGGGAG CCTGGGTGGT CTCAGGGAG CCTGGGTGGT CTCAGGGAG CCTGGGTGGT TCTCATGGG TCCTGGGGAG TTCCATGGG TTCTCATGGG TTCTCATGGG TTCTCATGGG TTCTCTCATGGG TTCTCTCATGGG TTCTCTTGGTAT TTCTCTCATGGGAG CCTGGCCAGAG CCTGGCCAGAG CCTGCCTGGTAG TTCTCCTCATGGG TTCTCTCATGGGAG CCTGCTGGAGT TTCTCCTCAGGAG CCTGGCCAGAG CCTGGGCCAGA TTCCTCAGTGG TTCTCCTCAGGAG CCTGGGCCAGG TTTAGTGGAT TCTCTCCTCAGTGG CCTGGGCCAGG CCTGGCCAGG CCTGGGCCAGG CCTGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGGCCAGG CCTGGCCAGG CCTGGCCAGGC CCTGGCCAGG CCTGGCCAGG CCTGGCCAGG CCTGGCCAGG CCTGGCCAGG CCTGGCCAGG CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGC CCTGGCCAGGCCA	21  CTCGGCTTTG CTCCACCAG GTGTCCGG TTCTGGCCA TGGGTTCCGG CTGGGAGCCC GGCTCCGAGT CTGACAGG CTGACAGG CTGACAGG CTGACAGG CAGGACGGG CAGGACGGG CCACGGGCC CCACGGCCCTCAG CCACGGGCC CCACGGCCCTCAG CCACGGGCCCAGGCCC CCACGGCCCTCAG CCACGGAGGCC CAGGACAGGCCCAGGCCC CACGACGCCCC CACGACGCCC CACGACGCCC CACGACGCCC CACGACGCCC CACGACACCCC CACGACACCCC CACGACACCCC CCACGACACCCC CCACGACCCCC CCACGACCCCC CCACGACCCCC CCACGACACCCC CCACGACCCC CCACGACCCC CCACGACCCC CCACGCCCCC CCACCCC CCACCCCC CCACCCC CCACCCC CCACCCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACCC CCACC	CCTGGACAGE CAGGCCTGAG GAGCCCCAG GAGCCCCAG GATCACCCA GAGCTGCCCAA AGCTGCCCAA AGCTGCCCAA AGCTGCCCAA AGCTGCCCAA AGCTGCCCAA AGCTGCCCAA AGCTGCTGGAG ATAGGACCCT AGAGCTGGGAC TCATTGTTA ATATAGTCAA CAGTCATTGT CAGGCCCTCAT CAGGCCCTCAT CAGGCCCTCAT CAGGCCCTCAT CAGGCCCTCAGGCCCT CACCCCAGGCT CACCCAGGCT CACCCAGGCT CACCCACAGCT CACCACAGCT CACCCACAGCT CACCACAGCT CACCACAGCT CACCACACACACACACACACACACACACACACACACA	I TCCTGCCTCC CCCCTCTCTG ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTTGTC ACAGCTCTG CCCAGCTCTG GTGCAGTCCA ACCCTGCCCT CCCAATGTGT CGCGTGCTGC GAGTCAGAGC GAGGAATGT CAACAGGTT GGCGTGCTGC CAACAGGTT GGCGTGCTGC CAACAGGTT GGAGGACGCCC CTCCACAGTT GGGTATCGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CAACAGGTC CTCAACAGTC CTTGCGCGTAAC AAAA  41    CAATGGAGCC CTTGTTTACCG TTGTTACCGCT CAATGGAGCC CTTGTTTACCGCT TTTTTACCGCT CAATGGAGCC CAATGGCGGAA AGGCCACTC CAATGGCGGAA AGGCCAACTC CAATGGCGGAA AGGCCACTC CAATGGCGGAA AGGCCAACTC CAATGGCGGAA AGGCCAACTC CAATGGCGGAA AGGCCAACTC CAATGCCGGAA AGGCCAACTC CAATGCCAGAA ACACCTACTGCAACTC AAACACTACTC CAATGCCAGAACCAACTC CAATGCCAGAACCAACTC CAATGCCAGAACCAACTC CAATGCCAGAACCAACTC CAATGCCAGAACCAACTC CAATGCCAGAACCAACTC CAACACTC CAACACT	CGCAGGGCCC CTGCCAGACA ACACCAGGC AGTTCCTCTG GGCATGGAGC GCTTTAGGC CCGTCCTGCA GGCTGCAGCA GGCCCAGCA CACCAGCA CACCAGCA GGCCCTCCGG GGCCCCCGG GGCCCCCGG GGCCCCCGG GGCCCTCCGG TGGCTGAAAC CCTGGGATG GGCTGAAAC CCTGGGTAAT CCCTTGCA GGAGGATGTA CCCTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGGTGGCTG GGAGGATGTA  51   CCCTGGGTG ATTGAATTCC GGAGGATGTA  52 A CATGCCTTCC ATCATCTTTG A CATGCCTTCC ATCATCTTTG TACCCTTCC TACCTTTCC TACCTTTCC TACCTTTCC TACCTTTCC TACCTTTCC TTGCATCTTTTG TACCCTTTCC TTGCATCTTTC TTGCATCTTC TTGCATCTTC TTGCATCTTTC TTGCATCTTC TTGCATCTTTC TTGCATCTTC TTGCATCT TTGCATCTTC TTGCATCT TTG	120 180 240 300 360 420 480 660 660 720 780 840 960 1080 1140 1250 1320 1320 1440 1560 1560 1724

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	AGGCCAACAC CC	GCAAGCGT C	GCATCTCTT TO	STCCTTGGT (	ATCTGGGTG	CCATTGTGG	480 540
	GAGCTGCATC CT CAGGCAACGT CA	ACTICCIC A	NTCCTGGACT C	CACCAACAC /	CAGCGTGCCA (	STOCTCATCA	600
_	TOTACATOTT CA	TOTTOTTC A	AGCTTCTTCC T	GGTCTTCCT (	CATCATCCTC 1	PTCTGCAACC	660
5	TGGTCATCAT CO	CTACCTTG (	TCATGCAGC O	GGTGCAGCA (	GCAGCGCAAC (	SCTGAAGTCA	720 780
	AGCGCCGGGC GC	TGTGGATG (	STGTGCACGG T	TECTEACET (	GGGCTTCCAG	GACAGCAAAT	840
	TCCACCAGGC CA	TTAATGAT	GCACATCAGG T	CACCCTCTG (	CCTCCTTAGC A	ACCAACTGTG	900
	TOTAL NOOF TO	TTATCTAC '	TOTAL CARREST	CARGARGTT	CCCCAAGCAC (	CTCACCGAAA	960
10	AGTTCTACAG CI	ATGCGCAGT	AGCCGGAAAT G	CTCCCGGGC	CACCACGGAT	ACGGTCACTG	1020 1080
	CAGGCCTGAA GT	CTTCTCCT (	CCATGAACAT C	ATGGACTGA	GCTGGGGGAA	GAAGGGATAT	1140
	CTACTICTICGT CT	CCCCACCA !	CCTCTGTGGG C	ACTGGTGGG	CCATTAGATT	TGGAGGCTAC	1200
1.5	CTCACCTGGG C	TASTANONA	CCCACACCCA C	GCTGTTGGA	AAATCCAGAA	CTCAAATGAG	1260 1320
15	CCCCTTCATC CO	CCTGTGGG	CGCATACTAC A	CACCCCCAC	GTGCAGACCT	TGGGGGAAGA	1380
	CTTTABACCA CI	CTAGTTCTC	CCCGATGGGG (	CATCGGTCTA	AAGCTTTGGG	GGAGTGGGCG	1440
	CACTGGCTCA C	TAATOTOO	CCCAGCACTT 7	rgggaggccg	AGGTGGGCAG	ATCATGGGTC	1500
20	AAGAGATCGA G	ACCATCCTG	GCCAACATTG 7	CTCCCA	ACTORGRAGE	CTGAGGCAGG	1560 1620
20	AGAATCGCTT G	AACCTGGGA	GCCAGAGGTT (	CAGTGAACC	TAGATTGCAC	CATTGCACTC	1680
	TAGCCTGGCA A	CAGAGCGAG	ATTCCATCTC A	AAAAAAAAA	AAAAAAAAA	AAAAAAAGCT	1740
	TTGGGCAACT A	CTCTCAAGT	GATAGAGGTA (	ACTGGGTTA	GGAAAGGACA	CTGCCCTCAC	1800 1860
25	TCCGGCACAA G	CTCTTTCTC	ACCUTTURE A	COCARGOGG	CTTGATGGAA	CCTTCTCTGA	1920
25	CTCATCTGGC A	ACCTGTCCC	TAATGGTGAC	CAAAGAAGAT	AAAACATGAA	CAGACCAAAA	1980
	GCTAGGACAA G	AGCTTGCTT	CCCAAGACAG	ACGTGTCTGT	CTGCAAAGGC	CTTGCCTCTA	2040 2100
	GTCCAGTCAG C TAGTCCCTAA T	TCTGGGGGA	TCTCTCCCCC	BGCCACCACC	TGAGGGTGGG	CAAAGGCCCC	2160
30	TTGABAGCAA A	ATTGGGGCT	GGGCTCAGTG (	GCTCATGCCT	ATAATCCCAG	CACTTTGGGA	2220
	GGCCAAGGCA G	GCAGATCAC	CTGAGGTCCG	GAGTTCGAGA	CCAGCCTGGC	CAACGTGGTG	2280
	AAACGCCATC T GGAGGCTGAG G	CCACTAAGA	ATACAAAAAT	ATGGCTCATG	AGACCAGCCT	GACCARTATG	2340 2400
	GTAAAACCCC G	TCTCTACTA	AAAATACAAA	AAAATTAGCC	TGGCGTGGTG	GCGCATGCCT	2460
35	GTAGTCCCAT A	GCTGTAGC	TACTGGGAGG	AGGCGGAGCT	TGCAGTGAGC	CGAGATCACG	2520
	CCACTGCTCT C	CAGCCTGGG	CGACAGAGTG	AGACTCTGTG	TCAAAAACAA	GGCTTCCATA	2580 2640
	CGAACAGGCA C	CANTIGGAGE CATEGGCTGG	GAAGTACATG	AGGCCCCTGG	GTAGAAGGGT	CTGTCAGTTC	2700
	TCTCCTCCCT 1	rgcccrcrgg	GAGGGTCCTC	CTAACATAGC	TTCCAGGAGG	TGGGAGGAGC	2760
40	AGTTACTGTC !	AGCAGGTGTC	AGCCAGGTGT	CAGCTTCTCC	TGGGGATCTC	TAGATGTCTG	2820 2880
	CTTGTGATTT T	TTGGCAAGTA	CTCAGACCCA	AGCGGCTCAG	AGGAAACTTC	TCTGGTTTCT	2940
	AGAGCTCTGT (	CTCCTTCAG	AGAAGTCTTC	CTTCCTTCCA	GTCAGTGTCC	CTGTGAAGCT	3000
45	GGGATACTCA T	TTTCCTGTGT	ACCGGGCAAA	CACCGGATTG	CTGATTTTGA	GAAATGCCTC	3060 3120
45	TCGATGGACC	TGTAACCTGC	TGGAGTCTGG	GATGGTAGCT	TTCARCTCTT	GGCTGTGTCA	3180
	TTTCCTGCTG /	AGGGACCAGG	CACTGAATTT	CCTACCTCTT	AGGGTCATTA	CCTATGAGGT	3240
	TARAGCTACC '	TCATGGGATT	GTTATACGCC	ACTAATGTTG	AGGCAGACAC	CTCTTGGCAG	3300
50	GGTGACTGCT	CATCTTAGAC	CCTCCCCTTT	TOTGCGAATT	TGGGCCCCTT	GATCCTCTGA	3360 3420
50	GGTCCCTTAC	CTGAACACAT	· AGAAACCCTG	GAGCTGTGAC	: TGTGTCCATC	TGTGTGTGTT	3480
	TOTOTOTOTO	TGTTGCGGGG	GATGGGCACC	TGCATGAATG	: TGGTAGAGAA	AATGGCTCTG	3540
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55	TOTTOTTA	GGCCCTGTGA	GCGTCCCTTG	TCAGGATACA	TTCTCTCATT	TTGCTGAAGC	3720
•	TCATTTGATT	GGGTGTCTGT	TTCTCGCAGC	CAAAAGAGCT	CTGAATGAGG	BAAAGTGCTTC	3780
	TGTGCTAACT	CCCCGCGTCT	CCTGAATTTC	AGTCATTCAT	r gtacccgcc	CGAAATTTTT	3840 3900
	GCAATATCTG ACTTTTAA	TGTACCAACT	GTCCATTTAC	TTAATAAGA	A MOITHCELL	AMITAMOTO	3908
60	•					•	
	Seq ID NO:	119 DNA Se	equence				
	Coding sequ		on #: NM_003 853	211.2			
	1	11	21	31	41	51	
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	ACTECTCAGE	CTTCAGGGA	C CCTGAGCACC	GCCTGGTCT	C TTTCCTGTG	G CCAGCCCAGA	120
	ACTGAAGCGC	TGCGGCATG	G CGCGCGCCTG	CCTCCAGGC	C GTCAAGTAC	C TCATGTTCGC	180
70	CTTCAACCTG	CTCTTCTGG	C TGGGAGGCTG	TEGESTECT	G GGTGTCGGC	A TCTGGCTGGC	240 300
70	CGCCACACAG	GGGAGCTTC	G CCACGCTGTC	CTCTTCCTT	c engrecers	T CGGCTGCCAA T GCCTGGGTGC	360
	CATCAAGGAG	AACAAGTGC	C TCCTGCTCAC	TTTCTTCCT	G CTGCTGCTG	C TGGTGTTCCT	420
	GCTGGAGGCC	ACCATCGCC	A TOCTOTTOTT	CGCCTACAC	G GACAAGATT	G ACAGGTATGC	480
75	CCAGCAAGAC	CTGAAGAAA	G GCTTGCACCT	GTACGGCAC	C CAGGGCAAC	G TGGGCCTCAC	540 600
13	CAACGCCTGG	GTGTACAAC	C AGACCGACTI	ACCTGACTO	C TGCTGCTTG	A ACTACACTGA G AGTTCAGTGA	
	GAGCTGTGGG	CTGCACGCC	C CCGGCACCTC	GTGGAAGGC	G CCGTGCTAC	C AGACGGTGAA	720
	CGTGTGGCTT	CAGGAGAAC	C TGCTGGCTG1	GGGCATCTT	T GGGCTGTGC	A CGGCGCTGGT	780 840
80	GCAGATCCTG	TAGGOGG	T TOGCCATGAG	CATGTACTG	A AAGGACGCC	A AGGCAGACAC C ACGGGGAGAT	900
30	GGCCGCACCC	ACAGCTGCC	T TTCCCACCA(	CAGCCTCGC	FT GCTCTGCCC	C ATGCTGGGAG	960
	GAGGGAGGGA	GGGACAGGT	'G CCTGGAGCC	CCGGAACCC	T GTTTCTGG/	LA GGCCCTAGCT	1020
	CAGGTGGCTT	CAGGGCCTC	C GGACCCCCC	TGGGAGGG	T GGCCACGTC	SC TGGCTGCGGA NT TCTCCAAAGC	1080
	ACCUAGGGCA	- ADDOLUGE	in onecticcy				

		CGGGAGCCAG TCTTGGCATC					1200 1260
	CGTGGACCCC	TCACCTACAT	TCCATAGTGG	GCCCGTGGGG			1320
5	AGTGTGAGCA	GCAAAAAAA	AAAAAAAAA	AAA			1353
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10	1	11	21 	31 	41 j	51 	
	TAGTCGGAGC	GAGGTGGCGA	GTCGCTGAGC	COGCCGCGGG	CCCGAGAGCG	GCTGCAGCCG GCCACCGCCG	60 120
	CCGCCGCCAC	CACCGCCACC	GGAGTCGCGG	GCCAGCCGGG	CAGCCTCCGC	GGGCCCCGGC	180
15						ACCGCGGGCG CGCCGCAGCC	240 300
	GCCGCCGCCC	GAGCCGCGGG	CAGGAGCCTC	GGGAGCCGCC	<b>GCCGCCGCCG</b>	CCCCCCCCCC	360
						ATTCTTCAGG CGCACCCCGC	420 480
20	CGTCCGCCCG	CCGCCCCGTC	CCCCGGCCCG	ecceccccc	GGCCCCCGGC	CCCCTGAGGC	540 600
20	GCCGCGACCC	OGGCCCGGCC	GTGCGGCCCG	CCGGGGCCAT	GGCGAAGAAG	AGCGCCGAGA	660
						CCCGGGCCCG	720 780
25	CCGTGCCGCC	GCGCGAGACC	TGGACGCGCC	AGATGGACTT	CATCATGTCG	TGCGTGGGCT	840
25						AACGGCGGAG ATTTTCTTCT	900 960
	TAGAGATCTC	GCTGGGCCAG	TTCATGAAGG	CCGGCAGCAT	CAATGTCTGG	AACATCTGTC	1020
						ACCACCTACT	1080 1140
30	CCTGGGCCAC	ATGTGGCCAC	ACCTGGAACA	CTCCCGACTG	CGTGGAGATC	TTCCGCCATG	1200
						GACCGCCGGT CTGGAGGTGC	1260 1320
	CAGGGGCCCT	CAACTGGGAG	GTGACCCTTT	GTCTGCTGGC	CTGCTGGGTG	CTGGTCTACT	1380
35						GCTACATTCC	1440 1500
						GTGTGGATAG ACAGCCCTGG	1560 1620
	GCAGCTACAA	CCGCTTCAAC	AACAACTGCT	ACAAGGACGC	CATCATCCTG	GCTCTCATCA	1680
40						TTCATGGCTG GCCTTCATCG	1740 1800
40						CIGITCITCI	1860
						TTCATCACCG ATCTCTGTGG	1920 1980
4.5	CCCTCTGTTC	TGCCCTCTGC	TTTGTCATCG	ATCTCTCCAT	GGTGACTGAT	GGCGGGATGT	2040
45						GACGACATTG	2100 2160
	CCTGTATGAT	CGGGTACCGA	CCTTGCCCCT	GGATGAAATC	GTGCTGGTCC	TTCTTCACCC	2220
						CTGGTCTACA GCCCTGTCCT	2280 2340
50	CCATGCTGTC	CGTGCCGCTC	CACCTCCTGC	GCTGCCTCCT	CAGGGCCAAC	GCCACCATGG	2400
						GAGTACCGAG GAGCAGCAAGG	2460 2520
	TOGTCGTGGT	GGAGAGTGT	ATGTGACAAC	TCAGCTCAC	TCACCAGCTO	ACCTCTGGTA	2580 2640
55						CACTAAAACA	2700
						A TAGATGCCTC	2760 2820
	CAGTGCTGC	A CTCCTCCTG	CCCTGCCAC	CCCACCCCC	C GCCCACCTC	CCAGGCTCTG	2880
60						A GCTTGGGAAA G GGAGGCAGGG	2940 3000
••	GAGGGGCAG	CAGAACCAAG	CAAATATTT	AGCTGGGCT	A TACCCCTCT	C CCCATCCCTG	3060
						G CCAATCGCCA C GGAGAGTATA	3120 3180
65	TATAGATCT	C TATCTCTTA	CAAAGGTGA	A TGCCAGATG	T AAATGGCGC	C TCTGGGCAAA	3240
03						C TGCTTGTATA T CCCTGTGAGC	3300 3360
	CCTACCTTA	C CCCTCTGCC	C CTAGCCAAG	G AGTGTGAAT	T TATAGATCT	A ACTTTCATAG	3420 3480
						G TGCGTGTGTG G CTGTCCCCAC	3540
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80		cid Accessi quence: 206		3332.1			
- •	1	11	21	31	41	51	
	I GCACGAGGG	) C GCTTTTGTC	I T CCGGTGAGT	T TTGTGGCGG	 G AAGCTTCTG	C GCTGGTGCTT	60
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	AAAAAAAA AAAAAAAAA AAAA	1284
50	•••••	
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	1 11 21 31 41 51	
55		60
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	TECCTACAC TEGRAAGGAA ACAGCTACAT GATTCAGCGC AAGGAGTEGG ACTTATCTGA	
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	GININGTING MODUCCON MODUCCOND MANGETCINI ATTOOLISM CONTESTED	

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	TGCCTACAAC TGGAAAGGAA ACAGCTACAT GATTO GTATAGTTAC AAGGACCCAG AGGACCAAGG AAACO		
	GINING INC MOUNCECAG MOUNCECAMOG ARACT	TOTAL ALTOURING CONTOCNOOL	340

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		: 126 DNA S					
65		cid Accessi		3786			
05		quence: 71.	.4654	21	41	51	
	1	11	11	31	7.	7.	
	CALCUSCUSCO	יר ומודודונות	c eccectece	T COCACOGO	- 10000000	TGCAGCCGCG	60
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	CONCCOMME AMIGIGATION MODECUMENT CONTRIBUTION TO THE PROPERTY OF THE PROPERTY	1860
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10	TTTGTATTTT	ATAATATGAA	ACAAGGGGGG	AGGGTAATAG	CAATGTGTTT	TGCAACATAT	4260
	TAAGAGTATG	TGAAGGAAGC	AGGGATGTCG	CAGGAATCCG	CTGGCTAACA	TCTGCTCTTG	4320
	GTTTCTGCTG	CCCTGGAGCC	TGACCCTCAG	TCTCCATTCT	CCCTCCTACC	CAGGCCTCCT	4380
20	CAACCTTCAC	CTCCTTTCCC	ACCAAGGAGG	AGAAGTAGGA	AGTTTTCTTA	AAGGGCCAAT	4440 4500
20	TCAAAGCCAA	GTCGTGGGGT	GCAGATTGTT CCTTCCAGGT	ATGGTGACAG	TTCTCACACAT	CTGACATGGC	4560
	CACCTTCTCA	CACTOCOCCA	GAGAAAAGAG	CCTCAGCAAG	AGAGTTTTGC	CAACAATTCC	4620
	CCTTAAAAGG	AAACAGATCA	ACTACACCGC	ATCCCAACAA	CCCAGGTTCT	TTTCCTTCCT	4680
			TCTTTCCTGC				4716
25							
		137 DNA Se					
			n #: NM_0051	883.1			
	Course sed	uence: 1714 11	21	31	41	51	
30	î	î	ï	ī	ï	Ī	
	GCCTTTGGGG	AGCAGGAGGC	AGACATGTGT	TGCTTTGCAC	GTCATCTGGT	CCTTCCACCT	60
	GGCTGGGCAT	GGGATGGTGA	CCTCAGCTGG	AACATGGGGC	TCGAGCCAGA	CCTCAGGGTC	120
	TCCCTGCGTG	TAGCCCCCAA	CCCCAAGCCT	GATCCCCACC	GGAGACCTGA	ACAGCCTTGG	180 240
35	ACATCATCGG	ATCAGGGTGG	GAGGTGCCAG	CCTCTGCCAC	CTGACTTCCA	GTCCCTGTGC GCAACCCAAA	300
23	CCCTCCCACC	CIGCCCTIGG	GCACICCIGC	CAGCCTGGAC	TTCCCAGCCC	CTCTGGGGCA	360
	GCATCTGGGT	GCCAGACCTC	GGTTCCTAGG	GCCTCGTTTC	TCCCTCTGGG	AACAGCCAAA	420
	TGGTGGTCCC	TGAGACTCAG	GACAGACCAA	GAAGAAGCCG	GATGACATGG	CAAGCCACAC	480
40	ACTGCGTCCC	CTGAGCAGGA	CGGGACAGCC	CGACTCCATC	CTCCCACCTC	CGACTGAGCC	540
40	CCCACCCCTA	CTCCTGTCCC	AGCCGTGCCC	CTGGTGACAT	TTGGGTGGG	GGGGAGGGGA	600
	TGAGGGGGCA	CCTGGGGGTG	AGAGAACAAA	TGACGGGTGA	ATACATGTGT	GTGGCCAGGT	660 720
	CTCCCACCCC	CACCTCCCA	CACCCATCCC	CTCCCATTGG	TGGTCTGAG	GGGGCTCAGG CAAAGGCGGA	780
	CIGGCAGGG	GAGGGGCTGAT	GGGAAAGGAA	CAAAGAGGGA	AGGGGGGCGT	GAAGGGGGTT	840
45	CCGGCGGGAG	GGCCGAGCCC	AGGGAGGAGG	CGCCGGCCAG	CTGGACAGAG	GGAGGAGGCC	900
	AGGCCAGAGG	CAGAAGACG	CCAGAGGCAC	AAAGAAGCCA	GCCCCCTGGG	GGAGTCAAGG	960
	GATGGGGCAC	AGACTGCCC	GCCAGCAGG	GACCAGCTGA	AGGCTGCGC	A GGGGGTGCGG	1020
	GCCACACAG	TAGCCACCC	r GAGCTCAGCC	ACCGATGGAG	GCTCGTGGG	CTGCTGCGGT	1080 1140
50	GATGGCGGTC	GCTTGGGT	CATCIGICCI	CCCGTTTCTC	CACAGCIIA	GTGTCACCCA TGTCTGCCCC	1200
50	COCCUTC	COGTORICA	CTGGGCAGG	TIGCTITTAL	GGGGGAGGG	CCTGTCTGTC	1260
	TGTCTGTCG	CCTCTCTGG	C TGTGAGCCTC	GGGGTGCTG	GCTGGCCAG	r ccccrrccrc	1320
	GGTTAGGCTC	3 TCCCAGCTG	T CTGAGTGTTT	GTCCGGCTG1	CAGGATGTG	r cctgggggct	1380
<i>E E</i>	GGGAAGGAG	A GGCCGACCC	A TNGTCTGTCC	GTCGACTGG1	CAGTTGGAC	TTCAGCTGTC	1440
55	TGTACGTCT	TCTGCTGGC	C CATCTGTCT	CCCTTGGGG	CACCTCTCA	C TCCACCTGCC	1500 1560
	CCTCTGCGC	COGGATIGO	C CCCAACCCA	CACGIGGGC	CACCCCCCC	C CACACCAGTG G GCTTAGGTCA	1620
	GGGGCGTC	T GTCCCCCC	G CATCACCON	COCTOCCOA	ACCATCAGO	T GAACCCTCTG	1680
	ACCCTGTGA'	T CCCAGACGC	T GCAGGAGCTY	3 AAGATGGCG	A GCTCCGTGG	C GCCCTACGAG	1740
60	CAGCTGGTG.	A GGCAGGTGG	A GGCCTTGAA	G GCTGAGAAC	A GCCACCTGA	G GCAGGAGCTA	1800
	AGGGACAAC	T CCAGCCACC	T GTCCAAGCT	G GAGACAGAG	A CGTCGGGCA	T GAAGGAGGTC	1860
	CTGAAGCAC	C TACAGGGAA	A ACTGGAGCA	G GAGGCCCGA	G TGCTGGTGT	C CTCGGGGCAG	1920 1980
	ACGGAGGTG	C TGGAGCAGC	T GARGGCCCT	A CAGAIGGAC	C CERCOCOCC	T GTACAACCTC A GGGCAGCCCA	2040
65	GTACACCCC	T COCCCACCC	C CARCECCEGA	C TTTCCCGAG	C TGAGCCGGG	C CACCATCCGG	2100
•••	CTGCTGGAG	G AACTGGACC	G GGAACGGTG	T TTCCTGCTG	A ATGAGATTG	A GAAGGAGGAG	2160
	AAGGAGAAG	C TCTGGTACT	A CTCTCAGCT	G CAGGGCCTG	T CCAAGCGCC	T GGACGAGCTG	2220
	CCGCACGTG	G AGACGCAG1	T CTCGATGCA	G ATGGACCTG	A TCCGGCAGO	A GCTTGAGTTC	2280
70	GAGGCCCAG	C ACATCCGCT	C GCTGATGGA	G GAGCGCTTC	G GCACCTCGC	A CGAGATGGTG	2340 2400
70	CAGCGGGCA	C AGATCCGCC	C CTCGCGCCT	G GAGCAGATT	G ACAAGGAGG	T GCTGGAGGCG C GGTGCCGGTG	2460
	CAGGACCGA	C CCCAGACAC	A GCTCCCCA	A CACCCTGAG	G ATGGCACCO	C TCAGCCGGGC	2520
	AACAGCAAG	G TGGAGGTG	T CTTCTGGCT	G TIGTCCATG	T TGGCGACG	G CGACCAGGAG	2580
	GATACAGCO	C GCACGCTG	T GGCCATGTC	C AGCTCGCCC	G AGAGCTGC	T GGCCATGCGC	2640
75	CGCTCGGGG	T GTCTGCCTC	T GCTGCTGCA	A ATCCTCCAC	G GCACCGAGO	SC CGCGGCCGGG	2700
	GGTCGCGCC	G GGGCCCCAC	G GGCACCGGG	C GCCAAGGAC	G CACGCATG	CGCCAACGCG	2760
	GCGCTGCAC	A ACATOGTO	TT CTCGCAGCC	GACCAGGGC	TGGCGCGC	A GGAGATGCGC	2820 2880
	GTCCTGCAC	G GCGGGCCCC	LA GOGLOGOGO	C GCCCCCAC	G CCCCGATC	BA CTGGCTGCAG CC CATCGAGCCG	2940
80	CAGATCTG	C AGGCCACC	IG TGCTGTTAT	G AAGCTGTCC	T TTGATGAG	A GTACCGCCGT	3000
	GCCATGAAG	G AGCTAGGT	GG GCTGCAGGG	C GTGGCAGAC	C TGCTGCAG	T TGACTATGAG	3060
	ATGCACAAC	A TGACCCGG	GA CCCGCTGA	AC CTGGCGCTC	C GCCGCTAC	C GGGCATGACC	3120
	CTCACCAA	C TCACCTTT	GG GGACGTTG	C AACAAGGCC	A CCCTGTGT	SC GCGCCGCGGC	3180
	TGCATGGAG	SG CCATCGTG	GC CCAGCTGGG	C TCCGACAGT	TO AGGAGCTC	CA CCAGGTGGTG	3240



	TCCAGCATCC '	TTCGGAACTT (	STCCTGGAGG (	GCCGACATCA	ACAGCAAGAA	GCTGCTGAGG	3300
	GAGGCGGGCA						3360
	CTGAAGAGCG						3420
-	GCCATCTGCC .						3480
5	CAGAGCAACT	CGCTGGCCAT (	CATCGAGAGC (	GGCGGCGCA	TCCTCCGCAA	TGTGTCCAGC	3540
	CTCGTCGCCA	CCCGTGAGGA (	CTACAGGCAG	GTGCTCCGGG	ATCACAACTG	TCTGCAGACG	3600
	CTGCTGCAGC						3660
	TGGAACCTGT	CGGCCCGCAG (	CGCCCGTGAC	CAGGAGCTGC	TGTGGGACCT	GGGCGCCGTG	3720
	GGCATGCTGC	GTAATCTGGT	GCACTCCAAG	CACAAGATGA	TCGCCATGGG	CAGOGCOGCC	3780
10	GCCCTGCGCA	ACCTGCTGGC	CCATCGGCCC	GCCAAGCACC	AGGCGGCCGC	CACCGCCCTG	3840
	TCCCCAGGCA	GCTGCGTGCC	CAGCCTGTAC	GTGCGCAAGC	AGCGGGCGCT	GGAGGCCGAG	3900
	CTGGACGCAC	GGCACCTCGC	GCAGGCGCTG	GAGCACCTGG	AGAAGCAGGG	CCCGCCGGCA	3960
	GCCGAGGCCG	CCACTAAGAA	GCCGCTGCCG	CCCCTGCGAC	ACCTGGACGG	CCTGGCCCAA	4020
	CACTATGCTT	CCGATTCGGG	CTGCTTTGAC	GACGACGATG	CACCGTCATC	CCTGGCTGCG	4080
15	COCCOCCOCA	CCGGGGAGCC	AGCCAGCCCT	GCCGCGCTGT	CCCTCTTCCT	GGGCAGCCCC	4140
	TOTTECAGE	GGCAGGCGCT	CCCTCCCACC	CCCCCACCC	GCCGAGGCGG	CAAGGAGGCA	4200
	CACAACCACA	CCAGTGGGGA	CCACOCAGE	COCCOCCARCO	CCAACCCCAA	CCTCCCCCTT	4260
	GAGAAGGACA	GCATCGACCA	CCTCCTCCAG	CACATCTCCC	CCTGCACAC	CTCCTCCGAC	4320
	GCAGTGGCGC	GCCTCAGCTC	GC100100W0	CCACATCTCCC	CCCTOCTCG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	4380
20		CGCCATGCCG					4440
20	CAGTCCTGCT	CGCCATGCCG	COGCCCCGGAG	GOCGGGGGGGG	CALACCACAC	CCTCAACACC	4500
	CACCOGCTGC	TGCGGCTCAA	GGCGGCCCAC	GCCAGCCICI	TOTALONG	CCTCACCAC	4560
	CCCACTCCCA	GCGACGGGTA	CTGCCCACGC	GAACATATGC	1GCCC1GCCC	GC I GGCCGCA	4620
	CIGGCTTCGC	GCCGCGAGGA	CCCCAGGIGI	GGGCAGCCTC	GGCCCAGCCG	GCTTGACCTT	
25		GCTGCCAGGC					4680
25	GTGCGCACCA	TCAAGCTGTC	GCCTACCTAT	CAGCACGTGC	CACTGCTTGA	GGGTGCCTCA	4740
	AGGGCGGGTG	CAGAGCCCCT	CCCCCCCCT	GGAATCTCTC	CAGGGGCCCG	GAAGCAGGCC	4800
	TGGCTGCCGG	CAGACCACCT	GAGCAAGGTT	CCCGAGAAGC	TGGCCGCTGC	CCCCCTGTCT	4860
		AGGCACTGCA					4920
••	TGCAGCTCCC	TTTCCTCGCT	GTCCTCGGCC	GGCCGCCCAG	GCCCCAGCGA	GGGTGGTGAC	4980
30	CTGGATGACA	GTGACTCCTC	CCTGGAGGGG	CTGGAGGAGG	CCGGCCCCAG	CGAGGCTGAG	5040
	CTGGACAGCA	CGTGGCGGGC	GCCCGGGGCC	ACCTCGCTGC	CCGTAGCCAT	TCCGGCTCCC	5100
	CGGCGTAACC	GAGGCCGGGG	CCTGGGGGTG	GAAGACGCCA	CGCCGTCCAG	CTCGTCGGAG	5160
	AACTACGTGC	AGGAGACACC	<b>GCTTGTGCTG</b>	AGCCGCTGCA	GCTCTGTGAG	CTCGCTGGGC	5220
	AGCTTCGAGA	GCCCGTCCAT	CGCCAGCTCC	ATCCCCAGTG	AACCTTGCAG	CGGGCAGGGC	5280
35	AGCGGCACCA	TCAGCCCTAG	CGAGCTGCCC	GACAGCCCCG	GACAGACCAT	GCCTCCCAGC	5340
	CGGAGCAAGA	CGCCACCGCT	GCCCCCCCC	CCACAGGGTC	CCCCCGAGGC	CACCCAGTTC	5400
	AGCCTGCAGT	GGGAGAGCTA	CGTGAAGCGC	TTCCTGGACA	TCGCCGACTG	CCGGGAGCGC	5460
	TGCCGGCTGC	CATCTGAGCT	GGACGCAGGC	AGCGTGCGCT	TTACCGTGGA	GAAGCCAGAC	5520
	CAGAACTICT	CCTGCGCCTC	CAGCCTCAGC	GCGCTGGCCT	TGCACGAGCA	CTACGTGCAG	5580
40	CACCACCTCC	ACCTCCCCT	CCTCCCCTCC	CCCTCCCCC	ACCORPORAGE S	GGGCGCCGGG	5640
40	CAGGACGIGG	MOCIOCOGCI	ACCCCACCCC	CCCCCCCCCCC	ACCCCCCCCC	GCCCACGGGT	5700
	***************************************	CONTITION	CCACCACCAC	CTCCAACTCC	TOCCCACTO	CCTGGGAGCC	5760
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COCCCCCCC	CARCCTCCCC	TOCCOCOTO	TOCCAGGTOG	CCGCGCACTC	5820
	GCCGIGCCIG	**************************************	CONGREGACE	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCACCACCA	CGACTCCTGC	5880
45	CCCG1GCCCG	COCACAIGII	COCCOCC	THOROTACO	CCCAGGAGGA	CACCCACCAC	5940
73	ACTGACTCCG	CUGAGGGCAC	GCCGGTCAAC	COCCOCACCAC	CCCCCTCCCT	CAGCGACGAG	6000
-	ACGCTGCAGG	GACCCCCCAG	GGACCAGCCC	GGGGGACCAC	A CONTRACTOR	AAGACCCACC	6060
						AGGCGCCGGC	
	CGCAGCGCGG	AGCAGTCTCG	GGGCGCGGGC	AAGAACCGAC	CAUGUCTUSA	GCTGCCCCTG	6120
50						GACCCGCGG	6180
50	GACGGGGCGC	TCCAGTCGCT	GTGCCTCACG	ACGCCCACTC	AGGAGGCCGT	GTACTGCTTC	6240
	TACGGCAACC	ACTCGGACGA	GGAGCCCCCG	GCGGCCGCGC	CCACGCCAAC	CCACCGGCGC	6300
	ACATCGGCC	A TCCCTCGCGC	TTTTACGCGG	GAGCGTCCGG	C AGGGCCGGA	GGAGGCCCCT	6360
	GCCCCGTCC	AGGCTGCACC	AGCTGCCCCC	CCCCCCCCCCCC	C GGACCCAGC	CAGCCTCATT	6420
	GCTGACGAGA	CCCCGCCCTG	CTACTCCCTG	AGCTCCTCC	G CCAGCTCCCT	CAGCGAGCCC	6480
55						CACCAAGGAC	6540
	CCGGGCCCAC	GAGGCGGACG	CGACAGCTCC	CCCAGCCCG	c gegeegeggi	GGAGCTTCTG	6600
	CAGCGGTGC	A TCAGCTCGGC	CCTGCCCAGG	CCCCCCCCCC	C CCGTGTCTGC	CCTGCGGCGC	6660
	CGCAAGCCCC	GAGCCACCCC	GCTGGATGAC	CGGCCCGCA	G AGGGGTCCC	GGAACGCGGC	6720
	GAGGAGGCAG	CGGGCTCGG2	CCGGGCCTCC	GACCTGGAT	A GCGTGGAGT	GCGCGCCATC	6780
60						CACGCGGGAG	6840
	GCCTCGTCC	G AGTCCGACTC	CATCCTGTC	TTCGTATCO	G GGCTGTCAG	I GGGATCCACC	6900
	CTACAGCCC	CCAAGCACAG	GAAGGGACGA	A CAGGCGGAG	G GAGAAATGG	CAGTGCCCGG	6960
	CCCCAGAG	A AAAGGGGCG	AGCCTCAGT	C AAGACCAGO	G GGAGCCCCC	G TTCCCCTGCA	7020
						C TGTGCTCCGG	7080
65	CCACCAACA	G TGATCTACG	CCCCAGCCC	GCACCCCGT	G CCCAGCCCA	A AGGGACCCCC	7140
05	GCCCCCCC	G CEACACTOC	CAACGTGGC	CCCCCTTGC	C TGGCACAGO	C CGCGGCTCCA	7200
	CCCAAAGTC	C CCAGCCCCCC	CCACCACCC	TOCOCCACO	C TACACOGGO	C TGCCAAGACC	7260
	TOTAL	C CCACCCTCA	CCAGCCCCC	CAGAAGGGC	A CACCECCCE	C CCGCCTCGCC	7320
						T GCCCAGAAAG	7380
70						C CCCGGTGCCC	7440
70						C GCCCGTGCGG	7500
	AAAACGCCG	A TOCOCALCE		T CCCCCCCC	C CCCCCCCC	G GGCAGTCCCG	7560
							7620
						G CGGGGGGGGG	
75						C CGACCGCTCG	
13						G CCGCCGCTCC	
						c cccccccccc	
						T CCGAGCGGCA	
						C CAGCCCTGGC	
00						T GCGCGCGCCCC	
80						C CCTGGCCCGC	
						G CCGCAGCAGC	
						G GCGGCGCATC	
	CGAGATGAG	G ACGTGCCCC	A CATCCTGCG	C AGCACGCT1	C CCGCCACGC	C CCTGCCACTG	8220
						C CAGOGACGCC	

	GTGGTCCAGA	TODADOADO	recorded l	AAGACCAACT	CCAGCACGTC	CCCGAGCCTG	8340
	GAGACCAGGG .	AGCCCCCCGG	GCCCCCCCCCCCCCC (	GGCGGCCAGC '	TCTCCCTCCT	CGGCAGCGAC	8400
	GTGGACGGTC	CCAGCCTCGC	CAAGGCTCCC	ATCTCCGCAC	CCTTCGTGCA	CGAGGGCCTG	8460
•	GCGGTCGCCG						8520
5	GTACCCCCCT GCGGAGAAAG	TCAACTATGT	GCCCAGCCCC	ATGGTGGTCG	CAGCCACCAC	TACCOCCCC	8580 8640
	GCGGAGAAAG	TTCTCTCCCC	GCCCTGCGGC	GCGCTCTGG	TOTOTOTOG	GCCTGCGCTG	8700
	TAGACGTCCC	CCATAGGTCG	CCCCAGGGCC	TCTGCCCACC	CGAGCCCCAC	CACTCTCAGA	8760
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10	GAGGTCCAGG	AGGAAACGGG	GCGGCCGCTA	GGCCTCAAGT	CCCGACCGTG	GAGCGCTGGC	8880
	AAGGGCGTCC	TGGCCCAGCC	CTGAGCGCGC	GCCCCTTCCC	CTGTCGGAAG	CCGTTGCTTG	8940
	ACCCCGGGCG	AGGGAGGCGG	TAGCCTCCGG	GTCCGGGTCT	CCCCCACC	CCGCTGCTTC	9000 9060
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20	GGCAGCGGGC	TGCGTACGAT	GGGACCTGGT	GCAGACGCCG	GGCCGGCTGA	TOCACTCACT	9420 9480
20	CCATCCCAGA	GGAGATGCTG	GCTACCAGCT GCGGGCGAGG	CCAATCCAAA	CCAGACTGAG	GGGAGTCCCG	9540
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	CACGTTACGG	AGACCATCAC	ATGTGGGCGT	GGTCAGTGCC	CAGGACCGCA	CCGCTGCTCA	9660
	TCTTGTCCCT	TTTCAATTCC	CTTCTGGTTC	<b>ATGATGCATA</b>	AAGCGCTAGG	CCCTAGAACT	9720
25	CCAGAAACAG	CACAGCTGGG	GCGGGGACCC	AGCCTTGCCC	TCCACCCGAG	GCTCTGGGAC	9780
	AAGGCGGGAG	GTTCGGGGGC	CTTCCGGCAG	GTGAACGCAG	GGCTGGAGAG	TATTTGGTGC	9840 9900
	CAGATGAGGT	GAAAGCTTAT	AGAAGGGCCT	GAGGGGCTCG	CCACCCCCCC	GGTCTCCGTG	9960
	PLACECCUP P	CCCTCCTCC	TCCIGCGIGG	GCCGACAACC	TCTTTTCTGC	AGAAAAGCTC	10020
30	CAGCAGGCGC	TGCCTTCACC	CACGGATCTG	CCCAGGCTGA	AGGCACACGC	TCAATGCCCC	10080
	ACCTGCCTTC	TCCAGGAGGA	ACGAACCAGG	GTTTGAGGGT	TGGGTGGATG	GAGCTCAAAA	10140
	GGAAACCCCCA	GCCCCACCAC	GGATGACCCA	TCCCTCCCCT	CCCATCCCCA	GCATGGGCAA	10200
	GGCCAGCCTT	TCTGGCAAAA	GGAGCTGTCC	TCAACTCAGG	GCCGCTGTGA	GCAAAGCTGA	10260 10320
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55	CAIGCICCGG	CACCCACACCC	GTGCTGGAGG	TGCCCAATGC	TCCCTCCTAG	GACCTCGCAG	10440
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40	TCTTCTGAGC	TTTTGGACTT	GGGGATGCCA	AACACGTGCT	CACCCTCACA	CTCGCCCCGG	10680 10740
	CCCGCTGCGC	CCCTAATIGC	CAAAGGGTAG	CCTCCCCCAT	TOCOTTOCA	CCAGGTCGCT ATATGTAAGT	10800
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						A TGGCGCGCGC	11460
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55	ATCTCTCCC	CTABGGSO	C ACACCETCAC	CTGTCCGAC	CGCACACAT	TAATAAACTG	11640
	AGCTCTTGC	Corrections	- nanccoran				11649
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	CTCCTCACA	G AAGCCTGGA	G CTGGGCATC	AAGAAGAAG	C AGCCTCATT	T GTTTTCTGGT	60
65	GTCATCGTA	G GTGGCCACC	T ATGGCTTTT	G GGAATGTAA	A AAGGGCAGC	T CTCTGGCATG	120
	TTCCTGACT	G AGGATCTCA	T AACATTTAA	C TTGAGGAAC	T TOOTCOTT	T CCAGCTTTGG	180 240
	GAGTCAAGC	T TOTCACCIG	G GGCGGGTGG	C ACCGACACC	T CCCCCCCC	C TTCATCTCCTC	300
						A ACGGTGCCTC	360
70	TGCGTCCTG	C CACTCAGGA	C CTCTCAAGT	CCCGATGTG	A TGGCTCCTC	A GCATGATCAG	420
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	GATCTATAT	G GCTATAGCA	C CAGCTCTTT	G GCTCTTGGC	T TGGCATGGC	T AAGTTGGGAG	540
						A AGCCTTCCCA	600 660
75	GTTGACTGA	A AUATUAUGO A GABTGABOT	AGGCTCTAG	C AGCTTOTAG	C CCAGGAAGG	T CCTTCAAGAA C CACTGTACCT	
, ,	GGAGCCATC	T GGGATAAGA	C TTTGACCCA	T GACTCCCAT	A TCCACAGCO	T GTCCATCCTA	780
	GCCCATCCC	A GTTTATCCT	G TATCATTIC	A GCTGGGATT	C CCACATCC	C TGAGTTGGAA	840
			A TAAAGACTC				879
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	CCACGCGTCC GGAACGTCTT TTTGCCGACG CCCTCGGAGC AGCCGCGATG GCCAGCACCA	60
	GGACTATOGA GCTGGAGCAC TTTGAGGAAC GGGACAAAAG GCCGCGGCCG GGGTCGCGGA GAGGGGCCCC CAGCTCCTCC GGGGGCAGCA GCAGCTCGGG CCCCAAGGGG AACGGGCTCA	120 180
	TCCCCAGTCC GGCGCACAGT GCCCACTGCA GCTTCTACCG CACGCGGACC CTGCAGGCCC	240
5	TCAGCTCGGA GAAGAAGGCC AAGAAGGCGC GCTTCTACCG GAACGGGGAC CGCTACTTCA	300
	AGGGCCTGGT GTTTGCCATC TCCAGCGACC GCTTCCGGTC CTTCGATGCG CTCCTCATAG	360
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	CCATCGACGG CAGCCGGAAG GTCACCAGCC TGGACGAGCT GCTGGAAGGT GAGAGTTACG	480 540
10	TGTGTGCATC CAATGAACCA TTTCGTAAAG TCGATTACAC CAAAAATATT AATCCAAACT GGTCTGTGAA CATCAAGGGT GGGACATCCC GAGCGCTGGC TGCTGCCTCC TCTGTGAAAA	600
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	GAGTGAAGCC TAGAAAAGCC GTGCGGATCC TTCTGAATAA AAAGACTGCT CATTCCTTTG	720
	AACAAGTCTT AACAGATATC ACCGAAGCCA TTAAACTAGA CTCAGGAGTC GTCAAGAGGC	780
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15	TTTTTATTGC ATGTGGACCA GAAAAATTTC GTTATGCCCA AGATGACTTT GTCCTGGATC	900
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	GCCTCTCCCT GGCTCGAATG CCCCCTCCAC TCCCGACCCG GGTGGATTTC TCCCTGGCTG	180
	GGGCACTCAA TGCTGGCTTC AAGGAGACCC GGGCCAGTGA GCGGGCAGAG ATGATGGAGC	240
	TCAATGACCG CTTTGCCAGC TACATCGAGA AGGTTCGCTT CCTGGAACAG CAAAACAAGG	300
	CGCTGGCTGC TGAGCTGAAC CAGCTGCGGG CCAAGGAGCC CACCAAGCTG GCAGACGTCT	360

	ACCAGGCTGA GCTGCGAGAG CTGCGGCTGC GGCTCGATCA ACTCACCGCC AACAGCGCCC	420
	GGCTGGAGGT TGAGAGGGAC AATCTGGCAC AGGACCTGGC CACTGTGAGG CAGAAGCTCC	480
	AGGATGAAAC CAACCTGAGG CTGGAAGCCG AGAACAACCT GGCTGCCTAT AGACAGGAAG	540
-	CAGATGAAGC CACCCTGGCC CGTCTGGATC TGGAGAGGAA GATTGAGTCG CTGGAGGAGG	600
5	AGATCCGGTT CTTGAGGAAG ATCCACGAGG AGGAGGTTCG GGAACTCCAG GAGCAGCTGG	660
	CCCGACAGCA GGTCCATGTG GAGCTTGACG TGGCCAAGCC AGACCTCACC GCAGCCCTGA	720
	AAGAGATCCG CACGCAGTAT GAGGCAATGG CGTCCAGCAA CATGCATGAA GCCGAAGAGT	780
	GGTACCGCTC CAAGTTTGCA GACCTGACAG ACGCTGCTGC CCGCAACGCG GAGCTGCTCC	840
	GCCAGGCCAA GCACGAAGCC AACGACTACC GGCGCCAGTT GCAGTCCTTG ACCTGCGACC	900
10	TGGAGTCTCT GCGCCGCACG AACGAGTCCC TGGAGAGGCA GATGCGCGAG CAGGAGGAGC	960
	GGCACGTGCG GGAGGCGGCC AGTTATCAGG AGGCGCTGGC GCGGCTGGAG GAAGAGGGGC	1020
	AGAGCCTCAA GGACGAGATG GCCCGCCACT TGCAGGAGTA CCAGGACCTG CTCAATGTCA	1080
	AGCTGGCCCT GGACATCGAG ATCGCCACCT ACAGGAAGCT GCTAGAGGGC GAGGAGAACC	1140
	GGATCACCAT TCCCGTGCAG ACCTTCTCCA ACCTGCAGAT TCGAGAAACC AGCCTGGACA	1200
15	CCAAGTCTGT GTCAGAAGGC CACCTCAAGA GGAACATCGT GGTGAAGACC GTGGAGATGC	1260
	GCGATGGAGA GGTCATTAAG GAGTCCAAGC AGGAGCACAA GGATGTGATG TGAGGCAGGA	1320
	CCCACCTGGT GGCCTCTGCC CCGTCTCATG AGGGGCCCGA GCAGAAGCAG GATAGTTGCT	1380
	COGCOTOTIC TOGGACATTT CCCCAGACCT GAGCTCCCCA CCACCCCAGC TGCTCCCCTC	1440
	CCTCCTCTGT CCCTAGGTCA GCTTGCTGCC CTAGGCTCCG TCAGTATCAG GCCTGCCAGA	1500
20	COGCACCCAC CCAGCACCCA GCAACTCCAA CTAACAAGAA ACTCACCCCC AAGGGCAGTC	1560
20	TGGAGGGGA TGGCCAGCAG CTTGCGTTAG AATGAGGAG AAGGAGAGAA GGGGAGGAGG	1620
	TGGAGGGCA TGGCCAGCAG CTTGCGTTAG AATGAGAGG AAGGAGAGA GGGAAGAGAG	1680
	GCGGGGGCA CCTACTACAT CGCCCTCCAC ATCCCTGATT CCTGTTGTTA TGGAAACTGT	1740
	TGCCAGAGAT GGAGGTTCTC TCGGAGTATC TGGGAACTGT GCCTTTGAGT TTCCTCAGGC	-
25	TGCTGGAGGA AAACTGAGAC TCAGACAGGA AAGGGAAGGC CCCACAGACA AGGTAGCCCT	1800
25	GGCCAGAGGC TTGTTTTGTC TTTTGGTTTT TATGAGGTGG GATATCCCTA TGCTGCCTAG	1860
	GCTGACCTTG AACTCCTGGG CTCAAGCAGT CTACCCACCT CAGCCTCCTG TGTAGCTGGG	1920
	ATTATAGATT GGAGCCACCA TGCCCAGCTC AGAGGGTTGT TCTCCTAGAC TGACCCTGAT	1980
	CAGTCTAAGA TGGGTGGGGA CGTCCTGCCA CCTGGGGCAG TCACCTGCCC AGATCCCAGA	2040
20	AGGACCTCCT GAGCGATGAC TCAAGTGTCT CAGTCCACCT GAGCTGCCAT CCAGGGATGC	2100
30	CATCTGTGGG CACGCTGTGG GCAGGTGGGA GCTTGATTCT CAGCACTTGG GGGATCTGTT	2160
	GTGTACGTGG AGAGGGATGA GGTGCTGGGA GGGATAGAGG GGGGCTGCCT GGCCCCCAGC	2220
	TGTGGGTACA GAGAGGTCAA GCCCAGGAGG ACTGCCCCGT GCAGACTGGA GGGGACGCTG	2280
	GTAGAGATGG ACGAGGAGGC AATTGGGATG GCACTAGGCA TACAAGTAGG GGTTGTGGGT	2340
	GACCAGTTGC ACTTGGCCTC TGGATTGTGG GAATTAAGGA AGTGACTCAT CCTCTTGAAG	2400
35	ATGCTGAAAC AGGAGAGAAA GGGGATGTAT CCATGGGGGC AGGGCATGAC TTTGTCCCAT	2460
	TTCTAAAGGC CTCTTCCTTG CTGTGTCATA CCAGGCCGCC CCAGCCTCTG AGCCCCTGGG	2520
	ACTGCTGCTT CTTAACCCCA GTAAGCCACT GCCACACGTC TGACCCTCTC CACCCCATAG	2580
	TGACCGGCTG CTTTTCCCTA AGCCAAGGGC TCTTGCGGTC CCTTCTTACT CACACAAA	2640
	ATGTACCCAG TATTCTAGGT AGTGCCCTAT TTTACAATTG TAAAACTGAG GCACGAGCAA	2700
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-10	CCACCCCAGT GCACCCACTC TGCTTTGACT GAGCAGACTG GTGAGCAGAC TGGTGGGATC	2820
	TOTAL CATOCOLOGO COLCECCO CTTCACCCT CTCCTCTCCC CTCTACCCC	2880
	TGTGCCCAGA GATGGGACTG GGAGGGCCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC	2880 2940
	TGTGCCCAGA GATGGGACTG GGAGGGCCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC	2940
45	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAGAAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG	2940 3000
45	TGTGCCCAGA GATGGGACTG GGAGGGCCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC	2940
45	TGTGCCCAGA GATGGGACTG GGAGGGCCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA	2940 3000
45	IGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA Seq ID NO: 149 DNA Sequence	2940 3000
45	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1	2940 3000
	TGTGCCCAGA GATGGGACTG GGAGGGCCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845	2940 3000
45 50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCGAGAAAGGT CTCCTCTCCC CTCTAAGGCT GAGAAAGGT CTCTCCTCCC TCTCAAGACT GACTGCTGCTG CTCAACTCTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGGAAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3000
	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3000 3033
	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGGC GAAGAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3000 3033
	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 445.1845 1 11 51	2940 3000 3033 60 120
50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding Bequence: 4451845 1 11 21 31 41 51	2940 3000 3033 60 120 180
	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTCCCCTC CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 445.1845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240
50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300
50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300 360
50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300 360 420
50 55	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCG GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGTGCG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 445.1845 1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300 360 420 480
50	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 420 480 540
50 55	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTCCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGATTGT CCCTCTCAAC CTCCAGCCGG GCGCTGTTGG CCTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCTCA GCCTGGTAGA CGTCTGCCAG CTTGGTGGGC TCCTTGGCC GCAGCTGCTT CAGCCTCAG AGCCAGCCG TTGGTTTTCT GTTCAGGAA GGAACCTTC TCGATGTAGAC GCCTGGTAGA CCATCATCTC TGCCCGCTCA CTGGCCCGGG TCCCTTGAA GCCAGCATGA AGTGCCCCAG CCAGGAGCAA ATCCACCCGG GTCGGAGTGG AGGCGGGCAT TCAGCCTGGA AGAGCGGCCA CCAGGGCCCA GACGCGGCC AGGAGCCTGC TCCCCCCCA TCATCTCCCC TGAGGAGAGG TAGGAGCCCC GACGCGGCC AGGAGCCTC TCCCTCTCCA CCTCCCCCCAGGAGACGC TAGGAGCGCC GAGCAGGGGA GGTGATGGGT CTCCTCTCCA CCTCTCCCC TGAGGAGAGG TAGGAGCCCC GCCGCGGGCC AGGGCCCCCCCCCCACA TCATCTCCCC TGAGGAGAGG TCCTCCCAGTG CTGAAGAATA CCAGCCTCCT ATATGGAAAT CATACTTATA TCAGTTACAGC CAAGAGGCAC CTCCTCCCCAA AGAAATCATT TGTCCTCGGG AGGGGGAAAA CAGACCCAAAA	2940 3000 3033 60 120 180 240 360 420 480 540
50 55	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 360 420 540 660
50 55	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAAGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 445.1845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300 420 480 600 660 6720
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGATTGT CCCTCCACC CTCCAGCCGGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCCTCA GCCTGGTAGA CGTCTGCCAG CTTGGTGGGC TCCTTGGCC GCAGCTGGT CAGCCTCAGC AGCCAGCGCC CTTGGTTGC CTTCAGGAA GGCAACTTC TCGATGTAGAC GGCTGGTAGA CCATCATCTC TGCCCGCTCA CTGGCCCGGG TCCCTCTGAA GCCAAGCGGCCC CCAGGGAGAA ATCCACCCCGG GTCGGAGTGG AGGGGGGATT AGTGCCCCAG GCAGGACCA GACGCGGCC AGGACCTCT CAGCCCAGGA GAGGGGGGAT TAGGAGCCGC GAGGCGGCA GCTGCTCTCCAC TCATCTCCCC TAGGAGAAGA TAGGAGCGCC TCCTCCAA GAGAATCAT TCTCTCCCC TAGGAGAACA TATTATGGAA GAGAGTTTCA TGGGATCATC TCTCGGGAGC AGCCGCAAAA TATTATGGAA GAGAGTTTCA TGGGATCATC TCTCGGGAGC AGCCGAATG CCCTCCAGGT TTGGAAACACA CCTCTAAGAAA ACCAGCGAGC AACCAGAATG CACAGGAGCAC TCCTCCCCAA GAGAATCATC TCTCGGGAGC AGCCGGATGA GCTCTCTGGA GCCTTCTAGGT TTGGAAAACCA CCTCTAAGAAA ACCAGGAGT CTACCTCTTGAG GCCTCCAGGGT TTGGAAACCA CCTTAAAAC TACAGGAGG GAAACCACTT	2940 3000 3033 60 120 180 240 360 420 480 540 660 660 720 780
50 55	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCG GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845  1 11 21 31 41 51	2940 3003 3033 60 120 180 240 360 420 540 660 720 780 840
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGCTGCT CCCCTCCAC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCCTCA GCCTGGCAGCTG GCGCTGTTCG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCACCTCAC ACCCAGCAGC CTTGGTTTTCT GTTCCAGGAA GCGAACCTTC TCGATGTAGC TCCAGCAGCA CCATCATCTC TGCCCCGCTCA CTGGCCCGGG TCTCCTTGAA GCCAGCATTG AGCCAGGCC CCATCATCTC TGCCCCGCTCA CTGGCCCGGG TCTCCTTGAA GCCAGCATTG AGTCCCCCG CCAGGAGCAA ATCCACCCGG GTCGGAGTGG AGGGGGGATT CGAGCAGGGA AGCCAGCGGT TAGGAGCCCA GACGGCGGCC AGGAGCCAGG CCCCCCACCA TCATCTCCCC TGAGGAGAG TCCTCCGATG CTGAACAAATA CCAGCCTCCT ATATGGAAAT CATACTTTATA TCAGGTGCAAAGGCAC CTCGTCCCCAA AGAGACCATA TCATCCCCC TGAGGAAAACATTATTATGGAAA GAGAGTTTCA TGGGATCATT TGTCCTCGGG AGGTGGAAAA CAGACCAAAA TATTATGGAA GAGAGTTTCA TGGGATCAT TTCTCTGGGA AGCGGAGTG ACCAGGATG GCCTGCAGGAG GCCTCTCACAC CTCTTAGAGAAA AGCCAGCGCG AACCAGGATG CTCCTCTGGG GCCTCTCAGGT TTGGAAACCA GACCTTAAAC TACAGGCTCT TCCACGACGG GAAACACATTT GTGGGTGAGA AGAGGCTTCAT CCTTTAGAGAA AGCCAGCGC AACCAGGATG CTACACCCCT GTGGGTGAGA AGAGGCTTTCA TGGGATCATT CTTCAGGAGAG CACCAGGATG CTACACCCCT TCCTCGAGAG GGCCTTACAT CCTTTAGAGAA AGCCAGCGCG AACCAGGATG CTACACCCCT TCCTCGAGAG GTGCCTTACAT CCTTTAGAGAA AGCCAGCGCG AACCAGGATG CTACACCCCT TCCTCGAGAGA AGAGGTTTCA TGCAGTACAT TCCTCGGGA CACCAGGATG CTACACCCCT TCCTCGAGAA AGAGGTTTCAT GATCTCGGTGA AGAGGCCTCT TCCACGACGC GACCAGAAACACTTT TCCTTCGAAAACA AGACCTTTCATT CAAAATGAACCC ACTTTATGAAACCC ACTTTATGAAA	2940 3000 3033 60 120 180 240 300 420 480 600 660 720 780 840 900
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGCTGCT CCCCTCCAC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCCTCA GCCTGGCAGCTG GCGCTGTTCG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCACCTCAC ACCCAGCAGC CTTGGTTTTCT GTTCCAGGAA GCGAACCTTC TCGATGTAGC TCCAGCAGCA CCATCATCTC TGCCCCGCTCA CTGGCCCGGG TCTCCTTGAA GCCAGCATTG AGCCAGGCC CCATCATCTC TGCCCCGCTCA CTGGCCCGGG TCTCCTTGAA GCCAGCATTG AGTCCCCCG CCAGGAGCAA ATCCACCCGG GTCGGAGTGG AGGGGGGATT CGAGCAGGGA AGCCAGCGGT TAGGAGCCCA GACGGCGGCC AGGAGCCAGG CCCCCCACCA TCATCTCCCC TGAGGAGAG TCCTCCGATG CTGAACAAATA CCAGCCTCCT ATATGGAAAT CATACTTTATA TCAGGTGCAAAGGCAC CTCGTCCCCAA AGAGACCATA TCATCCCCC TGAGGAAAACATTATTATGGAAA GAGAGTTTCA TGGGATCATT TGTCCTCGGG AGGTGGAAAA CAGACCAAAA TATTATGGAA GAGAGTTTCA TGGGATCAT TTCTCTGGGA AGCGGAGTG ACCAGGATG GCCTGCAGGAG GCCTCTCACAC CTCTTAGAGAAA AGCCAGCGCG AACCAGGATG CTCCTCTGGG GCCTCTCAGGT TTGGAAACCA GACCTTAAAC TACAGGCTCT TCCACGACGG GAAACACATTT GTGGGTGAGA AGAGGCTTCAT CCTTTAGAGAA AGCCAGCGC AACCAGGATG CTACACCCCT GTGGGTGAGA AGAGGCTTTCA TGGGATCATT CTTCAGGAGAG CACCAGGATG CTACACCCCT TCCTCGAGAG GGCCTTACAT CCTTTAGAGAA AGCCAGCGCG AACCAGGATG CTACACCCCT TCCTCGAGAG GTGCCTTACAT CCTTTAGAGAA AGCCAGCGCG AACCAGGATG CTACACCCCT TCCTCGAGAGA AGAGGTTTCA TGCAGTACAT TCCTCGGGA CACCAGGATG CTACACCCCT TCCTCGAGAA AGAGGTTTCAT GATCTCGGTGA AGAGGCCTCT TCCACGACGC GACCAGAAACACTTT TCCTTCGAAAACA AGACCTTTCATT CAAAATGAACCC ACTTTATGAAACCC ACTTTATGAAA	2940 3000 3033 60 120 180 240 300 420 480 600 660 720 780 840 900
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCTCAC TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3003 3033 60 120 180 240 360 420 540 660 720 840 960
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1 Coding sequence: 4451845 1 11 21 31 41 51	2940 3003 3033 60 120 180 240 360 420 540 660 720 780 900 900 900
50 55 60 65	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAAGGCC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGATTGT CCCTCTCAAC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCCTCA GCCTGGCAGCTG GCGCTGTTCG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCCTCA GCCCGGGC GCGCTGTTCG CTTGAGGTGGC TCCTTGGCC CAGCTCGTC CAGCCTCAGC ACCCAGCAC CGTCTCCCAG CTTGGTGGGC TCCTTGGCC CAGCTGGTT CAGCCTCAGC ACCCAGCAC CCATCATCTC TGCCCCGCTCA CTGGCCCGGG TCTCCTTGAA GCCAGCATTG AGTCCCCCG CCAGGAGAA ATCCACCCGG GTCGGAGTGG AGGGGGGATT CGAGCAAGGG AGAGGCGGGT TCCTCGAGG AACCACCGG GTCGGAGTGG AGGGGGGATT CGAGCAGGG AGAGGCGGGT TCCTCCGATG CTGAACAAACCCGG GCCCCCCCCCCACA TCATCTCCCC TGAGGAAGAC TATTATATGGAA AACAACCCGG AGGAACTAT TGTCCTCGGG AGGTGGAAAA CAAGAGCAC CTCGTCCCAA AGAAATCAT TGTCCTCGGG AGGTGGAAAA CAGACCAAAA TATTATGGAA GAAGATTTCA TGGGATCAT TCTCGGGAC AACCAGGATG CTCCTTGGG GCCTGTAGAG GGCCTTACAT CCTTAGAGAA ACCAACCGAT CAACACCAGAT GGCTGGAGG GGCCTCATAC CCTTAAACA TGCCCTCT TCCAGGAGG AGCCGGGT GGCCTGGAGG GGCCTAAAC CTTCAGAGAA AGCCACCGC AACCAGAGT CTACACGCTC GTGGGTGAGA AGAGGCTTGA GCCATCATA TCATTGGTAA CAACACCTAACCC CTCTCAGGT TTGGAAACCA GACCTTAAAC TACAGGCTC TCCCGGG GAAACACTTT TCCTTGGAAA CAAAACCAC CACGTTCAT TCAAAACACC CATCTTGGAA AAGAACCAAAACACAC CACCACCAT AATGAAACACA CAGACCAAAA AATGAACCAA AGAACACAA CGCCTCAAACACACACACACACACACACACACACACACAC	2940 3000 3033 60 120 180 240 300 420 480 660 660 660 720 780 840 900 900 900 1080
50 55 60	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CTTCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 360 420 540 660 720 840 960 1020 1020
50 55 60 65	TITISCCCAGA GATGGGACTIG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTCCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCT GCTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 720 780 900 900 901 1080 11080 11200
50 55 60 65	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTCCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 300 420 480 660 660 660 660 840 900 900 900 900 1080 1140 1140 1126
50 55 60 65	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTCCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51	2940 3000 3033 60 120 180 240 360 420 540 660 720 780 840 906 1020 1020 1120 1200 1200 1200
50 55 60 65 70	TITISCCCAGA GATGGGACTIG GGAGGGCCA CTICAGGGTT CTCCTCTCCC CTCTAGGGC GAGAAAGGGT CTCCTCTCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTCTCTGCC ACTGCTGCTG CTGACTGCTG CTAAACTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 445.1845  1	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 720 780 900 900 901 1080 11080 1120 1120 1120 1120 1120 1
50 55 60 65	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTCCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGCTGTG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCTCAA GCCCAGCCGT GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCTCAA GCCCAGCCGT TGGTTTTGCT GTTCCAGGAA GGCAACCTTC TCGATCTAGC GCCTCAGC AGCCAGCCGC CTTGTTTTCT GTTCCAGGAA GGCAACCTTC TCGATCTAGC GCCAGCATTG CCATCATCTC TGCCCGCTCA CTGGCCCGGG TCTCCTTGAG GCCAGCATTG AGTCCCCAG CCAGGAGAA ATCCACCCGG GTCGGAGTGG AGGGGGATT CGAGCAGGGA AGGCGCGGT TGCAGGACCA GACGGGGGCC AGGGACCTTC TCGATCTCCCC TCAGGAGAG TAGGAGCACC AGCGAGCCGG GGGAACCTTC TCCTCTCCAG AGCCAGCGGG TCCTCCCAGT CTGAGCAGGA GGTGATGGGT CTCTCTCCCA GCTCAGCCGGG TCCTCCCAGT CTGAAGAATA CCAGCCTCCT ATATGGAAAT CATACTTATA TCAGTTACAG TATTATAGGAA GAAGATTCA TGGGATCATC TCTCGGGAGG AGGCGGGT GCCTCCAGG GGGCCAAGACTA CCTTAGAGAA ACCAGCAGCA ACCAGGATG TACCACAGA TATTATGGAA GAGAGTTTCA TGGGATCATC TCTCGGGAGC AGCCAGGATG CTACACCCTA GCCTCCAGGT TTGGAAACCA GACCTTAAAC TACAGGCGCT TCCAGGCGG GCCTCCCAAACA CACATTGGAT ATGCCACCCT ACTCAGAGAA AAAGAACCA CACCAGAAAC CACATTGGAT ATGCCACCCT ACTCAGAGAA AAAGAACCA CACGCGGG AAACCACTT AATGAAACAAAAACCAC CACCTTAAAC TACAGGACACA CACGCGGG AAACCACTT AATGAAACAAA GAAAACCAA CACCACAACA CACCACAAA AAAGAACACA CACCACAAAA CACATTGGAT ATGCCACCCT ACTCAGAGAA AAAGAACAC CACGCGGG CACACACTTA AATGAACCAC ATCATCATTA TGCAGAGCCT CACAGATTATA AGGCCCCCC ACCACACA CACGCACACA CACTCATATTA TGCAGAGCCT CACAGATTCAA GAAAACCAAA CCTCCACACA AAAGAACAAC CACTCAATTA TGCAGAGCCT CACACACTTTA AGGCCCCCC AACGCACACA CACTCAATTA TGCAGAGACCAC CACACTTTA AGGCCCCCC AATGCACTGC CAACCACTAT TGCAGAGGAT CACCACATTA TGCAGAGACCAC ACCACAGAAC CACTCAATTA TGCAGAGACCAC CACACTTTA AGGCCCCC CAACACAC CACCACACAC CACTCAATTA TGCAGAGACCAC CACACTTTA AGGCCCCCCAACACACACACACACACACACACACACAC	2940 3000 3033 60 120 180 240 420 480 540 660 720 840 900 1080 1140 1140 11260 11320 11320 11320
50 55 60 65 70	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGATTGT CCCTCCACC CTCCAGCCGGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC CCCCCACCAC CTCCAGCCGGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGAGCTC CAGCCTCAGC AGCCAGCGCC CGTCTGCCAG CTTGGTGGGC TCCTTGGCC GCAGCTGGTT CAGCCTCAGC AGCCAGCGCC CCATCATCT TGCCCCCTCA CTGGCCCGG TCCCCTCTGAA GCCAGCAGCGCC CCAGGAGAA ATCCACCCGG GTCGGAGTGG AGGGGGACTT CGAGCCAGG AGCCAGCGCC CCAGGAGAA ATCCACCCGG GTCGGAGTGG AGGGGGATT CGAGCCAGG AGGCGGGC TAGGAGCCC GACGCGGCC AGGGCCCCCCACCAC TCATCTCCC TGAGGAGAC TAGGAGCCC GAGCACTCT ATATGGAAA CACACCGGA AGGCGGGG CACAGAGCAC CACCTCCCAA AGAGACCAAA TCATCTCCC TGAGGAGAAC TATTATGGAA GAGAGTTTCA TGGGATCAT TCTCCGGGAG AGGCGGGGAAAC CACACCAAAA TATTATGGAA GAGAGTTTCA TGGGATCAT CTCCGGGAGG AGGCGGAGAAA CACACCAAAA TATTATGGAA GAGAGTCTC CCTTAGAGAAAT CACCCACCGC AGCCCCCCCCCC	2940 3000 3033 60 120 180 240 360 420 360 420 780 840 900 960 1020 1140 1200 1200 1200 1200 1200 1300 1200 1300 13
50 55 60 65 70	TITISCCCAGA GATGGGACTIG GGAGGGCCA CTICAGGGTT CTCCTCTCCC CTCTAGGGC GAGAAAGGGT CTTCCTCTC CCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACTGCTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 445.11845  1	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 720 780 900 900 901 1080 1190 1190 1190 1190
50 55 60 65 70	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGCTCTACC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCTCAC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC TCGCAGCTCAC GCCTGGTACA CGTCTGCCCAG CTTGGTGGGC TCCTTGGCC GCAGCTCGT TGGCCTCAGC AGCCAGCCGC TTGGTTTTCT GTTCCAGGAA GGAACCTTC TCGATTAGC TGGCCCAGC AGCCAGCGCT CCATCATCTC TGCCCGGTCA CTGGCCCGGG TCTCCTTGAA GCCAGCACTCA CCAGGGAGAA ATCCACCCGG GTCGGAGTGG AGGGGGATT CGAGCAGGGA AGGCGGGGT TAGGAGCGCC GACGCGGCC AGGAGCCTCT TCCATCTCCC TGAGGAGAG TAGGAGCGCC GACGCGGGCC AGGAGCCTCT TCCTCTCCAG AGCCAGCGGG TCCTCCCATG CTGAGCAGGA GGTGATGGT CTCTCTCCCA GCTCTCCGG CTCGTCGGGT TCCTCCAGT CTGAAGAATA CCAGCCTCCT ATATGGAAAT CATACTTATA TCAGTTACAG CAAGAGGCAC CTCGTCCCCAA GAGAATCAT TGTCCTCGGG AGGCGAGTGA ACCACCAAAA TATTATAGGAA GAAGATTTCA TGGGATCATC TCTCGGGAGC AGGCGGGGT GCCTCCAGG GTGCCTACAT CCTTAGAGAA ACCAGCGCGC AACCAGGATG CACACCAAAA TATTATGGAA GAGAGTTTCA TGGGATCATC TCTCGGGAGC AACCAGGATG CACACCAAAA TATTAAGAA CAAAAGCTGC CGGTTCAATT TCAAAATAGA CAACACCAAC GCCTGTGAGA AAGCGTCC CAGTCAATT TCAAAATAGA CAACTACCC CATCATAGCA CACATTGGAT ATGCCACCCT ACTCAGAGAA AAAGAACAC CAGGCGTGG GAACCCCTT AATGAAACAAA GAAAACAAA CGTCACACAT GAAGAACACA CATCAATTA TGCACACCT CCTGGTTC GAGGGGTCC CCTCACACA AACGACAACA CATCAATTA TGCAGAGCCC CACACTTTA AGGTCCACAC GTTCCAGAGAA AAAGAACACA CATCAATTAT TGCAGAGGCTC CACACACTTTA AGGTCCAACA CATCTCAACA CACCACAAC CATCAATTAT TGCAGAGACC CACACTTTA AGGTCCAACA CATTGTGAGG CCACACCATTA TTCAAGAACCA CATCAACAC CACCTATATA TGCAGAGACAC CACACTTTA AGGCCCCC AACGACACA CACCACACAC CATCAACCC CACCACACAC CACACTTTA AGGCCCCCC AACGACACAC CACCACACAC CACCACACAC CACCACACAC CACCAC	2940 3000 3033 60 120 180 240 360 420 480 540 660 720 960 1080 1140 1260 1140 1260 1320 1380 1420 1380 1420 1380 1420 1380 1420 1380 1420 1380 1420 1420 1420 1420 1420 1420 1420 142
50 55 60 65 70 75	GARGAAGGGT CATTCCTCT CCCCAAGACT TETCAGGGTT CTCCTCTCCC CTCTAAGGGC GAAGAAGGGT CATTCCTCT CCCCAAGACT TEGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1 11 21 31 41 51    GAATTCCGCC TCACAGTGGC CAGGTCCTGT GCCAGATTGT CCCTCCACC CTCCAGCCGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC CGCCCCCACC CTCCAGCCGGG GCGCTGTTGG CGTGAGTTGA TCGAGCCGCA GCCGCAGCTC CGCCCCACC CTCCAGCCGGG CCCTTTCCT TGCCCGCCC CTCCTCGGCC GCAGCTGCT CGAGCCCAAG GCCCCCCCCCC	2940 3000 3033 60 120 180 240 360 420 540 660 720 780 840 900 1020 1140 1200 1140 1200 1320 1320 1320 1320 1320 1320 132
50 55 60 65 70	TITITICCCAGA GATGGGACTIC GCACAGACT CTCAGGGTT CTCCTCCACC TCTTAGGGC  ACAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC  ACAGAAGGGT CCTGCTGCTG CTAAATCTTCA GGGCACTGCT TCCCTCACT TCTTCCTGCC  ACAGAAGGGT CCTGCTGCTG CTAAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG  AAAATAAAG ACAAATGCTG CGCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1	2940 3000 3033 60 120 180 240 300 420 480 660 720 780 900 900 900 900 900 1080 1120 1200 1200 1120 1120 1120 11
50 55 60 65 70 75	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1	2940 3000 3033 60 120 180 240 360 420 660 720 660 780 840 960 1020 1140 1260 1120 1120 1120 1120 1120 1120 112
50 55 60 65 70 75	TITISCCCAGA GATGGGACTIG GGAGGGCCA CTICAGGGTT CTCCTCTCCC CTCTAGGGC GAGAAAGGGT CTTCCTCTCT CCCCAAGACT TGGTGTCTT TCCCTCCACT TCTTCTGGC ACTGCTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT TCCCCTCACT TCTTCCTGCC ACACTGCTG CTGCTGCTGC CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1	2940 3000 3033 60 120 180 240 300 360 420 780 660 720 780 900 1020 1140 1260 1320 1320 1320 1320 1320 1320 1320 132
50 55 60 65 70 75	TGTGCCCAGA GATGGGACTG GGAGGGCCA CTTCAGGGTT CTCCTCTCCC CTCTAGGGC GAAGAAGGGT CCTTCCCTCT CCCCAAGACT TGGTGTCCTT TCCCTCCACT TCTTCCTGCC ACCTGCTGCTG CGTGCTGCTG CTAATCTTCA GGGCACTGCT GCTGCCTTTA GTCGCTGAGG AAAAATAAAG ACAAATGCTG CGCCCTTAAA AAA  Seq ID NO: 149 DNA Sequence Nucleic Acid Accession #: L29126.1  Coding sequence: 4451845  1	2940 3000 3033 60 120 180 240 300 360 420 480 660 720 780 900 900 900 900 900 900 1080 1120 1260 1320 1320 1320 1320 1320 1320 1320 132

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	CCCCTCAGGT TGGGTCTTTT GC					2100
	TTAATACATC TTTAATTTAT TA					2160
	AATAAAAGGG AACTTAATTC AT	ACACCTAC T	TCATACAGT '	TATACATTTT	CACTTACAA	2220
5	AAAGAAGACA ATTCTGTTAA AT					2280
,	AGAATGTTGT TATTTTAGCA AT	OWWCGIG I	TECNENTEC	ATTGGTTATT	ACCCTGTGTA	2340
	CCTTGTCCCT CATTTTGCTG TG					2400
	TTGACATACC TCTGTCCTCC TC					2453
	HONORING TELBRECICE TO					- 100
10	Seg ID NO: 150 DNA Segue	nce				
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15	CCCAGGAACC CCCAGGGAGC CA	GCATGAAG (	GAGCTCACC	CCGAGTACAG	CTCCTCGGAC	60
	AGCGAGCTGG ACGAGACCAT CO					120
	AGTTCGGCTC TAGGTTCCAT GI	CCCCAACT A	ACATCTTCCC	AGATTTTGGC	CAGAAAAAGA	180
	CGGAGAGGAA TAATTGAGAA GC					240
	AGAAGGCTGG TACCCAGTGC TT					300
20	ATCCTGCAGA TGACCGTGGA TO					360
	TTTGACGCGC ACGCCCTTGC TA					420
	GAAGTTGCGC GTTATCTGAG CA					480
	CGACTGGTTT CGCATCTCAA C	AACTACGCT 1	TCCCAGCGGG	AAGCCGCGAG	CGGCGCCCAC	540
	GCGGGCCTCG GACACATTCC CT	rgggggacc (	GTCTTCGGAC	ATCACCCGCA	CATCGCGCAC	600
25	CCGCTGTTGC TGCCCCAGAA CC	GGCCACGGG A	AACGCGGGCA	CCACGGCCTC	ACCCACGGAA	660
	COGCACCACC AGGGCAGGCT GC	GGCTCGGCA (	CATCCGGAGG	CGCCTGCTTT	GCGAGCGCCC	720
	CCTAGCGGCA GCCTCGGACC GC	GTGCTCCCT (	GTGGTCACCT	CCGCCTCCAA	ACTGTCGCCG	780
	CCTCTGCTCT CCTCAGTGGC C	TCCCTGTCG (	GCCTTCCCCT	TCTCTTTCGG	CTCCTTCCAC	840
••	TTACTGTCTC CCAATGCACT G	AGCCCTTCA (	GCACCCACGC	AGGCTGCAAA	CCTTGGCAAG	900
30	CCCTATAGAC CTTGGGGGAC G	GAGATCGGA (	GCTTTTTAAA	GAACTGATGT	AGAATGAGGG	960
	AGGGGAAAGT TTAAAATCCC A	GCTGGGCTG	GACTGTTGCC	AACATCACCT	TAAAGTCGTC	1020
	AGTAAAAGTA AAAAGGAAAA A					1080
	TTTGTTGGTT TACTTTTATC T	TTTTTAATG	TTTTTTTCAT	CATGTCATGT	ATTAGCAGTT	1140
25	TTTAAAAACT AGTTGTTAAA T					1200
35	AACACTTTGT GATAGGTTTG T					1260
	TTTTGCCTCA AAATTTGGGG A					1320
	TATAGTTATG GTCTGTTTTT A					1380
	ATTCTGTTTG TTAATATTTT G					1440
40	GAGGGGAACT ATATTGAATT T	TATATTTCT	GAGCAAAGCG	TTGACAAATC	AGATGATCAG	1500
40	CTTTATCCAA GAAAGAAGAC T					1560
	CAAACTGTTG GTGGCCCTGA A					1620
	TTCTGATTTA GTTAGGAGAG A	GCCGCTGAT	AGGTTAGGTC	TCATTIGGAG	TGTTGGTGGA	1680
	AAGGAAACTG AAGGTAATTG A	<b>LATAGAATAC</b>	GCCTGCATTT	ACCAGCCCCA	GCAACACAAA	1740
15	GAATTTTAA TCACACGGAT C	TCAAATTCA	CAAATGTTAA	CATGGATAAG	TGATCATGGT	1800
45	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A	TCAAATTCA GTACAGTGG	CAAATGTTAA AAACTGTTAA	CATGGATAAG ATGCATAACC	TGATCATGGT TAATTTTCCT	1860
45	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T	TCAAATTCA GTACAGTGG AACTGGAAA	CAAATGTTAA AAACTGTTAA TTTTTATGTG	CATGGATAAG ATGCATAACC AGTTTTCCTT	TGATCATGGT TAATTTTCCT TTGGTGCATG	1860 1920
45	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T	TCAAATTCA GTACAGTGG TAACTGGAAA TTTAAAAGGG	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC	CATGGATAAGG ATGCATAAGG AGTTTTCCTT TCCTTCTCTT	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT	1860 1920 1980
45	GAATTTTAA TCACACGGAT C GTGCGACTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A	TCAAATTCA LGTACAGTGG TAACTGGAAA TTAAAAGGG LTATCATTTT	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040
	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTCAGT A GGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G	TCAAATTCA LGTACAGTGG TAACTGGAAA TTAAAAGGG LTATCATTTT	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040 2100
45 50	GAATTTTAA TCACACGGAT C GTGCGACTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A	TCAAATTCA LGTACAGTGG TAACTGGAAA TTAAAAGGG LTATCATTTT	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040
	GAATTTTAA TCACACGAT C GTGCGAGTGG TCAATTCAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA	TCAAATTCA IGTACAGTGG PAACTGGAAA PTTAAAAGGG ITATCATTTT GTTTGACCTC	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040 2100
	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA Seq ID NO: 151 DNA Sequ	TCAAATTCA GTACAGTGG AACTGGAAA TTTAAAAGGG ATATCATTTT STTTGACCTC	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040 2100
	GAATTTTAA TCACACGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA Seq ID NO: 151 DNA Sequ Nucleic Acid Accession	TCAAATTCA GTACAGTGG AACTGGAAA TTAAAAGGG ATATCATTTT STITGACCTC  Lence #: NM_001!	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040 2100
50	GAATTTTAA TCACACGAT C GTGCGAGTGG TCAATTCAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782	TCAAATTCA GTACAGTGG CAACTGGAAA TTTAAAAGGG NTATCATTTT GTTTGACCTC  Jence #: NM_001!	CAAATGTTAA AAACTGTTAA TTITTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG	CATGGATAAG ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA ATGTGTTGTG	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA	1860 1920 1980 2040 2100
	GAATTTTAA TCACACGAT C GTGCGAGTGG TCAATTCAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782	TCAAATTCA GTACAGTGG AACTGGAAA TTAAAAGGG ATATCATTTT STITGACCTC  Lence #: NM_001!	CARATGITAA AAACTGITAA TITITATGTG CTITCCTGCC TCAGGITTAT TGTTGTACTG	ATGCATAACC ATGCATAACC AGTTTTCCTT TCCTTCTCTT TCTTTTAGCA	TGATCATGGT TAATTITCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA	1860 1920 1980 2040 2100
50	GAATTTTAA TCACACGGAT CGTGCGAGTGG TCAATTGAGT AGGGACTGCCA TATTTTCTTT TGAACTGTGGT TGCCAAGGTA TAATTTGATTT GGGCTATAAA AACGACCTCC ACTGAACTGG GAAA  Seq ID NO: 151 DNA Sequenceic Acid Accession Coding sequence: 1782	TCAAATTCA GTACAGTGG AAACTGGAAA TTTAAAAGGG ATATCATTTT STITGACCTC Lence #: NM_001: 5589	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG	CATGGATAAG ATGCATAACC AGITTTCCTT TCCTTCTCTT TCTTTTAGCA ATGTGTTGTG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA	1860 1920 1980 2040 2100 2103
50	GAATTTTAA TCACACGGAT CGTGCGAGTGG TCAATTGAGT AGGGACTGCCA TATTTTCTTT TGAACTGTGGT TGCCAAGGTA TAATTGATTT GGGCTATAAA AACGACTCC ACTGAACTGG GAAA  Seq ID NO: 151 DNA Sequencia Action Accidence Acid Accession Coding sequence: 1782  1 11  AGCAAACTCG TCTTGTCTAC	TCAAATTCA GTACAGTGG TACAGGAAA TTAAAAGGG TTAAAAGGG TTAAAACGG TTAAAACCTC TTAAAACGG TTAAAACGG	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC	CATGGATAAG ATGGATAACA AGTITICCTI TCTTTTAGCA ATGTGTTGTG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGGTTA ACTAAATAAA	1860 1920 1980 2040 2100 2103
50	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAACGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11         AGCAAACTG TCTTGTCTAC C TTTCCGGAGT ATGGACTAAA	TCAAATTCA GTACAGTGG AACTGGAAA TTAAAAGGG ITATCATTTT STTTGACCTC  #: NM_001: 589 21	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCCTTACCTT	ATGGATAAG ATGGATAAG AGTITICCTI TCCTTCTCTT TCTTTTAGGA ATGTGTTGTG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA	1860 1920 1980 2040 2100 2103
50	GAATTTTAA TCACACGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11   AGCAAACTGG TCTTGTCTAC G TTTCGGAAGT ATGGACTAAA A TCCCAACTGG CCGTCAGACCC	TCAAATTCA GTACAGTGG TAACTGGAAA TTAAAAGGG NTATCATTTT STTTGACCTC  Lence #: NM_001: 2589 21 21 21 22 24 25 26 26 26 26 26 26 26 27 26 26 26 26 26 26 26 26 26 26 26 26 26	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTTGTGTGCC	ATGGATAAG ATGGATAAG ATGTTCCTT TCTTTTAGCA ATGTGTTGTG  41   CTCCCCAAAAAT ACCGCTTGGG AAGCGCCTGG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGCCATG	1860 1920 1980 2040 2100 2103
50	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCAAATTCA IGTACAATTGA IGTACAGTAGA ITTAAAAAGGG ITATCATTTT STITTGACCTC  LEENCE #: NM_001: 2589 21	CAAATGTTAA AAACTGTTAA TTTTTATAGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGGTGGTGC AAATCCGTGG	ATGGATAAGC AGTITICCTT TCTTTTAGGA ATGGTTGGG ATGGTTGGG  41 1 1 1 TCCCCAAAAT ACGGCTTGGG AGCAGGCCCGG AGCAGCAGGAGGCCGGG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGACCATG ACAGGACCATG	1860 1920 1980 2040 2100 2103 60 120 180 240
50	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAACGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCAAATTCA IGTACAGTGG ICAACTGGAAA TTAAAAAGG ITATAAATGG INTTGACCTC  H: NM_001: 5589  CCACCCTCCC ATCACCTCCC CCACCTCCCC CCACCTCCCC CCACCTCCCC CACCTGCCC CCACCTGCCC CCACCTGCCC CCACCTGCCC CCACCTGCCC CACCTGCCC CACCTGCCC CACCACATTCGGG	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGGC AAATCCGTGGC	ATGGATAAG ATGGATAACG AGTITICCTI TCCTTCTCTT TCTTTTAGGA ATGGTTGTG  41	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA ACTGGTGGC ACAGGACCATG ACAGGACCATG ACAGGACCATG ACAGGACCTG ACAGGACCTG ACAGGACCTG ACAGGACCTG	1860 1920 1980 2040 2100 2103 60 120 180 240 300
50	GAATTTTAA TCACACGGAT CGTGCGAGTGG TCAATTGAGT AGGGACTGCCA TATTTTCTTT TGAACTGGGT TGCCAAGGTA TAATTGATTT GGGCTATAAA AACGACCTCC ACTGAACTGG AAA  Seq ID NO: 151 DNA Sequence of the control of th	TCAAATTCA IGTACAATTCA IGTACAATGG CAACTGGAAA TTTAAAAGGG #: NM_001: S589 21   CCACCTCCC ATCACACTCC CCACTTCGCCC CGCTTCGGGG GAGGAATTGG	CAAATGTTAA AAACTGTTAA AAACTGTTAT TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGTGGG AAATCCGTGG AAATCCGTGG AAAGGAATACTT	ATGGATAAGC AGTITICCTT TCCTTTGTT TCTTTTAGCA ATGTGTTGTG  ATGTGTTGTG  ATGCCTTGGG AGCGCTTGG AGCAGCAGG AGCAGCAGG CTGACCAGAAATGCACC TGACACCAGC	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA ACTGGTGGA ACAGGAGCTG ACAGGAGCTG ACAGGAGCTG CGGAAGATAAT CGGAAGATAAT	1860 1920 1980 2040 2100 2103 60 120 180 240 360
50 55 60	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequence: 1782 1 11   11   ACCAACTGG TCTTGTCTAC C TTTCGGAAGT ATGGACTAAA A TCCCAACTGG CCGTCAGACC C ACCACAGCCA AGGAGCCAAG GTGGGGAGTA ACCTCCCGCA C CTGGTCATCT GCTCCTTGAT C AGTCTGTCTCT CAAAAGAGAAA A	TCAAATTCA GTACAATTCA GTACAGAAA GTACAAGAGG ATATCAATTT STITGACCTC  SENCE #: NM_001: SS89 21	CAAATGTTAA AAACTGTTAA TTTTTATAGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCGC AAAGCATAACTG GAAGATACTG GAAGATCTC GAAGATCTC	ATGGATAAGC AGTITICCTT TCCTTTAGCA ATGGTTGGT TCTTTAGCA ATGGTTGGT  41 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGGGG ACAGGACCATG ACAGGACCATG ACAGGAGCTG GGTGTGATATAAA CTTCAAAATT	1860 1920 1980 2040 2100 2103 60 120 180 240 300 360 420
50 55 60	GAATTTTTAA TCACACGGAT CGTGCGAGTGG TCAATTGAGT AGGGACTGCCA TATTTTCTTT TGAACTGGGT TGCCAAGGTA TAATTGATTT GGACTGTGT TGCCAACTGG CAAAACGACCTCC ACTGAACTGG CAAAACGACTCC ACTGAACTGG CAAAACTGG TCTTTCGGAAGT ATGGACTGACTGACTGGAACTGG CGTCGGAACTGACTGAACTGGAACTGAACT	TCARATTCA IGTACAGTGG IGTACAGTGG ITACAGTGGAA TTTARAAGGG ITATCATTTT STTTGACCTC  SESB9 221	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGGG AAATCCGTGG AAATCCGTGG GAAATTCL ACAGAATTCL ACAGAATTCL ACAGAATTCL ACAGAATTCL ACAGAATTCL ACAGAATTCL ACAGAATTCL	ATGGATAAG ATGGATAACC AGTITICCTI TCCTICTCTI TCCTITTAGGA ATGGGTTGGG  41   CTCCCCAAAAT ACCGCTTGGG AACGGCCTGC TGACACCAGG CAATTGCACCAGGAGAGGAG	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   ACTCTGGTGGC ACAGGACCATG ACAGGACCATG ACAGGACCATG CGTTGTGAT ACAGGACATAT ACAGAAAGGT ACAGGAAGGT ACAGGAGGAGGAGATAAT ACAGAAAGGT	1860 1920 1980 2040 2100 2103 60 120 180 240 360
50	GAATTTTAA TCACACGGAT CGTGCGAGTGG TCAATTGAGT AGGGACTGCCA TATTTTCTTT TGAACTGTGGT TGCCAAGGTA TAATTTGATTT GGACTATTAA AACGACCTCC ACTGAACTGG GAAA  Seq ID NO: 151 DNA Sequence of the sequence of th	TCAAATTCA IGTACAATTGA IGTACAATGG ITAAAAAGGG ITAAAAAGGG ITACATTT STITGACCTC  IEECCE #: NM_001: S589 21   CCACCCCCCC ICCACCCCCCCCCCCCCCCCCCCCCC	CAAATGTTAA AAACTGTTAA AAACTGTTAT TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CGGTGGTGGG AAATCCGTGG AAATCCGTGG AAAGGAATAC GCAAGATCC ACAGGAATTC ACTCTTACTT	ATGGATAAG ATGGATAACC AGTITICCTT TCCTTTGTT TCTTTTAGCA ATGTGTTGTG  41	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGCCATG ACAGGAGCTG CGAAGAATAAA ACGCAAAAAAA	1860 1920 1980 2040 2100 2103 60 120 180 300 360 420 480
50 55 60	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11           AGCAAACTGG TCTTGTCTAC TTTCGGAAGT ATGGACTAAA A TCCCAACTGG CCGTCAGACC C GTGGGGGAGTA ACCCTCCGCA C CTGGTCATCT GCTCCTTCAT C AGCTGTCTCT CAAAGAAGAAC CATGACCCC AGGCTAAGTG C ACCACTGCC AGGCTAAGTG C ACCACTGACCC TGGGATTTTCCTAACTGCTCTC CAAAGAAGAAC CATGACCCC AGGCTAAGTG C ACCATGACCCC TGGGATTTTCAAGAGCATAT T ATGATTTCTC AAAAGAAGAAC ATGAACTCT TATGGAATCT TATGGAATCAT TAAGAGCCAT	TCAAATTCA  GTACAGTGG  ACTACAAATGG  ATATCAATTTT  STITGACCTC  SEENCE #: NM_001: 2589 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CAAATGTTAA AAACTGTTAA TTTTTATAGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCGC AAATCCGTG AAATCGTG AAAGGAATCC ACAGAATTCC ACTGTACTC ACTGTACTC ACAGAATTCC ACTGTACTC ACTGTACTC ACAGAATTCC ACTGTACTC ACTGTACT ACTGTACT ACTGTACT ACTGTACT ACTGTACTC ACTGTACT ACTGTAC	ATGGATAAG ATGGATAACC AGTITICCTT TCTTTTAGGA ATGGTTGTG  41	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT CGTGTAGTTA ACTAAATAAA  51   CTCTGGTGGC ACAGCACTGT ACTGTGACTAT CGTTGTAGT CTCTGAGTGA CTCTGAGTGA CTTGTAGT CTTCAAATT ACAGAAAGGA ACAGCAAAAGGA ACAGCAAAAGGA ACAGCAAAAGGA ACAGCAAAAGGA ACAGCAAAAGGA ACAGCAAAAGGA ACAGCAAAATT ACAGAAAAGGA ACAGCAAAATT ACAGCAAAATT ACAGCAAAATT ACAGCAAATT ACAGCAATT	1860 1920 1980 2040 2100 2103 60 120 180 240 360 420 480 540
50 55 60	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT I GAACTGTGGT TGCCAACGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA IGTACAGTGG ICACTGGAAA TTARAAGGG ITATCATTTT STITTGACCTC  H: NM_001: 2589 251	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACTTC CGTGGTGGG AAATCCGTGG AAATCCGTGG GAGAATTCT ACAGAATTCT ACAGAATTCT ACTTCTACTC TCCTTACTC TCCTTACTC TCCTTACTC TCCTTACTC TCTTACTC TCTTATACTC TCTTATACTC TCCTTATACTC TCCTTATACTC TCCTTATACTC	ATGGATAAG ATGGATAACC AGTITICCTI TCCTTCTCTT TCTTTTAGGA ATGGCTTGG  41	TGATCATGGT TAATTTTCCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   ACTAGATGGA CTCTGGTGGC ACAGGACCATG ACAGGACCATG GCTTGTCATT CGTGAAATAAA ACGAAAAGAAAA	1860 1920 1980 2040 2100 2103 60 120 180 240 300 360 420 480 540 600
50 55 60 65	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11           AGCAAACTGG TCTTGTCTAC TTTCGGAAGT ATGGACTAAA A TCCCAACTGG CCGTCAGACC C GTGGGGGAGTA ACCCTCCGCA C CTGGTCATCT GCTCCTTCAT C AGCTGTCTCT CAAAGAAGAAC CATGACCCC AGGCTAAGTG C ACCACTGCC AGGCTAAGTG C ACCACTGACCC TGGGATTTTCCTAACTGCTCTC CAAAGAAGAAC CATGACCCC AGGCTAAGTG C ACCATGACCCC TGGGATTTTCAAGAGCATAT T ATGATTTCTC AAAAGAAGAAC ATGAACTCT TATGGAATCT TATGGAATCAT TAAGAGCCAT	TCAAATTCA IGTACAATTGA IGTACAATGG ITAAAAAGGG ITAAAAAGGG ITACATTT STITGACCTC  IEECC #: NM_001: 2589 21   CCACCCTCCC ATCACACTCCC CCACCTGCCC CCCCTCCCGGG GAGGAATTGG GGTCACTTGA GGTCACTTGAACAAAAT CAGATATGAA ATATCAACAC AAGTCTGAACAAAAT CAGATATGAAAAAT CAGATATGAAAAAT CAGATATGAAAAAT CAAGATATGAAA	CAAATGTTAA AAACTGTTAA AAACTGTTAT TTTTTATGTG CTTTCCTGCC 936.2 31   TCCCCCATCC TCCTTACCTT CCGTGGTGGG AAATCCGTGG AAATCCGTGG AAATCCGTG GAAGATTCC ACTCTTACCT ACTCTTACCT ACTCTTACCT ACTCTTACCT ACTCTTACCT ACTCTTACCT ACTCTTACT CCACCAGAAT CCACCACAGAAT CCACCAGAAT CCACCAGAAT CCACCAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACCAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACCAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACCAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACACAGAAT CCACCACAGAAT CCACCACAGAAT CCACCACACACACACACACACACACACACACACACA	ATGGATAAG ATGGATAACC AGTITICCTT TCCTTTGTT TCTTTTAGCA ATGTGTTGTG  41	TGATCATGGT TAATTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGACATG ACAGGAGCTG CGAAGATAAT ACTAAAATT ACAGGAAGATAAT ACGCAAAAAAA ATGCACTTTTT CCTGAGCAAA AAGGCAAAAAA AAGGCAACAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAA AAGGCACAAAAAAAA	1860 1920 2040 2103 2103 60 120 180 240 360 420 540 660
50 55 60	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TICARATTCA  IGTACAGTAG  IGTACAGTAG  ITTARAAGGG  ITTARAAGGG  ITTARATTTT  ITTGACCTC  IEECE #: NM_0019 2589 21 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CAAATGTTAA AAACTGTTAA TTTTTATATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CGGTGGTGGCG AAATCGTG AAAGGAATAC GAGGATTCI ACTGTACTTC ACTGTACTC CACGAGATTCI CACGAGATTCI CACGAGATTCI TCGTATACTC TCGTATACTC CACCAGAA CTGTATACTC TCGTATACTG	ATGGATAAGC AGTITICCTT TCCTTTATCT TCTTTTAGCA ATGGGTGGG AGCGCTGG AGCGCTGGG AGCGCTGGG TCAGCAGGG TCAGCAGGG ATTATAGG ATTATAGG ATTATAGG TCTCAGCAGGAGG TTATATAGG TCTGAGAGAGT TTTTTGAAA	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT CGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGACCATG ACAGGACCATG ACAGGACCATG CTTTGATATT ACTAAAATT ACTAAAATT ACTAAAATT ACGCAAAAGGA ATGCACTTTTT CCTGAGCAAA ATGCACTTTTT CCTGAGCAAA AAGCATAAAAAAAAAA	1860 1920 1980 2040 2100 2103 60 120 180 240 300 420 480 600 600 720
50 55 60 65	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAACGTA T AATTGAATT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1	TCARATTCA IGTACAGTGG IGTACAGTGG ITATCATTTT STITTGACCTC  SEND SEND SEND SEND SEND SEND SEND SEN	CAAATGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  936.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGGG AAATCCGTGG AAATCCGTGG AAATCCGTGG AAATCCGTG CGAGAATACT ACAGAATTCT CCCCCATCC TCGTATACTC CACAGAATCC TCGTATACTC CCACAGAATCC CCCACAGAATCC CCGTGTGGGT CCGTGTGGGT CCGTGTGGGT CCGTGTGGGT CCGTGTGGT CCGTGTGGTC CCGTGTGGTC	ATGGATAAG ATGGATAACC AGTITICCTI TCCTTCTCTI TCCTTTTAGGA ATGGGTTGGG  41   CTCCCCAAAAT ACCGCTTGGG AACGGCCTGG AGCAGCAGGG CAATTGCAC TCACACAGG TCTAATAGG TTCAGAGAGG TCTTAATAGG TTCAGAGAGG TTTAATAGG TTCAGAGAGG TTTATTAGAA TCCACTGGCA TTTTGAAA TCCACTGGCA TCTAGCAGGG TCTTGAGAGGT TCTAGTAGGG TTTATTGAAA TCCACTGGCA TCTTGGCAATG	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   ACTAGACCATG ACGCCATGTGA CTCTGGTGGC ACAGGACCATG CTTTGAAATTAA ACGAACCATG ACAGGAGGTG CTTTCAAAATTAA ACAGAAAGGA AGGCAAAAAA AGCCATTTTT CCTGAGCAAA AAGGTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AAAGCTTCAG AGAAGGTGTG	1860 1920 1980 2040 2100 2103 60 120 180 240 300 420 480 600 660 600 660 720 780
50 55 60 65	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAACGTA T AATTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA  IGTACARTGA  TTARAARGGG  TATATATT  STITGACCTC  IENCE #: NM_001: 2589 21   CCACCCTCCC  CCACCTCCCC  CCCTCCCGGG  GAGGAATTGA  CAGATATGAA  TATAAAGAAT  CAGATATGAA  TATACACACT  CAGATATGAA  TATACACACT  CAGATATGAA  TATACACACT  CAGATATGAA  TATACACACT  CAGATATGAA  CAGATA	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGGTGGC AAAGGATTAC GGAAATCCC ACTCTACCT ACTCTTACTC ACTCTTACTC ACTGTTACTC ACTGTTACTC ACTGTTACTC ACTGTTACTC ACTGTTACTC ACTGTTACTC CCGTGTATACTC CCGTGTATACTC CCGTGTGTGCT CCACCAGGAA CCGATATTT CGGTGTGTC CGAGAGGAGGGG CGAAAGGAGGAG CGAAAGGAGGAG CGAAAATTT CGGTGGTGT CGAAGAGGAGGAG CGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	ATGGATAAG ATGTTTCCTT TCCTTTCTTT TCCTTTAGCA ATGTGTTGTG  41	TGATCATGGT TAATTTCT TTGGTGCATG TGATTTATTT GGTGTAGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGCCATG ACAGGACCATG ACAGGAGCATA ACTAAAATT ACTAAAATT ACTCAAAATT ACGAAAAGGA ATGCACTTTTTA ACAGAAAGGA ATGCACTTTTA CTTCAAAATT ACGAAAAAAA ATGCACTTTTTA CTTCAAAATT ACGAAAAAAA ATGCACTTTTTA CTTGAGCAAAA ATGCACTTTCA CTGAGCAAAA AAAGGTTCAG CAATATCTAC GGAAGGTGTG CACAATCGCA	1860 1920 2040 2103 2103 60 120 180 240 300 360 420 540 660 720 780 840
50 55 60 65	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1 11    IACCAACTG TCTTGTCTAC TTTCGGAGT ATGGACTAAA A TCCCAACTG CCGTCAGACC GTGGGAGTA ACCTCCGGA GTGGGAGTA ACCTCCTGGA CCTGGTCATCT GCTCCTTGAT AGTCTGTCAAGACCAA ATTGAATCAT TAAGAGCAAT TCATACAATG TGGAACTAT TCTATCAATG TGGAACCAT TATGCACGAT GGGGCCCTAA TATCCTCTCTGT GGGATCCTCA TATGCAGGAT GGGGCCCTAA TATCTCTCTGAT GGGATCCTCA TATGCAGGAT GGGGCCCTAA TATCTGTCCAATGAACCAATGATGCAATGATGAACCAT TATGCAGATGAACCAATGAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACAATGAACCAATGAACAATGAACCAATGAACAATGAACAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACCAATGAACAATGAACCAATGAACAATGAACCAATGAACCAATGAACCAATGAACAATGAACCAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAATGAACAAAAAAAA	TCARATTCA  IGTACARTGG  CAACTGGARA  TTARARGGG  TATACATTT  TTTTGACCTC  IEECE  #: NM_0019  2589  21    CCACCCTCCC  ATCACACTCC  CACCTTCCC  ATCACACTCC  CACCTTCCC  GGTCACCTCC  GGTCACCTCGGG  GAGGAATTGG  CCTCACCTCG  ATTARACACT  AAATTCAACAC  AAGTCTGATCAC  ACAGGCATC  CCGCTCCACCC  CCTCCCC  CCTCCCC  CCTCCCC  CCCCTTCCC  CCCCCTCCC  CCCCTCCC  CCCCCC	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATAGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGGTGCC AAACCGATC AAACGAATAC ACTATACTT CAGGATTC ACTATACTT CAGGATTC ACTATACTT CAGGATTC CTGATACTT CCGTGTGGCC TCGATACTTC CGAGGATCC TCGATATTC CGTGTGGCC GAGGAGGAG GCGAGGAGGGC GGACACCC GGAAGAGGAGC CGCTACCCC CGAACACCC CGAAGAGGAGC CGCTACCCC CGAACACCC CGAACACCC CGAACACCC CGAACACCC CCACCACCC CGAACACCC CCACCACCC CGAACACCC CCACCACCC CGAACACCC CCACCCC CGAACACCC CGAACACCC CGAACACCC CGAACACCC CGAACACCC CGAACACCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC C	ATGGATAAG ATGTTTCCTT TCCTTCTCTT TCCTTTAGCA ATGTGTTGTG  41   CTCCCAAAAT ACCGCTTGGF AGCGCTGGF AGCAGCAGG TTCAGTGAGG TTCAGTGAGG ATTTCAGGG TTCAGTGAGG ATTTTAGAGG TTCAGTGAGG TTCAGTGAGG TTCAGTGAGG TTCAGTGAGG TTCAGTGAGG TTTTTAGAGG TTTTTGAGAG TTTTTGAGG ATTTTTGAGG TTGACAATG CCATCAATG	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT CGTGTAGTTA ACTAAATAAA  51   ACCCTTGTGA CTCTGGTGGC ACAGGACGTG ACAGGACGTG ACAGGACATA ATGCACTTTTT CCTGAAAATT ACTAAAATT ACTAAAATT ACTAAAATT ACGAAAGGA ATGCACTTTTT CCTGAGGAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTTTT CCTGAGCAAA AAAGCTTCAG ACAATGCA CAAAATCTAC AGGAAGGTGTG CACACATGGCA ATTCCCGTGTC	1860 1920 1980 2040 2100 2103 60 120 180 240 300 420 480 600 720 780 840 900
50 55 60 65 70	GARTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAACGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1 11    1 12    ACCAACTCG TCTTGTCTAC TTTCGGAGT ATGGACTAAA A TCCCAACTCG CCGTCAGACC GTGGGAGTA ACCTCCGGA CTGGTCATCT GCTCCTTGAT AGTCTGTCATCAAAAAAAAAAAAAAAAAA	TCARATTCA  GTACATGA  TTARAAGGG  **ACTIGARA  TTARAAGGG  #*: NM_001:  \$589  21    CCACCCTCCC  ACCACCTCCC  ACCACCTCCC  GGGGAGAATTGG  GGTCACCTGCC  GGTCACCTGCC  GGTCACCTGTA  GATAAGTGAT  TGAAACAAAT  CAGATATGAA  ATATCAACA  AGGCCATC  AGGCCATC  CTGGGCGTACGGC  CTCACCTGTA  GATAAGTGAT  CAGATATGAA  ATATCAACA  CAGGCAACG  ACAGCCATC  CTGGCTGTAT  CACAGACCT  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  CACAGACC  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  TACACCGGC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCCACC  CTGCCCTGTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGC  CTGCCCTGTTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGCC  CTGCCCCCCC  CTTACCCCCC  CTTACCCCCC  CCCCCCCC	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGGTGGC AAAGGATTAC ACTCTTACTC ACTGTTACTC ACTGTTACTC ACTGTTACTC CGTGTGTGC CGTGTATCTC CGTGTGTGC CTGTATACTC CTGTGTGTC CGAGGAGATC CGAGGAGGGG CCCCTGTGGTGC CGAGGAGGGG CGCTACGCC CTGTGTGTC CGAGGAGGGG CGCTACTACC CATCTCACTC CGAGGAGGGGG CGCTACTACC CTCCATCTACC CTCCATCTACTACC CTCCATCTACTACC CTCCATCTACTACT	ATGGATAAGC AGTITICCTT TCCTTTCTTT TCCTTTAGCA ATGTGTTGTG  41	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGAGGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGACCATG ACAGGACCATG ACAGGAGCTAT ACTAAAATAA TGCACTTTTT CCTCAAAATT ACGAAAAAAA ATGCACTTTTT CCTCAAGATCAA ATGCACTTTTT CCTCAGCAAA ATGCACTTTTT CCTCAGCAAA ATGCACTTTTT CCTCAGCAAA ATGCACTTCAG CAATATCTAC GGAAGGTGTG CACAATCGCA ATTCCCCTGTGC CACACTCGCA CTTAAATGGA	1860 1920 2040 2040 2103 2103 60 120 180 240 360 420 480 540 660 720 840 900 960
50 55 60 65	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1	TCARATTCA  GTACATGA  TTARAAGGG  **ACTIGARA  TTARAAGGG  #*: NM_001:  \$589  21    CCACCCTCCC  ACCACCTCCC  ACCACCTCCC  GGGGAGAATTGG  GGTCACCTGCC  GGTCACCTGCC  GGTCACCTGTA  GATAAGTGAT  TGAAACAAAT  CAGATATGAA  ATATCAACA  AGGCCATC  AGGCCATC  CTGGGCGTACGGC  CTCACCTGTA  GATAAGTGAT  CAGATATGAA  ATATCAACA  CAGGCAACG  ACAGCCATC  CTGGCTGTAT  CACAGACCT  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  CACAGACC  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  CACAGACCC  CTGGCTGTAT  TACACCGGC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCACC  GAACCCCCACC  CTGCCCTGTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGC  CTGCCCTGTTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGCC  CTGCCCTGTTAT  CACCAGCC  CTGCCCCCCC  CTTACCCCCC  CTTACCCCCC  CCCCCCCC	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGGTGGC AAAGGAATACC ACTCTACCT ACTGTATACT ACTGTATACT CCGTGTGTGC CCGTGTGTGC CCGTGTGTGCT CCGTGTGTGCT CCGTGTGTCC CGTGTATACT CGTGTGTC CGGTGTGTGCT CGAGGAGTCC CGGTGTGTGCT CGAGGAGGGG CCCCTGTGTGTC CGAGGAGGGG CGCTACTAC CTCCTATCACC TCCTATCACC CTCCTATCACC CTCTATCACC CTCCTATCACC CT	ATGGATAAGC AGTITICCTT TCCTTTCTTT TCCTTTAGCA ATGTGTTGTG  41	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGAGGTTA ACTAAATAAA  51   AGCCTTGTGA CTCTGGTGGC ACAGGACCATG ACAGGACCATG ACAGGAGCTAT ACTAAAATAA TGCACTTTTT CCTCAAAATT ACGAAAAAAA ATGCACTTTTT CCTCAAGATCAA ATGCACTTTTT CCTCAGCAAA ATGCACTTTTT CCTCAGCAAA ATGCACTTTTT CCTCAGCAAA ATGCACTTCAG CAATATCTAC GGAAGGTGTG CACAATCGCA ATTCCCCTGTGC CACACTCGCA CTTAAATGGA	1860 1920 2040 2103 2103 60 120 180 240 300 360 420 780 660 720 780 840 900 960 1020
50 55 60 65 70	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAACGTA T AATTGATTT GGGCTATAAA A AACGACCTC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1	TCAAATTCA IGTACAATTCA IGTACAATGG INATCAGAATGG INTATCATTTT STITGACCTC  IEECCE #: NH_001! SSB9 21   CCACCCCCCC CCCCTCCCCC CCCCTCCCCCCCCCC	CAAATGTTAA AAACGTTAA AAACGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31    TCCCCCATCC TCCTTACCTT CGGTGGTGGG AAATCCGTGG AAATCCGTG AAAGGAATAC GTCATACTC CACAGAATCC CTCATACTC CACAGAATCC CGACAGAATCC CGAGAATCC CGACAGAATCC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGA	ATGGATAAG ATGTTTGTG  41	TGATCATTGT TAATTTTCT TTTGGTGCATG TGATTTATTT GGTGTAGTTA ACTANATANA  51   AGCCTTGTGA CTCTGGTGGA CTCTGGTGGA CTCTGGTGGA ACAGCATG ACAG	1860 1920 1980 2040 2100 2103 60 120 180 240 300 420 480 660 720 780 840 900 960 1020 1020 1080
50 55 60 65 70	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCAAATTCA IGTACAATTCA IGTACAATGG INATCAGAATGG INTATCATTTT STITGACCTC  IEECCE #: NH_001! SSB9 21   CCACCCCCCC CCCCTCCCCC CCCCTCCCCCCCCCC	CAAATGTTAA AAACGTTAA AAACGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTTAT TGTTGTACTG  31    TCCCCCATCC TCCTTACCTT CGGTGGTGGG AAATCCGTGG AAATCCGTG AAAGGAATAC GTCATACTC CACAGAATCC CTCATACTC CACAGAATCC CGACAGAATCC CGAGAATCC CGACAGAATCC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGAGAATC CGAGAATCC CGA	ATGGATAAG ATGTTTGTG  41	TGATCATTGT TAATTTTCT TTTGGTGCATG TGATTTATTT GGTGTAGTTA ACTANATANA  51   AGCCTTGTGA CTCTGGTGGA CTCTGGTGGA CTCTGGTGGA ACAGCATG ACAG	1860 1920 2040 2103 2103 60 120 180 240 360 420 480 540 660 720 660 780 840 900 1020 1020 1020
50 55 60 65 70	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA  IGTACARTGA  IGTACARTGA  ITTARAAGGG  ITTACACTC  IEECE  #: NM_001: 2589  21    CCACCCTCCC  ATCACACTCC  CACCTCCCC  ATCACACTCC  GGCTCCGCGG  GGGGAATTGG  GGTCACTGGG  GGTCACTGGG  GGTCACTGTAC  GGTTACACTGAC  CTGCACCACACACACACACACACACACACACACACACACA	CAAATGTTAA AAACTGTTAA TTTTTATAGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCGC AAACGGATTC ACAGAATTC ACTCTACCTC CAGGAATTC ACTCTACCTC CAGGAATTC CAGGAATTC CAGGAATTC CAGGAATTC CGAGGAATC CGAGGAATC CGAGGAATC CGAGGAATC CGAGGATTC CGAGGAGGGAG CTGATATTT CCGATCGCC TCCATCTAC CGAGGAGGGAG CGAGGAGGGAG CGAGGAGGGAG CGAGGAGGGAG	ATGGATAAG ATGTTTCCTT TCCTTTCTTT TCCTTTTAGCA ATGTGTTGTG  41   CTCCCAAAAA ACGCCTGG AGCGCTGG AGCGCTGG AGCAGCAGG ATGCACGAG ATTTAACG TCACCAGG ATTTAACG TCACCAGG ATTTAACG TCACCAGG ATTTTAAGG CCACCGGAA ATTTTGAAA ATTTTGAAA CCACTGGCAA ATTTTGAAG CCACCGGCA ATGCAATG CCACCGTGA CCACCGTGA CCATCAATG CCACCGTGA CCATCAATG CCACCGTGA CCACCGCTGA CCACCGTGA CCACCGCTGA CCCTGCCTGA	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT CGTGTAGTTA ACTAAATAAA  51   CACCTTGTGA CTCTGGTGGC ACAGCATGA ACAGACCATG ACAGCACATG ACTGCAAATTA ACGAAAAGGA AGGCAAAAAT ACGCAATCACAC CACACCGCA ATTCCCCTGTC ACACATCGCA ATTCCCGTGTC ACCCTTAAATGGA AGAACACGGC CAAGAACACGGC CAAGGATGGC CAAGGATGGC CAAGGATGGC CAAGGATGGC	1860 1920 2040 2103 2103 60 120 180 240 360 420 480 540 660 720 780 840 900 1020 1020 1140 1200 1200 1200
50 55 60 65 70	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT GAACTGTGGT TGCCAACGTA TA AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1	TCARATTCA  IGTACARTGG  CAACTGGAA  TITARAAGGG  #: NH_001!  SS89  21  CCACCCCCC  CCACCTCCC  CCACCTCCCC  CCACCTCCCC  CGCTCACCTCCC  CGCTCACCTCCC  CGTCACCTCGCC  CGTCACCTCGCC  CGTCACCTCGCA  AGACCACACAC  AGACCACACAC  CACCACACAC  CACCACACAC  CACCAC	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  31    TCCCCCATCC TCCTTACCTT CGGTGGTGGG AAATCCGTGG AAATCCGTGG AAATCCGTG AAATCCTACTG GCAGAATTCC ACTCTTACTT CCACCAGAATCC CTCGTATACTC CGAGAATTCC CGAGAATTCC CGAGAATTCC CGAGAATTCC CGAGAATCC CGAGAACC CGAGAACC CAGGAGACC CACCAGGGG ACCACGGGG AATCAGAACA CAGGGGGGAGAAC CAGGGAGGAGAC CAGGGAGGAGAC CAGGGAGGAGAC CAGGGAGGAGAC CAGGGAGGAGAC CAGGGAGGAGAC CAGGGAGGAGAACAACAACAACAACAACAACAACAACAAC	ATGGATAAG ATGTTTGTG  41	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGATGATTA ACTANATANA  51   CTGGTGGGC ACAGCATG ACAGGAGCTG ACAGCATGATA ATTANATA ACTANATANA  TGGACTTGTGA CTGAGCANA AGGCANANAN AGGCANANAN AGGCANANAN CGGAAGGTGGC ACAGCATCGCA ATTCCCCTGTC CGAGCATCGCA ATTCCCCTGTC CGTATATGGA AGGCATCGCA ATTCCCCTGTC CGTATATCGAC CGTTANATGGA AGGTACCAC CCTANATGGA CCAGGGCGCAG AGANACACGGC CCAAGGATGGC CCAAGGATGGC CCAAGGATGGC CCAAGGATGGC CTATCACATC	1860 1920 1980 2040 2100 2103 60 120 180 240 300 420 480 660 660 720 780 960 960 1020 1020 1040 1140 1260
50 55 60 65 70	GAATTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA  IGTACARTGA  IGTACARTGA  ITARAARGG  ITATATTT  ITTTGACCTC  IEEECE  #: NM_001: 2589  21    CCACCCTCCC  RTCACACTCC  CGCTCCCGGG  GAGGAATTGG  GGTCACTGTA  GATAAGTATT  CAGATATGA  ATATCAACAA  ATATCAACAC  CCTCCCCGGGT  CGGCTCCCGGG  GGTCACTGTA  GATAAGTATT  CAGATATGA  ACAGGCATC  CTGGCTGTAC  CTGGCTGTAC  CTGGCCTGGG  GACCCCCAGC  GACCCCCAGC  CTGCCAGACAC  CCACCAGCAC  CCACCAGC  CCACCAGC  CCACCAGC  CCACCAC  CCACCAGC  CCACCAC  CCACCAGC  CCACCAC  CCACCAC  CCACCAC  CCACCAC  CCACCA	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  916.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCC AAACGATTCL ACTTCTACTC ACTTCTACTC ACTTCTACTC ACTTCTACTC ACTTCTACTC CGTGATACTTC CGTGTGGTCC TCGTATACTTC CGTGTGGTC CCACCAGGATTCL CTGATATTT CGTGTGGTC TCGAGAGGAGG CCCCCTGC TCCTCTCC TCGTATACTC TGAGAGGAGG ATTCCCTACTC ATTCCCTACTC ATTCCCTACTC ATTCCCCCTG AATTCCCCTG AATTCCCCTG ACTCCCCTG ACTCCCCGGG AATTCACGGGG AATCAACGAGA	ATGGATAAG ATGTTTTTTTTTTTTTTTTTTTTTTTTTT	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGAGTTA ACTAAATAAA  51   AGCCTTGTGA CTTGTGGGC ACAGACCATG ACAGACCATG ACAGACCATG ACAGACCATG ACAGAGAGATAAT ACTCAAAATT ACTCAAAATT ACTCAAAATT ACTCAAAATT CCTTGAGAAAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTCACACC CACACTGCA ATCCCCGGCGCGAA ATTCCCCGGGCGCAA AGGAAAAAAAAAA	1860 1920 2040 2103 2103 60 120 180 240 300 360 420 480 540 900 960 1020 1080 1080 1080 1080 1140 1260 1320 1340
50 55 60 65 70	GAATTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA  IGTACARTGA  IGTACARTGA  ITTARAAGGG  ITTACACTC  IEECE  #: NM_001: 2589  21    CCACCCTCCC  ATCACACTCC  CACCTTCCGGG  GAGGAATTGA  GGTCACTGCT  GGTCACCTGGG  GGTCACTGTA  GGTCACTGTA  GGTAACTGAC  CTGCCCACCACACA  AGCCAACACA  AGCCAACACA  AGCCAACAC  GAACCCAGCC  CAGCACCAC  CAGCACCAC  CAGCACCAC  CACCAGCAC  CCCCCCCC	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCGC AAATCGTG AAAGGAATCC AAAGGAATCC ACAGGAGGAG CTGATACTTC CGTGTGGCC TCCTTACCTT CAGAATTCCAA ATATCTCAA CTGATACTTC CGAGAATCC TCATACTTC CGAGAATCC TCATACTC CCACCAGAAA CCACAGAAG CAGAATCC TCATACTC CACAGGAGGA CCACAGGAGG AATGAAGAA CAGGGAGGA CAGGGAGGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGGAGAA CAGGAGAAA CAGGAAAGAA CAGGAAAACAA CAGAAAACAA CAGGAAAACAA CAGGAAAACAAAAAAAA	ATGGATAAG ATGTTTCCTT TCCTTTCTTT TCCTTTTAGCA ATGTGTTGTG  ATGTGTTGTG  ATGTGTTGTG  ATGTGTTGTG  ATGTGTTGTG  ACCGCTTGGA ATGTGCAGGA ATGTACAGGG CAATTACAGG ATGTACAGGG ATGTACAGGG ATTTGAGA ATTTTGAGA ATTTTGAGA ATTTTGAGA CCACTGGCA ATTTTGAGA CCACTGGCA ATTTTGAGA CCACTGGCA CCACGGTGA CCACGGT	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT CGTGTAGTTA ACTAAATAAA  51	1860 1920 2040 2103 2103 60 120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1200 1380 1380 1380 1380 1380
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50 55 60 65 70	GARTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAAGGTA T AATTGATTT GGGCTATAAA A AACGACTCC ACTGAACTGG G AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782 1 11	TCARATTCA  IGTACARTGA  IGTACARTGA  ITARAARGG  ITATAARGGG  ITATATTT  ITTGACCTC  IEEECE  #: NM_001: 2589  21    CCACCCTCCC  ATCACACTCCC  CGCTCCCGGG  GAGGAATTGG  GGTCACTGTA  GATAAGTATT  CAGATATGAA  ATATCAACAC  TGAACACAT  CAGATATGAA  ATATCAACAC  CTGGCTGGGG  GAGCCACCAG  ACAGCCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CACACAGCACC  CCACAGACCAC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCACC  CCACACC  CCACAGCCACC  CCACACACC  CCACACC  CCACA	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  916.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCC AAAGCATCC AAATCCGTC AAATCCTACTC ACTGTACTC ACTGTACTC CGTGATACTT CCGTGTGGCC TCGTATACTT CCGTGTGGCC TCGTATACTT CGAGAGTTCC TCGTATACTT CGAGAGGGG CCCACCGGGG AATCACGCC TCGTATACTC TGGAGATCC TCGTATACTC TGGAGAGGGG CCCACCGGGG AATCACGCC TCGATACTC TGGAGAGGGG AATCACGGGG AATCACACGGGG AATCACACGGG AATCACACGGG AATCACACGGG AATCACACGGG AACCACACAC CGATCACAGT TGGAGAACTCC TGGAGAACTC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TG	ATGGATAAG ATGTTTTAGCA ATGTTTTAGCA ATGTTTTAGCA ATGTTTTAGCA ATGTGTTGTG  41 C TCCCCAAAAT ACGCTTGGF AAGGGCCTGG C AAGAGCAGG T TCAGTGAGG A TTTTAGAGA C TTACAGAGG T TCAGTGAGG A TTTTAGAGA C TCACTGGCA A TTTTGAGAG C CCACCGTGA A TTTTGAGAG C CCACCGTGA TTTTGAGAG C CCGTGTTATG C GGATAATG C CGACGGGA C TCTGGTTTA C CGGGTAGAGG C CTACACACGG G GAATAAGG C CTACTCCA C GGGGAATAAGG C CCACGTCA C TCTGGTTTA C CGGGGAATAAGG C CCACGTGA C CTACACACGG G GGAATAAGG C CCACCACGG C CACCGTGA C CTACACACGG C CACCACACGG C CACCACACG C CGACGACACACGG C CACCACCG C CACCACACCG C CACCACCG C CACCACACCG C CACCACCG C CACCACCG C CACCACCG C CACCACCG C CACCACCACCG C CACCACCAC C C CACCACACCG C CACCACCACCG C CACCACCACCACCG C C CACCACCACCG C C CACCACCACCACCG C C C C C C C C C C C C C C C C C C	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGATATA ACTAAATAAA  51   AGCCTTGTGA CTCTGGGGC ACAGACCATG ACAGACCATG ACAGACCATG ACAGACATAT ACTAAAATATA ACTAAAATATA ACTAAAATATA ACTAAAATATA ACTACAAATT CCTCGAGCAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTCACACC CACATGCA CACAATGCA ATTACCACGA CACAATGCA ATTACACACC CACAGATGGC CACAAGATGGC CAAGAATGGA CTTAAAATGA AGCAAAATAGA CTAAAATGCA CTTAAAATGA CACACCCGGGCGCAG CACACCTCCGGG CCTACTCCTC CACCTCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTACTTCCTG CGCTTCCTTC CCCTCCTCCTC CCCTCCTCCTC CCCTCCT	1860 1920 2040 2103 2103 60 120 180 240 300 360 420 480 540 900 1020 1080 1020 1080 1140 1200 1320 1380 1440 1500 1500
50 55 60 65 70	GARTTTTAA TCACACGGAT C GTGCGAGTGG TCAATTGAGT A GGGACTGCCA TATTTTCTTT T GAACTGTGGT TGCCAACGTA T AATTTGATTT GGGCTATAAA A AACGACCTCC ACTGAACTGG C AAA  Seq ID NO: 151 DNA Sequ Nucleic Acid Accession Coding sequence: 1782  1	TCARATTCA  IGTACARTGA  IGTACARTGA  ITARAARGG  ITATAARGGG  ITATATTT  ITTGACCTC  IEEECE  #: NM_001: 2589  21    CCACCCTCCC  ATCACACTCCC  CGCTCCCGGG  GAGGAATTGG  GGTCACTGTA  GATAAGTATT  CAGATATGAA  ATATCAACAC  TGAACACAT  CAGATATGAA  ATATCAACAC  CTGGCTGGGG  GAGCCACCAG  ACAGCCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CAGCACCACC  CACACAGCACC  CCACAGACCAC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCCACC  CCACAGCCACC  CCACAGCCCACC  CCACAGCCACC  CCACACC  CCACAGCCACC  CCACACACC  CCACACC  CCACA	CAAATGTTAA AAACTGTTAA AAACTGTTAA TTTTTATGTG CTTTCCTGCC TCAGGTTAT TGTTGTACTG  916.2  31   TCCCCCATCC TCCTTACCTT CCGTGGTGCC AAAGCATCC AAATCCGTC AAATCCTACTC ACTGTACTC ACTGTACTC CGTGATACTT CCGTGTGGCC TCGTATACTT CCGTGTGGCC TCGTATACTT CGAGAGTTCC TCGTATACTT CGAGAGGGG CCCACCGGGG AATCACGCC TCGTATACTC TGGAGATCC TCGTATACTC TGGAGAGGGG CCCACCGGGG AATCACGCC TCGATACTC TGGAGAGGGG AATCACGGGG AATCACACGGGG AATCACACGGG AATCACACGGG AATCACACGGG AATCACACGGG AACCACACAC CGATCACAGT TGGAGAACTCC TGGAGAACTC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TGGAGAACTCC TG	ATGGATAAG ATGTTTTAGCA ATGTTTTAGCA ATGTTTTAGCA ATGTTTTAGCA ATGTGTTGTG  41 C TCCCCAAAAT ACGCTTGGF AAGGGCCTGG C AAGAGCAGG T TCAGTGAGG A TTTTAGAGA C TTACAGAGG T TCAGTGAGG A TTTTAGAGA C TCACTGGCA A TTTTGAGAG C CCACCGTGA A TTTTGAGAG C CCACCGTGA TTTTGAGAG C CCGTGTTATG C GGATAATG C CGACGGGA C TCTGGTTTA C CGGGTAGAGG C CTACACACGG G GAATAAGG C CTACTCCA C GGGGAATAAGG C CCACGTCA C TCTGGTTTA C CGGGGAATAAGG C CCACGTGA C CTACACACGG G GGAATAAGG C CCACCACGG C CACCGTGA C CTACACACGG C CACCACACGG C CACCACACG C CGACGACACACGG C CACCACCG C CACCACACCG C CACCACCG C CACCACACCG C CACCACCG C CACCACCG C CACCACCG C CACCACCG C CACCACCACCG C CACCACCAC C C CACCACACCG C CACCACCACCG C CACCACCACCACCG C C CACCACCACCG C C CACCACCACCACCG C C C C C C C C C C C C C C C C C C	TGATCATGGT TAATTTTCT TTGGTGCATG TGATTTATTT GGTGATATA ACTAAATAAA  51   AGCCTTGTGA CTCTGGGGC ACAGACCATG ACAGACCATG ACAGACCATG ACAGACATAT ACTAAAATATA ACTAAAATATA ACTAAAATATA ACTAAAATATA ACTACAAATT CCTCGAGCAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTTTT CCTGAGCAAA ATGCACTTCACACC CACATGCA CACAATGCA ATTACCACGA CACAATGCA ATTACACACC CACAGATGGC CACAAGATGGC CAAGAATGGA CTTAAAATGA AGCAAAATAGA CTAAAATGCA CTTAAAATGA CACACCCGGGCGCAG CACACCTCCGGG CCTACTCCTC CACCTCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTAATTCCTG CACCTCCCGGG CTACTTCCTG CGCTTCCTTC CCCTCCTCCTC CCCTCCTCCTC CCCTCCT	1860 1920 2040 2103 2103 60 120 180 240 360 360 420 480 540 900 960 1020 1080 1020 1080 1140 1260 1320 1380 1440 1500 1500

TACTGTGTCT CATAGACATG CGCCACCTCC ACGTGAGAAC AAGGGTGAAG GTGAGGGAAG 2040

	GTGCACAACA C	CAACAGATAA	GAAAAAAATG	TTGACCTAG	AAACAAATGA	CATGTCAAG	1740
	AAGGCCATAA A	TGACCGACA	GATGCCTAAA (	STGGAATACA	GGGACATTGA (	SATTGATGAT	1800 1860
	TACAACCTGC C	CATGCAGAT	ACTGAAGCCA	ACCEACACTTCA	TAGETTERCAR	CTTCGAGGTG	1920
5	AGCTGGGAGA	CGTGATGGT	GAGCAGCCAC	GCCCCCGTGG	TGGTAAAGTG	TGACGGCCGT	1980
-	GGCAGCGGCT 1	TCCAAGGGAC	CAAGCTCCTG	CACGAAGTGA	GGCGGCGGCT	GGGCTTGCTG	2040
	GAGGAGAAGG	ACCAGATGGA	GCCCGTGCGG .	ACGATGCTGA	AGGAGCAGTA	CATTGACAGG	2100
	ACGCGCGTGG	CCCTGTTTGG	GAAGGATTAC	GGTGGCTACC	TGAGCACCTA	CATCCTCCCA	2160
10	GCAAAGGGAG	AAAATCAAGG	CCAGACATTC	ACCTGCGGCT	CTGCTCTCTC	TCCAATAACA	2220 2280
10	AACAGAGCAT	TOTATGCCTC	CARCCTACCC	CATCCACTCT	ASSETSO	AGAACAGCAG	2340
	TTCCTGATCA	TTCATCCCAC	TGCCGATGAA	AAAATTCATT	TCCAGCACAC	AGCAGAACTC	2400
	ATTACACAAC	TAATTAGGGG	AAAGGCTAAT	TACAGCTTAC	AGATTTACCC	GGACGAAAGC	2460
16	CATTACTTTA	CCAGCTCCAG	CCTCAAACAG	CATCTGTACC	GGTCCATCAT	CAACTTCTTC	2520
15	GTGGAATGCT	TCAGGATCCA	GGACAAACTG	CCGACAGTCA	CAGCGAAAGA	GGACGAGGAG	2580 2640
	GAGGACTAAG	CTCAGGTCGC	TCTAAGCACA CCTCTTCCCT	CCCACCCCCC	GGGGGGGGGG	CAGATOCAAC	2700
	TTCCATAGCA	TOTOTOTOTO	GGATGCGGAA	GGCAGTTTTG	CTTGGGAAAC	AAGCTCCTTC	2760
	CCCGGGGTCA	TCACTCACGG	CCTCCATGGC	ACCAGGGACA	ACCCTCTCCC	CGCAGCAGCG	2820
20	CCTCCTCCCC	GCGCCCGAGA	GACCGGCACG	CCACGGCCCC	TCCCCCCAAGG	AACAGAGCAA	2880
	AGGATGGTGG	CCGCAGGCCC	CACGCGAGCC	CACAGGACAC	CGGCCCCTAG	ATTCCAGCCA	2940
	CCAAGCGGAA	GCATGAGACC	CGCCCACACT	AGCCTCTGTG	TTCCCGTTAG	GGACATCACA	3000 3060
	CCCTGTCTCA	CGTCGCAGTG	CCATGGACGC CTACTTCCTG	TANTONCONC	GCACCATIGI	CTCAGGGGGT	3120
25	DAMAGAGA	CCTTTTCTCT	ACAGAGTCTT	ACTGTAGCTA	CGCTAATGGT	TAACCTGATA	3180
20	GAATTAACTC	GTATTTTTCT	ATGGTTTTAA	CCTGATGCTC	CACTGTCTCC	GTCATGGGGT	3240
	TGTTTTGCTG	TTTGGGGTTG	GGCCTTGTTT	CCCTTTCCTT	TCTCCAGTCC	ACGTGTAGAC	3300
	TTTGCGCTTG	ATGAAGAAGC	AGATCGGAAG	TAACTGCTCC	CTCCTCAAGG	TTGTCTTCAG	3360
30	ACGTCTTGGG	GACGITCCIA	AACACTGAGG	GGGAAGACAG	CCAATAGCAC	CCATTAAAAG	3420 3480
30	AAATACCTAA	TACATOCCTC	TCTCCCACTC	TOTTGTCT	CCTTGGTACC	GTATCAAGCT	3540
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	ccccccccc	GGGCGGCGG	GAACCCCAAA	CGCAACCGGG	TCTGGAGGGA	TCCCCGCGCC	60
40	GAGCCAGCCG	CCGTCACCGC	CTCCGCGCCG	CCCCTGCGGG	CTTGGCAGGC	CCCCCCCCCC	120
	CCCGCACTGC	GCCCGGCCGG	CGGCTCCCGC	GGTCCCACCC	TGAGCTCGCC	GGCCCGTCGC	180 240
			GCCGGCCTCG				300
	CCCCTGCTC	CCCCCCCTCC	TOGGGGTGCC	CTCCAATGCT	TCAGTCAACG	CGTCCTCCGC	360
45	GGCGAGCCCA	TCGCCCCGC	GCTGCTGGCC	TCGGCGGCCC	CCCCCCCC	CGAGCGCCCG	420
	GGCCCGGAGG	AGGCGGCGG	C GGCGGCGGCG	CCTGTGCAAC	: ATCAGCGTGC	AGCGGCAGAT	480
	GCTGAGCTCG	CTGCTCGTG	CCTGGGGCCG	CCCGCGGGGG	TTCCAGTGCG	ACCTACTGCT	540
	CTTCTCCACC	AACGCGCAC	GCCGCGCTTT	CTTCGCCGCC	GCCTTCCACC	GCGTCGGGCC	600 660
50	GCCGCTGCTC	ATCGAGCAC	TGGGGGTGG	COCCACCCC	COCCTCCCC	CCCCCCCCC	720
30	CTGCGTGGGC	GCCCCTCC	A CCGCCGGGGG	GCCCACCGC	CTGCCAGCCT	ACCCCGCGGC	780
	CGAGCCGCCC	GGGCCGCTG	T GGCTGCAGGG	CGAGCCGCTC	CATTTCTGCT	GCCTAGACTT	840
	CAGCCTGGAG	GAGCTGCAG	G GCGAGCCGGG	CTGGCGGCT	3 AACCGTAAGC	CCATTGAGTC	900
E E	CACGCTGGTG	GCCTGCTTC	A TGACCCTGGT	CATCGTGGT	TGGAGCGTGG	CCGCCCTCAT	960
55	CTGGCCGGTG	CCCATCATO	G CCGGCTTCCT A CCCCCGCCGC	GCCCAACGG	CATGGAACAGC	CACCOGACCAC	1020 1080
						CCAAGTGACC	1140
						TCCCGCCGGA	1200
	GACTCGGCCG	GTGTGCTTC	G TGCTGTAGT	TOATCGTTAGT	r ccrcrrccc	AGATGGGGCC	1260
60	GCCGAGAGAC	CCCAGCGCC	T TTGAAAAGC	A AGGTTTGTG	C TGCGCTTCC/	GTTCCGAAAA	1320
	GCAGATGTTT	AAGCCCTTG	G ACTGAGGGT(	GGATCGCAG	C TCCGAAGAC(	GAGAGGAGGG	1380
	AAATGGGGCC	CTTTCCCCT	C TATTGCATC	CCCTGCCCG	A CTCCTTCCC	GCACCCACGT	1440 1500
	GCCCTAGATT	CATGGCAGA	A AATGACCAA	A ICCIGIGIA	A BABAGATTA	TATTTAATAA ATTGCTATTG	1560
65	CIGITITADA	C IGAAAGIII	T TOTATOTGA	A CATAGTTGT	A TTTGAAATT	GTGGTTTTTT	1620
05	ATTTATTTA	AAATTGGGG	G GAGGGCATG	GAAGGATTT	A ACACCGATA	TATTGTTACCG	1680
	CTGAAAATGA	ACTITATGA	A CCTTTTCCA	A GTTGATCTA	T CCAGTGACG	r GGCCTGGTGG	1740
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	ACTAACCCT	G AAAAAGAT/	AT TOTOTOT	U CGGGAAAAT	C CCACCAACGT	G TCTCATGGCA A CGTAGATCTG	180 240
	ATCACAGAA	C ACCOCCATI	AT CCCATTCAC	י מעופופופו	G AGGTGAACC	A CGTAGATCTG G CCGCTGTGGC	
80	CACAGCCAG	T CGGAGCTG	CA AGTGTTCTG	G GTGGATCG	G CATATGCAC	T CAAAATGCTC	
	TTTGTAAAG	G AAAGCCAC	AA CATGTCCAA	G GGACCTGAC	G CGACTTGGA	G GCTGAGCAAA	420
	GTGCAGTTT	G TCTACGAC	IC CTCGGAGAA	A ACCCACTTO	A AAGACGCAG	T CAGTGCTGGG	480
	AAGCACACA	G CCAACTCG	CA CCACCTCTC	T GCCTTGGTG	A CCCCCGCTG	G GAAGTCCTAT	540
	GAGTGTCAA	G CTCAACAA	AC CATTTCACT	G GCCTCTAG	rg atccgcaga	A GACGGTCACC	600

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	ATGATCCTGT C	TGCGGTCCA	CATCCAACCT	TTTGACATTA	TCTCAGATTT	TGTCTTCAGT	660
	GAAGAGCATA A	ATGCCCAGT	GGATGAGCGG	GAGCAACTGG .	AAGAAACCTT	GCCCCTGATT	720 780
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5	TAG	CAACCAGG1	GCAGATCCCI	COGGACAGAI	CCCAGIAIAA	OCACA 1000C	B43
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	GGCACGAGGC (	CGGAGGCGCG	GTGCTCGGCC	CGGGAGCGCG	AGCGGGAGGA	GCAGAGACCC	60
	GCAGCCGGGA C	CCCGAGCGC	GGGCGATGCA	GGCTCCGCGA	GCGGCACCTG	CCCCTCCTCT	120
1.5	AAGCTACGAC (	CGTCGTCTCC	GCGGCAGCAG	CCCCCCCCC	AGCAGCCTCG	GCAGCCACAG	180
15	CCGCTGCAGC (	CGGGGCAGCC	TCCGCTGCTG	TOGCCTCCTC	CCCNACTOTT	TOTOGRAPHOT	240 300
	TCTTGCTTCC /	CCCTTTCCG	CTCCAAATCC	AGTGCTACCA	GTGTGAAGAA	TTCCAGCTGA	360
	ACAACGACTG (	TCCTCCCCC	GAGTTCATTG	TGAATTGCAC	<b>GGTGAACGTT</b>	CAAGACATGT	420
	GTCAGAAAGA	AGTGATGGAG	CAAAGTGCCG	<b>GGATCATGTA</b>	CCGCAAGTCC	TGTGCATCAT	480
20	CAGCGGCCTG '	TCTCATCGCC	TCTGCCGGGT	ACCAGTCCTT	CTGCTCCCCA	GGGAAACTGA	540
	ACTCAGTTTG	CATCAGCTGC	TGCAACACCC	CTCTTTGTAA	CGGGCCAAGG	CCCAAGAAAA	600 660
	GGGGAAGTTC TAGCCCTCTT	COCCOCCACAC	TECTEARCE	GAAGGAGATG	CACCATOCTC	CTGCATTGTT	720
	CTTCCAGCCC	TOGOCOCCAA	CCCCCCACCT	CCCTGAGTGA	GTTTCTTCTG	GGTGTCCTTT	780
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40	1		1	1	1	1	
	TGTGGGGCTG C	CCCGCCTCC	GCGGCGTCTG	CAGGCGCCAC	CCCTCCCTCT	TTCCGGCTGT	60
	GACCCTCCTC G						120
	GCTCCCGCTC O						180 240
45	CGCGGTCGTC C CTGTGACGCT G	TIGGIGGAA	GGAACCATGA	ACIGGCATCI	CCCCCICIIC	CARCTACCCT	300
73	CCAACACGGG G						360
	TGATCTCTCC C	CATGGGGTT	GCCTCCCTCC	TOGGGATGCT	TCAGCTGGGG	GCGGACGGCA	420
	GGACCAAGAA G	CAGCTCGCC	ATGGTGATGA	GATACGGCGT	AAATGGAGTT	GGTAAAATAT	480
	TAAAGAAGAT C						540
50	ACGCCGTGTT T						600
	ATGTGTTCCA G						660
	CCATCAATGC A	TGGGTTAAA	AATGAAACCA	GGGATATGAT	TGACAATCTG	CTGTCCCCAG	720
	ATCTTATTGA T						780 840
55	TGTGGAAATC A GGAAATCCTA T	CCGTTCCAA	CCCGAGAACA	CAAAGAAACU	CACTITUGIG	CCCTCCACA	900
33	GTGCCCCCAA T	CANDIGCCA	TACABCTTCE	TTGAACTGC	CTACCACGG	GAAAGCATCA	960
	GCATGCTGAT T	GCACTGCCG	ACTGAGAGCT	CCACTCCGC	GTCTGCCATC	ATCCCACACA	1020
	TCAGCACCAA G	ACCATAGAC	AGCTGGATG	GCATCATGG	GCCCAAGAGG	GTGCAGGTGA	1080
	TCCTGCCCAA G						1140
60	GCATTACTGA C	ATGTTTGAT	TCATCAAAGO	CAAATTTTG	C AAAAATAACA	AGGTCAGAAA	1200
	ACCTCCATGT T	TCTCATATC	TTGCAAAAA	G CAAAAATTG	A AGTCAGTGAA	GATGGAACCA	1260
	AAGCTTCAGC A						1320
	TAGACAGACC 1	TTTCTGTTT	TTCATCCGAC	ATAATCCTA	CAGGIGCIGIG	TTATICATEG	1380 1440
65	GGCAGATAAA ( GCTACGAAGA A	AAACCCTGA	AGAGTATAC	A AAAGAAACC	A TGCAAAGCAA	TTTTTTTACAT	1500
05	CGCTTCTTTT 1	TO A A A CT TO C	ASSATTOTT :	L LICAIAGIT	T GCAAGTGTTT	CTGTTCTGGG	1560
	AGGTATTGGA (						1620
	AAGGCTTCCA (						1680
	CCTGTTGAGT	ATTTGCTGTT	TGTCCAGTT	C AGGAATTTT	T GTTTTGTTT	TOTATATOT	1740
70	GCGGCTTTTC /	AGAAGAAAT1	TAATCAGTG	T GACAGAAAA	A AAAATGTTTT	ATGGTAGCTT	1800
	TTACTTTTTA '	TGAAAAAAA	ATTATTTGO	C TTTTAAATT	C TTTTCCCCC	TCCCCCTCCA	1860
	AAGTCTTGAT						1920
	GTTTTTGTTG						1980
75	TAAAAAACTC	CIGICITGC	AGACAAGGT	T GCTGTTGTG	C AGIGIGUETO	ACTOTTATO	2040 2100
13	TCTGTACTCC '	i i GONTTTG(	. ALTITIGTA	I ITIGTACAA	n vinanaia	- ACIGITATOA	2105
	GINGI						-143
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		11	21	31	41	51	
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						T GCAGGTGCCG	60
	GCGGCCGCCT	TITIGGGCT	CGGGACCCC	L GGGAGTGGG	in GCGGCAGTC	G GGGACGCCTC	120

	AACTOGTTCA	CTCAGGGAAT	CCTGCCCATC	CCCTTCTCCA	GGCCGACTTC	GCAGAACTAC	180
•	TGCTCCCTGG	AGCAGCCAGG	CCAGGGGGGGC	AGCACCAGCG	CCTTCGAGCA	GCTGCAGAGG	240
	TCCCGACGGC	GCCTCATCTC	CCAGAGATCT	TCCTTGGAGA	CCCTGGAAGA	TATTGAGGAG	300
5	AACGCCCCTC	TCCGGAGATG	TCGAACTCTC	TCAGGTTCAC	CCAGACCAAA	GAATTITAAG	360 420
,	AAGATTCATT	TTATCAAGAA	CATGCGGCAA CTGTAGTATA	CACGATACCA	TCCCCTATCC	CONCACTACC	480
			GGACGGAGGA				540
	CACATCATTC	CTCTGGAAGG	TGTGGAGCTG	GCTGCTGATG	GGAAGACTGT	TTCCTATACC	600
	CAATTTCTGT	TACCCACAAA	TGCCTTTGGA	GCCCGGAGAA	ATACCATAGA	CTCCACCTCC	660
10	TCTTTCTCCC	ACTTCCCTAA	CCTGAGCCAC	CGCAGCCTCT	CCATAGGCCG	GGCAAGCGGC	720
	ACCCAGGGGA	GCCTCGACAC	AGGTAGTGAC	CTGGGAGACT	TTATGGACTA	TGACCCAAAT	780
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			CTACGTGAAG				900
1.5			TCACATTAAG				960
15			GCAGGAGGAC				1020
	GCCTTCGTCT	ACTTTGAAAA	GCTCGCCCTC	AAGGGGAAAC	TCAACAAACA	GAACUGGAAG	1080 1140
	CIGIGIGCIG	GGGCATGTGT	GCTGTTAGCA CAAACTGGAA	CLCAAAATIG	GAAGIGACCI	COCAGAACTG	1200
	ATTOCATOO	ATTIANTIGA	GTTAGTGGCC	TTCCAATTC	CCTCCACTT	GCCCGAGCAC	1260
20			ACGGCTGGTC				1320
20	CAAGGGCA	TTTCTTCTCA	GCTTGGTGGA	GCAGCACTTA	CTTACTACTG	GAAATGAAAA	1380
						GAGAAGCAGT	1440
			TCTTGGGTGT				1500
	CCTCAAGCAC	GGGAAGAGGA	GGTGTGTGCT	GAGAACAGAG	AGGCCCTGCC	CTCTGTCCAC	1560
25			CCCAGCCCAG				1620
			CCAGATCTGT				1680
			GAAGTTGGGG				1740
	CAAAGAGTGT	GCCAATCTAT	TTTTGTATCA	GCATTGGAAG	TGCACTTTCC	CCTGGGGCGT	1800 1860
30	GTGGGTGTGT	GAATGTGCAA	GTGTCTGAGA CAGCCCTTAG	GATACTGCAT	CAGCCCTAGA	TCACCTTCAG	1920
50	CAGICCCGCC	TAGATGATT	CTGGATAAGA	ATTECTET	CCCTACCAGA	CAGTTTGACA	1980
						ACCAAGGGGA	
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			TCTGCCACCC				2160
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			GCATGATTGG				2340
						AACATTCCCA	2400
40						ACTGGGACAG	2460
40						GCACCAGCTG	2520
	AAGTTCCCCT	GACTGAAGAG	AGCCTGTGGC	CATGTAAAAA	GAGAATTAAA	CTCTTGTTGC	2580
	and the same of th						2587
	TTTTTGT						2587
							2587
45	Seq ID NO:	167 DNA Se	quence	26			2587
45	Seq ID NO: Nucleic Ac	167 DNA Se	quence n #: BC0088	26			2587
45	Seq ID NO: Nucleic Ac	: 167 DNA Se	quence n #: BC0088	26 31	41	51	2587
45	Seq ID NO: Nucleic Ac Coding sec 1	167 DNA Se id Accessio quence: 188. 11	equence on #: BC0088 .2695 21	31 	41 	1	
	Seq ID NO: Nucleic Ac Coding sec 1   GGCACGAGGG	167 DNA Serid Accessic quence: 188. 11     TCCGGCCTCT	quence n #: BC0088 .2695 21       GGACTAGGAA	31     CCGACAGCCC	41     CCCTCCCCGG	GTCCCTCCCT	60
45 50	Seq ID NO: Nucleic Ac Coding sec 1 GGCACGAGGG CTCTCTCCAC	167 DNA Se id Accessic quence: 188. 11   TCCGGCCTCTCGCCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCGCCCTCTCTCGCCCTCTCTCGCCCTCTCTCGCCCTCTCTCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	equence in #: BC0088 .2695 21 ) GGACTAGGAA GGAGGGGCTCT	31     CCGACAGCCC	41     ccctcccccc	GTCCCTCCCT GAGGGTCATC	60 120
	Seq ID NO: Nucleic Ac Coding sec 1 GGCACGAGGC CTCTCTCCAC CGCGCGCAC	167 DNA Secrit Accession puence: 188. 11	equence on #: BC0088 .2695 21     GGACTAGGAA   GAGGGGCTCT	31     CCGACAGCCC   CCACGCTCCC   CACCTGGATA	41     cccreccese   Gatagtrecca   Taattrecga	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC	60 120 180
	Seq ID NO: Nucleic Ac Coding seq 1   GGCACGAGG CTCTCTCCAC CGCGCCGCAC CCCCAGGATC	167 DNA Secrit Accession puence: 188. 11	equence n #: BC0088 .2695 21 i GGACTAGGAA GGAGGGCTCT GGTTTCGCCTT	31     CCGACAGCCC   CCACGCTCCC   CACCTGGATA   GCCCAGGATC	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA	60 120 180 240
	Seq ID NO: Nucleic Ac Coding sec 1   GGCACGAGGC CTCTCTCCA CGCCCGCAC CCCCCGGAT GAACTACCCC	167 DNA Secid Accession prence: 188. 11   C TCCGGCCTCTGCCTTTTCGCCTCTCGCCTTTTCGCCTGCCTGCGGGGGG	equence in 8: BC0088 .2695 21 if GGACTAGGAA G GAGGGGCTCT GCTTTCGCCTT C CCGCTGGG	31     CCGACAGCCC   CCACGCTCCC   CACCTGGATA   GCCCAGGATC   AGTGTCCACT	41 	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCCGCGT	60 120 180 240 300
50	Seq ID NO: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCGCGCAC CCCCAGGATT GAACTACCCC CAACCAGCTC	167 DNA Se rid Accessic puence: 188. 11     TCCGGCCTCT GCCGTTTCGG TCCACGCTGG ACCACGCTGG CGTGGCGGG	equence in #: BC0088 .2695 21	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCCGCGT TCCGCCACAA	60 120 180 240 300 360
	Seq ID No: Nucleic Ac Coding sec 1 GGCACGAGGG CTCTCTCCAC CGCCGCAGAT GAACTACCC CAACCAGCT GATCGTGGA	167 DNA Se id Accessic quence: 188. 11	equence in #: BC008B .2695 21	31	41 	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCGGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCGCGT	60 120 180 240 300 360 420
50	Seq ID No: Nucleic Ac Coding sec  1 GGCACGAGGG CTCTCTCCAC CCCCGCAGAT GAACTACCC CAACCAGCT GATCTGGAG GTCCCACGGGT GTCCACGGGT	167 DNA Secid Accessic puence: 188. 11	equence in 8: BC0088 .2695 21	31     CCGACAGCCC CCACGCTCCC CACCTGGATA GCCCAGGATC AGTGTCCACT CAGGCCGCTC GCCTGCGTT GCCGGTT CAGGTACCACT	41	GCCACAAA AGCTGCGCT TCCCCACAA AGCTGCGCGT CCATACGTCC	60 120 180 240 300 360
50	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession puence: 188. 11   C TCGGCCTTCG ACCACGTGG CGGGGGGGGGGGGGGG	equence in #: BC0088 .2695 .21 if GGACTAGGAA G GAGGGCTCT C GTTTCGCCTT C TTCCGCTGGA T TTATCAACG A AGATCCTGT A AGATCCTGT A AGATCCTGT A AGATCCAAGGA	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCGGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCGCGT	60 120 180 240 300 360 420 480
50	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTTCTCAC CGCCCCAGGAT GAACTACCC CAACCAGCT GATCGTGGAG GTCCCACGGG GGGATACAA GGGATACAA GGGATACAA	167 DNA Se id Accessic puence: 188. 11	equence on 8: BC0088 .2695 21	31	41	GTCCCTCCCT GAGGGTCATC GCGAGGCTGC GCCCGGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCGCGT CCATACGTCC AGAAAATTGA	60 120 180 240 300 360 420 480 540
50	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession puence: 188. 11 1	equence in #: BC0088 .2695 21 if GGACTAGGAA if GAGGGCTCT if TCCGCCTGG if TCCGCCTGG if TCCCGCTGGA if TATCAACGG if AGGCATCCC if AAGATCCTGTG if CCGGCATGTT if AACACCGTGCC if AAGACGAGGGG if CCGGCATGTT if AACACCGTGCC if AAGACGAGGGG if AAGAGAGGGG if AAGACGAGGG if AAGACGAGG if AAGACGAGGG if AAGACGAGGG if AAGACGAGG if AAGACGAGGG if AAGACGAGGG if AAGACGAGGG if AAGACGAGG if AAGACCAGGG if AAGACGAGG if AAGACGAGG if AAGACGAGG if AAGACGAGG if AAGACCAGGG if AAGACGAGG if AAGACGAGG if AAGACCAGGG if AAGACCAGG if AAGACCAGGG if AAGACCAGG if AAGACACAGG if AAGACCAGG i	31	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGCTGCGCT TCCGCCACAA AGCTGCGCT CCATAGGTCC AGAAAATTGA AATTACTCAA AGCATCCTGAG AGGCAGAGGGA	60 120 180 240 300 360 420 480 540 660 720
50	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTTCTCAC CCCCAGGAT GAACTACCC CACCAGGT GATCTGGAG GTCCCACGGG GTCCCACGGG GTCCCACGGG GGAATACAA GGACGCGGT AAGCAGATAAATT AAGCAGAGAAA	167 DNA Se id Accessic puence: 188. 11	equence in 8: BC0088 .2695 21	31   CCGACAGCCCC CACCTGGATE GCCAGGATC AGTGTCCACT GCGGGCGCTC GCCTCGGT GACAACGCC GACAACGCC CAGCTGGGA GTCAGTGGG GTCAGTGGGA GGCCGACTTC	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCAGGGGCA AGGGCCGCGT TCCGCCACAA AGGGCCGCT CCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG GAGCAGAGGA	60 120 180 240 300 360 420 480 600 660 720 780
50	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG CTCTCTCCAC CGCCCGCAC CCCAGGATT GAACTACCC CAACCAGCT GATGGTGCAT GTCCACGAG GTCCACGATACAAA GAGGAGGAA AAGTAAATT AAGGAGAAA CCAATCAGCA	167 DNA Secid Accessic guence: 188. 11	equence in 8: BC0088 .2695 21	31   CGGACAGCCC CACCTGGATA GCCCAGGATG GCCCAGGATG GCCCTGCGT CAGGCGCCT CAGCTGGGA GCCAGGCGC CAGCTGGGA GCCAGGCGCA GCCAGGCGCA GCCAGCTGGA GCCAGCGCACT CAGCTGGA GCCAGCCT CAGCTGGA GCCAGCCT CAGCTGGA GCCAGCATCA GCCAGCATCA GCCATCAG	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCAGGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCCGCT CCATACGTCC AGAAAATTGA AATTACTCAA GGATCCTGAG AGGCAGGGA CCTCAGCACC AGAGGAAACA	60 120 180 240 300 360 420 480 540 660 720 780 840
50	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession puence: 188. 11 1 1	equence in #: BC0088 .2695 21 i i GGACTAGGAA i GAGGGCTCT i CTTTCGCCTT i CCCGGGCTGT i TTATCAACGG i TTATCAACGG i AGATCCTGT i AGCCAAGGT i CCGGCATGTI i AGCCCAAGGT i CGGCATGTI i CGGGCATGTI i CGGGCATGTI i CAGGCATCGG i AAGAGGAGGG i AAGAGGAGGG i AAGACGAGGT i TCACAGCAGGT i TCACAGCAGGT i TCACAGCAGGT i TCACAGCAGGT i TCACAGCAGGT	31	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCCACAA AGCTGCGCT CCATAGGTCC AGAAAATTGA AATTACTCAA AGCATCTGAG AGCAGAGGA CCTCAGCACC AGAGAAACA CGTGCTTTTGA	60 120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	Seq ID No: Nucleic Ac Coding Sec I GGCACGAGGG CTCTTCTCA GCCCCACGATC GAACTACCC CAACCAGCT GATCGTGGAI GTCCACGGT GGAATACAA GGAGCGCGT AAGCAGGT AAGTAAATT AAGCAGAA CCAATCAGAG GGAGAAA GGAGAAATCA	167 DNA Secid Accessic puence: 188. 111	equence on 8: BC0088 .2695 21	31	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCGT TCCGCCACAA AGGGCCGCT CCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG CCTCAGGACC AGAGGAAACA AGGGAAACA GTGCTTTTGA GCGAAGCTCAC	60 120 180 240 360 420 480 540 660 720 720 780 840 900
50	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG CTCTCTCCAC CCCAGGATT GAACTACCAC CACCAGGAT GTCCACCAGGAT AGTATACACA GTCCACGG GAATACAA GACGAGGAT AAGTAAATT AAGCAGAAA CCAATCAGA GGCAGAAG GAGAACTCA CGAGGAGCCG CGAGAAGCCACA CGAGGCCCG	167 DNA Secid Accession process of the control of t	equence in #: BC0088 .2695 21	31	41	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCCGGGGCA AGGGCCGCT TCCGCCACAA AGCTGCGCGT CCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG AGCAGAGGA ACTCAGCACC AGAGGAACA GTGCTTTTGA CGAACCTCAC AGAGGAACCA AGCAAGCTGC	60 120 180 240 300 360 420 540 660 720 780 900 960
50 55 60	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession process 188. 11 11 11 11 11 11 11 11 11 11 11 11 11	equence in #: BC0088 .2695 21 j GGACTAGGAA GGAGGGCTCT GTTTCGCCTT GCCGGGCTGT TTATCAACGG AAGATCCTGT AAGCCAACGG AAGATCCTGT AAGACCAAGGT CCGGCATGTI CCGGCATGTI TCAAGGAGGA GAAGATCGG AAGATCGT AACACCTGCC GAAGGATCGT TCAAGCATCGT TTATACTAGT TTATACTAGT TTGATCAGCATCT TTATACTAGCAT TTCAACCATCT TTCAACCATCT	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCCGCT AGAAAATTGA AATTACTCAA AGCACCTGAG AGCAGAGGA CCTCAGCACC AGAGGAAACA GTGCTTTTGA CGARCTCAC AGAGCAACCA CGTGCTTTTGA AGCACCCACCC AGAGGAACCA AGCAAGCTGAC	60 120 180 240 300 420 480 540 600 650 720 780 940 960 960
50 55 60	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCCCCAGAGT GAACTACCCC CAACCAGCT GATCGTGGAG GTCCACCAGGG TGGTGCCAT AGGATACAA AGGCAGAAA CCAATCAGG CGCAGAAG CGAGCCCG GGCAATCA CGAGCCCG GGCAATCA CGAGCCCG GGCAATCA	167 DNA Secid Accession puence: 188. 111	equence on 8: BC0088 .2695 21 j GGACTAGGAA G GAGGGCTCT C GTTTCGCCTT TCCCGCTGGT TTCCCCTGGA AGATCCTGTC A AGATCCTGTC A AGATCCTGTC A AGATCCTGTC C AAGAGGAGGG C AAGATCCTGTC A ACACCATGCT TTCAACCAGT G AATATTAACTAC T TCAACCAGT T TCAACCAGT T TCAACCAGT C GGTTTAGCAC T TTCAACCACT C AGGTTTCGCAC C AGGTTCGCC C AGGTTCGCG C AGGTTCGCC	31   COGCOTGG	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCT TCCGCCACAA AGCTGCCCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG AGCAGAGGA ACTCCTGAG CCTCAGCACC AGAGGAAACA CGTGCTTTTCA CGAAGCTCAC AGCAGCTCAC AGCAGCTCAC CGAAGCTCAC CGAAGCTCAC CGAAGCTCAC CCACCCCCAT	60 120 180 240 360 420 540 660 720 840 960 1020 1080
50 55 60	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession and Ac	equence in #: BC0088 .2695 21	31	41	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTCC GCCCGGGGCA AGGGCCGCT TCCGCCACAA AGCTGCCGCT AGAAAATTGA AACTTCAA GCATCCTGAG AGCAGGAGGA AGCAGGAACA CGTGCTTTTGA CGAAGCTCAC AAGAGATCAC AAGAGAACTAC CGAAGCTCAC AAGAGCATCAC AAGAGCTCAC AAGAAGCTCAC AAGAAGCTCAC CAAGCACTGT	60 120 180 240 300 420 480 540 600 650 720 780 940 960 960
50 55 60	Seq 1D No: Nucleic Ac Coding Sec 1	167 DNA Se sid Accessic puence: 188. 11	equence in 8: BC0088 .2695 21    GGACTAGGAA G GAGGGCTCT C GTTTGCCCTT TTCCCCTTGGT TTCCCCTTGGT ACACCCAGGC ACACCCAGGC ACACCCAGGC ACACCCAGGC ACACCCAGGC ACACCCAGGC ACACCCAGGC TTCCCCAGGT TTCCCCAGGT TTCCCCAGGT TTCCCCAGGT TTCCCCAGGT TTCCCACCCTTC AGCCCGTCC AGCCCCTTC CCAACCCAGC TCCACCCCTTC CCACCCCTTC CCACCCCTTC TCCACCCCGTTC TCCACCCCTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCGTTC TCCACCCCTTC TCCACCCCTTC TCCACCCCTTC TCCACCCCTC TCCACCCCTTC TCCACCCCTTC TCCCACCCCTTC TCCACCCCTTC TCCACCCCTTC TCCACCCCTC TCCCCCCTTC TCCCCCCTTC TCCCCCCTC TCCCCCC	31	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCT TCCGCCACAA AGCTGCCCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG AGCAGAGGA ACTCCTGAG CCTCAGCACC AGAGGAAACA CGTGCTTTTCA CGAAGCTCAC AGCAGCTCAC AGCAGCTCAC CGAAGCTCAC CGAAGCTCAC CGAAGCTCAC CCACCCCCAT	60 120 180 240 300 360 420 540 660 720 780 960 960 1020 1080 1140
50 55 60 65	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CCCCAGGATT GAACTACCC CAACCAGCT GATCATCCAC GATCATCACC GATCATCACC GATCATCACC GATATACAC GGAGATACAA AGGCAGAAT AAGTAATT AAGCAGAAA CCATCAGA GCGCAGAAG GCGCAGAAG AGCACCT ACCTCTCT ACCTCTCT ACACCAAAG CCACCATT ACCACAAAG CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCATT ACCACAAAG CCACCATT ACCCACAC CCACCAC CCACCATT ACCCACAC CCACCAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCAC CCACCATT ACCCACAC CCACCATT ACCCACAC CCACCAC CCACCAC CCACCAC CCACCA	167 DNA Secid Accession puence: 188. 111	equence on 8: BC0088 .2695 21 j GGACTAGGAA G GAGGGCTCT CGTTTCGCCTT TCCCGCTGGA TTTATCACCGG A AGATCCTGTC C AAGATCCTGTC C AAGATCCT C AAGATCCTGTC C AGATTCACCAGC C AGATTCACCAGC C AGACCCTTCC C AGACCGTTCC C C AGACCCTTCC C C AGACCACTCC C T CCAACCACC C T C CAACCACC C T C CCAACCACC C T C CCAACCACC C T C CCAACCACC C T C CAACCACC C T C C C C C C C C C C C C C C C C C	31   COGCOTGG CAGACAGCTC CACCTGGATA GCCCAGGATC CACCTGGATA GCCCAGGATC CAGGCGCTC CAGGCGCTC CAGGCGCTC CAGGCGCTC CAGGCGCTC CAGGCGCACTC CAGGCGACTC CAGGCGACTC CAGGCGACTC CAGGCGACTC CAGGCGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGACTC CAGCCGGCGCC CATTCCCGG CATTCCCGG CAGCCGCGC CATTCCCGG CAGCCGCGCC CATTCCCGG CAGCCCCGACCC CAGCCCCGC CATTCCCGG CAGCCCCCG CATTCCCGG CAGCCCCCG CACCCCCCC CACCCCCCCCC CACCCCCCCC	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGCTGCGCT TCCGCCACAA AGCTGCGCT AGAAAATTGA AATTACTCAA AGCACGAGGAG CCTCAGCACC AGAGAAACA CGTGCTTTTGA CGATCCCAT CCATACCACC CCACTGCCAT CTATTCCACA CAGAGCACTGT CTATTCCACA CAGAGCACTGT	60 120 180 240 300 420 480 600 660 720 780 840 960 1020 1140 1200 1260
50 55 60 65	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession and Ac	equence in #: BC0088 .2695 21    GAGGGGCTCT GTTTCGCCTT GTTTCGCCTT GTTCGCCTGGA TTTCCCGGGCTCT TTCCCGGGCTCT TTCCCGGGCTCT CTCCGGGATCGT AACACCAGGGATCCC AACACCAGGGATCCC AACACCAGGATCCC TTCACACCAGGATCCC TTCACCAGCAGGATCCC TTCACCAGCAGGATCCC TTCACCAGCAGGATCCC TTCACCCAGCAGGATCCC AGCTCTCCGGAACCACCAGACACCAGACACCAGAACACCAGAACAAC	31	41	GTCCCTCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCT TCCGCCACAA AGCTGCCCATACGTCC AGAAAATTGA GCATCCTGAG ACCTCTGAG AGCAGAAGGA ACTTCTCAA CCTCAGCACC AGAGGAAACA CTGCTTTTCAA CGAAGCTCAC AGCAGCTCAC CAAGCACTCCCAT CTATTCCACA CAAGCACTGC CAAGCACCCC CCCCCAGCAC CCCCCAGCAC CCCCCCACCC CCCCCACCCC CCCCCACCCC CCCCCACCCC	60 120 180 240 300 360 420 540 660 720 840 960 1020 1080 1140 1200 1320
50 55 60 65	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CCCCAGGATT GAACTACCC CAACCAGCT GATCATCCAT GATTACCAC GATCATGGAG GTCCCACGGT GGTGCCAT AAGTAAATT AAGCAGAAA CCAATCAGA GGAGACCG GGCAATCA AGCAGAGA GAGACCCG GGCAATCA ACCACAGG GCCAATCA CCACCATGACCCC CCTACACAG CAGCATGAACCC CCTACACAG GCTCAATCC	167 DNA Secid Accession puence: 188. 111	equence on 8: BC0088 .2695 21 j GGACTAGGAA G GAGGGCTCT CGTTTCGCCTT TCCCGCTGGA TTTATCACCGA A AGATCCTGTC A AGATCCAGCAG G ATATTACTAC T TCAACCAG T TTAACTAC T GGTTTAGCA T TCAACCAG T TCAACCAG T AGATCTCG T CCAACCAG A TGGCTTCC T CCAACCAG A TGGCCTCTC C GTGTGCAGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGA A AGAGCGGGGA A AGAGCGGGGA	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCCGCGGGCA AGAAAATTGA GCATCCTGAG AGAACATTGA CCTCAGCACCA AGAGGAAACA CGTGCTTTTGA AGCAGCGCC AGAGGAACA CGAGCTCACC AGAGCACCG CCATCCCACC CTATCCCACCC CTATCCCACCC CATAATCTGTC CTCTTGGTGGAT CCTCTGGTGGAT CCTCTCACCCC CATAATCTGTC CCTCCAGCAC CCTCCCAGCCC CTTTGGTGGAT CATCCATGGAT CATCCATGGAT CCTCTCAGACC CCTCCAACCC CTTTGGTGGAT CATCCATGGAT CATCCATGCAT CATCCATCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATGCAT CATCCATCAT CATCCATCAT CATCCATCAT CATCCATC	60 120 180 240 300 360 420 540 660 720 780 840 900 1020 1140 11200 1232 1380 1440
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession process of the control of t	equence in 8: BC0088 .2695 .21	31	41	GTCCCTCCT GAGGGTCATC GAGGGTCATC GCCAAGCTCC GCCCGGGCCA AGGCCCCCT AGGACCTCC AGAAAATTGA AACTTCAA GCATCCTGAG AGCAGGAAGCA AGCAGGAACA AGCAGGAACCA AGAAGCTCC AGAAGCTCAC AGAAGCTCCC AGAACCTCGCAT CTATTCCACA CCACTGCCAT CTATTCCACA CAAGCACTGT CTATTCCACA CAAGCACTGT CTCCCAACCC ATAATCTTCCC ATAATCTCTCA	60 120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 11200 1260 13200 1380 1440 1560
50 55 60 65	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCCCCAGAGT GAACTAGCCC CAACCAGGT GGTCCACAGG GTCCACGGG TGGTGCCAT AGGTAACAA GGAGGCGGT AGGTAACAA CCAATCAGA GGAGACTCA CGAGGCCG GGCAATCA ACCCAAGG GCGCATCA ACCCAAGG CCGACAT AGCCACAGG CCGACAT AGCCACAGG CCTACCAGG CAGCCT CACACAAG CACCAAAG CACCAAAG CACCAAAG CACCAAAG CACCAAAG CACCAAAG CCTCACCAG CCTCACCAG CCTCACCACG CCTCACACAG CCTCACACG CCTCACACAG CCTCACACG CCTCACCG CCTCACCC CCTCACCG CCTCCCC CCTCCCCC CCTCCCC CCTCCC CCTCC CCTCC CCTCC CCTCC CCC CCCC CCTCC CCC CCCC CCC CCCC CCC C	167 DNA Se sid Accessic puence: 188. 11	equence in 8: BC0088 .2695 21    GAGCGGCTCT GGTTTGGCCTT TCCCCTGGA TTCCCCTGGA AGCCAAGGA AAGATCCTGTC AAGCCAAGGA ATTTACACGG AAGATCCTGCC CGCTGTCGGA AAGACCCGTCC CGTGTGCAGA AAGACCGGGA AAGACCGGGA AAGACCCGGAC AAGACCCGGAC AAGACCCGCGCC GGGGACAGCC	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCGT TCCGCCACAA AGGGCCGCT CCATACGTCC AGAAAATTGA GCATCCTGAG AGCTCGAGAACC AGAGGAAACCA AGGAGCTCAC CGAAGCTCAC CGAAGCTCAC CCAAGCACCC CAAGCACCC CAAGCACCC CTCCAACCC CATACCTGCAC CCATCCTCCAC CCATCCTCCAC CCATCCTCCAC CCATCCTCCAC CCATCCTCCAC CCATCCTCCAC CCATCCTCCAC CCTCCAACCC CATAATCTGTGT CCTTCGTGGT CCTTCCTACCAC CATCCTCCAA	60 120 180 240 360 420 480 660 660 720 780 840 1020 1140 1260 1320 1380 1500 1500
50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG GCTCTCTCCAC CCCCAGGATT GAACTACCC CAACCAGCT GATGTGGAATACAC GGCATACACG GGCATACACG GGCATACACA GGAGATACAA CCAATCAGG GGCAGATACA GGAGACCT AGGCAGATA AGGCAGAT AGGAGAAT ACACCAAAG GGCAATCA CCATCACCAG CAGCATC CAACCAAAG CAGCATCAC CAGCACATC CACCAGAG CAGCATT CCACCAGAG CAGCATT CCACCAGAG CAGCATT CCACCAGAG CAGCATT CCACCAGAG CCCTTCCCCCA CCCTCGCCCC CCACCAGC CCCTCGCCCC CCCTCGCCCC CCCTCGCCCC CCCCTCGCCCC CCCCTCGCCCC CCCCCCCC	167 DNA Secid Accession puence: 188. 111	equence on 8: BC0088 .2695 21    GAGGGGCTCT GGTTTGGCTT GGATTGGAT TATCAACGG AAGACCAAGGT AACACCAGG AACACCAAGG AACACCAAGG ATTATAACT GAACGAAGG AACACCAGG AACACCTTC AACACCAGG AACACCTCC AACACCAGG AACACCTCC AACACCAGG AACACCTCC AACACCAGG AACACCTCC AACACCAGG AACACCTCC AACACCCAGC AACACCTCC AACACCTCC AACACCTCC AACACCTCC AACACCTCC AACACCCAGC AACACCTCC AACACCCC AACACCTCC AACACCCC AACACCTCC AACACCT	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCGT TCCGCCACAA AGCTGCCCACAA AGCTGCCCACAA AGCTCCCAGGGGCA AGAAAATTGA GCATCCTGAG AGCAAGGAAACA CGTGCTTTTGA AGCAAGCTCCAAGCCCCACACACACCCCCCCCCC	60 120 180 240 360 420 540 650 720 780 960 1020 1080 1140 1200 1320 1380 1440 1560 1680
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Se id Accessic puence: 188. 11	equence in 8: BC0088 .2695 21    GGACTAGGAA GGAGGGCTCT CGTTTGCCCTT TTCCCCTTGGT TTCCCCTTGGT AACACCATGC AAGATCCTGTC AACACCATGC AACACCATGCC AACACCATGCC AACACCATGCC TTCACACCGGAA TTTATACTAC TTCACCCGGAA TTTATACTAC TTCACACCGT TCACACCATGCC AGGACCACCGTTCC CAGCCACCGTTCC CAGCCACCGTTCC CAGCCGACACCACCGTTCC CAGCCGACACCACCGTTCC CGTGTGCAGA AAGACCGGAA AGGACCGGAA GGGACAGCC GGGACAGCC AAGGACTGCC AACACCACGCAA GGGACAGCC AAGGACGCGAA AGGACCGGAA GGGACAGCC AAGGACGCGAA GGGACAGCC AAGGACGCGAA AGGACGGGAA GGGACAGCC AAGGACGCGAA GGGGACAGCC AAGGACGCGAA AGGACGGAA GGGGACAGCC AAGGACGCAA AGGACGGAA GGGGACAGCC AAGGACGCAA AGGACGGAA AGGACGGAA AGGACGGAA AGGACGGAA AGGACGGAA AGGACGGAA AGGACGCAA AGGACGGAA AGGACGCGAA AGGACGGAA AGGACGAA AGGACGGAA AGGACGAA AGGACGGAA AGGACGAA AGGACGGAA AGGACGAA AGGACGAA AGGACGAA AGGACGAA AGGACGAA AGGACAA AGGACGAA AGGACGAA AGGACGAA AGGACGAA AGGACAGAA AGGACGAA AGAA AGGACGAA AGGACAA AGGAC	31	41	GTCCCTCCCT GAGGGTCATC GCGAGGCTCA GCCGGGGCA AGGCCGCGT TCCGCCACAA AGCTGCCC AGAAAATTCA GCATCCTGAG AGCAGGAACA CCTCAGCACC AGAAGCTCC AGAAGCTCAC AGAGCACCC AGAGCACCC CCACTGCACC CCACTGCACC CTCGACCC CTTCGACCC CTTCGACCT CTCGACCT CTCGACCT CTCGACCT CTCGACCT CTCGACCT CTCGACCT CTCGACTAC CTCCAC CTCCAC CTCCACTAC CTCCACTAC CTCCACTAC CTCCACTAC	60 120 180 240 300 480 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1560 1620 1680
50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCCCCAGAGT GAACTACCC CAACCAGCT GATGTGGAG GTCCACCAGGG TGGTGCCAT AGGACGAGG CCAATCAGA CCAATCAGA CCAATCAGA CCAATCAGA CCAATCAGA CGAGCCCC ACACCAGG CCTGCAGAGG CCTGACACAG CTCTAGCAC CCTGCCCC CCTACACCA CCCTGGCCC CCTCACACG CCCTGGCCC CCCACACG CCCTGCCC CCCACACG CCCTGCCC CCCACACG CCCCCC CCCACACG CCCCCC CCCACACG CCCCCC CCCACACG CCCCCC CCCCCCC CCCACACG CCCCCC CCCCCC CCCCCC CCCCCC CCCCCC CCCC	167 DNA Secid Accession value of	equence in 8: BC0088 .2695 21    GAGGGGCTGT GGACTAGGAA G GAGGGCTGT TCCCCCTGGA TTCCCCTTGA A AGCCCAAGGT A AGATCCTGTC C AGGCAAGGT T TAACAGCAGG G T ATATGACT T TCAACCAGCAGG T TCAACCAGCAGG T TCAACCAGCAGG A GCACCGTTC C GGGGACACC C GTGTGCAGA A AGAGCCGAA A AGAGCCGAA A AGAGCCGGAA A AGAGCCGGA C GGGACAGCC G ATGACTTTG A GTGGGAGAC T CTATGGTGT T CTATGGTGT	31    CCGACAGCTCC CACCTGGATA GCCCAGGATG CACCTGGATA GCCCAGGATG CAGGCGCTCG CAGGCGCTCG CAGGCGCTCG CAGGCGCTCG CAGGTACA CAGGCGCAGTT CAGCTGGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA ACAGCTGGA CAGCTGCA CAGCTGCAGCTGC CACCTCAGGAA CAGCCTCAGAA CAGCAGCTGC CACCTCAGGAA CAGCTCAGGAA CAGCCATCAGCAA CAGCCATCAGCAA CAGCCACTCAGCAA CAGCCACTCAGCAA CAGCCACCACACA CACCCACTCAGCAA CACCCACCACACACA CACCCACCACACACACA	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCAGGGCA AGGGCCGCT TCCGCCACAA AGGGCCGCT CCATACGTCC AGAAAATTGA GCATCCTGAG AGCAGGAGGA AGTTACTCAA CCTCAGCACCA AGGAGCTCCA AGGAGCTCAC CCAAGCACTGC CCAAGCACTGC CTATCCCAC CCAAGCACTGC CTATTCCACA CCAAGCACTGC CTATTCCACA CCAAGCACTGC CTATTCCACA CCAAGCACTGC CTATTCCACA CCATGCCAT CCTCCAACCC CATAATCTGTC CTTGGGGT CATCCCTGCAACCC CTTCGAACTG CATCCCTGCAACCC CTTGGAACTGC CTTCGAACTGC CTTGCAACTGC CTTGCA	60 120 180 240 360 420 660 720 1020 1020 1140 1260 1320 1380 1500 1560 1680 1740
50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGG GCCCCCCAGGAT GAACTACCAC CCCCAGGAT AGTATACAC GCACCACG TGGTGCCAT AGGACAGC GGAATACAA AGGACGAA CCAATCAGG GGAATACAA AGGACGAA CCAATCAGG CCACCAGGAG GGCAGAG GCGCAGAG GCGCAGAC CCACCACAG CCACCAT AGCTGTCC CACCAGAG CTCTGCCCC CTCACACG GTCTGGCCC CTCAAATCC CCTCGGCTC CTCAAATCC CTCAGACAG TTTACCCAG	167 DNA Secid Accession value of	Equence in 8: BC0088 .2695 21	31	41	GTCCCTCCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCAGCGCACA AGGGCCGCGT CCCATACGTCC AGAAAATTGA AATTACTCAA GCATCCTGAG AGGCAAGGA AGCAGAGGA AGCAAGCTCC AGAACATTCAC CCACCCCACC	60 120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1860
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Se id Accessic puence: 188. 11	equence in 8: BC0088 .2695 21    GGACTAGGAA GGAGGGCTCT CGTTTGCCCTT ITTCCCCTTGGT TTCCCCTTGGT AACACCATGC AAGATCCTGTC AACACCATGC AACACCATGCC AACACCATGCC AACACCATGCC TTCACACCGGAA TTTATACTACG GATTTATACTAC TTCACACCGGAA TTTATACTAC TTCACACCGGAC AACACCATGCC AGCACCATCC AGCACCATCC AGCACCATCC CAACCCATCC CAACCCATCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGTCC CAACCCAGCC CAACACCAGCC CAACACCAGC CAACACCAGCC CAACACCAGC CAACACCAGC CAACACCAGC CAACACCAGC CAACACCAGCC CAACACCAGC CAACACCACCACC CAACACCACCACC CAACACCACC	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCGCGT TCCGCCACAA AGCTGCCC AGAAAATTGA GCATCCTGAG AGCAGGAGGA ACTTCACCCC AGAAACTGC AGAAGCTCC AGAAGCTCC AGAACCTCACCC AGAACCTCACCC AGACCCCCC AGACCCCCCCCCC	60 120 180 240 300 480 540 660 720 780 960 1020 1080 1140 1260 1320 1440 1560 1620 1680 1740 1800 1920
50 55 60 65 70	Seq ID No: Nucleic Ac Coding sec I GGCACGAGGG CTCTCTCCAC CGCCCCAGAGT GAACTACCC CAACCAGCT GATGTGGAG GTCCACCAGGG TGGTGCCAT AGGACGAGG CGATACAA AGGACGAGG CGAATACAA CCAATCAGA CCAATCAGA CCAATCAGA CCAATCAGA CCAATCAGA CCACCATCAGA CCGCCCCCCCCCC	167 DNA Secid Accessic puence: 188. 111	equence in 8: BC0088 .2695 21    GAGGGGCTGT GGACTAGGAA G GAGGGCTGT TCCCCTGGA TTCCCCTGGA TATCAACGG A AGATCCTGTC A AGATCCTGTC A AGATCCTGTC A AGATCCTGTC A AGATCCTGCC A AGATCCTGCC A AGATCCTGCC A AGATCCTGCC A AGATCCTGCC A AGATCCTGCC A AGACCAAGGAGGG T ATATTAACTA T TCAACCAGCAGG T TCAACGCAGG A TTTATACTA C GGGTTAGCA A AGACCGTTC C GAGGCCGTT C CAACCCAG G AGACCCTTC C GTGTGCAGA A AGAGCCGGAA A AGAGCCGGAA A AGAGCCGGAC C GTGTGCAGC A TAACTTTG A GTGCAGCAC C TTTATACTACTA T GGGAGAC T CTATGGTGT T TAACCATTA A TACCATTAC A CATCATTAC C CATGTTTG C C C C C C C C C C C C C C C C C C C	31	41	GTCCCTCCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCCGGGGCA AGGGCCGCT TCCGCCACAA AGGGCCGCT CCATACGTCC AGAAAATTGA GCATCCTGAG AGCAGGAGGA AGTTCCTAGC CCAAGCATCAC CGAAGCTCAC CGAAGCTCAC CCAAGCACCC CTATCCCCAT CCATTCCCAC CCAAGCACCC CATACCTGCAC CCATCCCAT CCATCCCAT CCATCCCAT CCTCCAACCC CATACTGCAC CCTCCAACCC CATACTCCCAC CCTCCAACCC CATACTCTCCAC CCTCCAACCC CATACTCTCCAC CCTCCAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACCC CTTCGAACTAC CTCCCAGGC CTTCGAACTAC CTCCCAGGC CTTCGAACTAC CTCCCAGGC CTTCGAACTAC CTTCGAACACT CTTCCCACACT CTTCCACACT CTTCCACA	60 120 180 240 360 420 540 660 720 1020 1020 1140 1200 1320 1380 1500 1680 1740 1860 1980
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding sec 1	167 DNA Secid Accession value of	Equence in 8: BC0088 .2695 21	31	41	GTCCCTCCCT GAGGGTCATC GCGAAGCTGC GCCCGGGGCA AGGGCGCGT TCCGCCACAA AGCTGCCC AGAAAATTGA GCATCCTGAG AGCAGGAGGA ACTTCACCCC AGAAACTGC AGAAGCTCC AGAAGCTCC AGAACCTCACCC AGAACCTCACCC AGACCCCCC AGACCCCCCCCCC	60 120 180 240 300 480 540 660 720 780 960 1020 1080 1140 1260 1320 1440 1560 1620 1680 1740 1800 1920
50 55 60 65 70	Seq 1D No: Nucleic Ac Coding Sec 1	167 DNA Se  id Accessic puence: 188.  11	equence in 8: BC0088 .2695 21    GGACTAGGAA GGAGGGCTCT CGTTTGCCCTT TTCCCCTTGGT TTCCCCTTGGT TTCCCCTTGGT ACACCCAGGA ACACCCAGGC ACAGCATCCC ACACCCAGGC ACAGCATCCC ACACCCTTCC ACACCCAGGC TTATACACCG TTATACACCG ATATCACCC CGGGCACCTTCC CGGCCCTTCC CGGCCCTTCC CGGCCCTTCC CGGCCCTTCC CGACCCCTTCC CGGCCGCCC TCCACCCCTCC CGCGCGCGCC TCCACCCCTCC CCACCCTTCC CGGCGGACACCC TCCACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CGACCCTTCC CACCCTTCC CACCCTTC CACCTTC CACCCTTC CACCCTTC CACCCTTC CACCCTTC CACCCTTC CACCCTTC CACCTTC CACCCTTC CACCTTC CACCTTC CACCTTC CACCTTC CACCTTC CACCTTC CAC	31	41	GTCCCTCCCT GAGGGTCATC GAGGGTCATC GCCAAGCTGC GCCAGCGCCACA AGGGCCGCGT CCCATACGTCC AGAAAATTGA GCATCCTGAG AGCAGAGGA ACTTCCTAGG AGCAGAGGA CCTCAGAGCA AGCAAGCTCC AGAACATTCAC CAACACCCACCC AGAACATTCACCCAT CTTCCTCAGCACC CATCCCATCC	60 120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1340 1500 1560 1680 1740 1860 1920 1980

		2220 2280
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25	CCCGTGTGGC GGTCGGAGCA AGCCATCGGA GCCATCGCGG CGAGCCAGGA GGACGGCGTG	420
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30	GGCCTCGGGG GGCTGCTGCT CACCGGCTGG ACCTTCGACC GGGGGGCCTG CGAGGTGCGG CCCCTGGGCA ACCTGAGCCG CAACTCCCTG CGCAACGCA CCGAGGTGGT GTCGTGCCAC	720
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60	CACATGAAAT TCTCTCTTCC ATCAAGCCGG AAAGAATGA AGGATGTGTG TATCCAGTTT GATGGTGGGA ACTGCTCTTC TGTGGGATCC TTATCCTACA TTGCTCTGCC ACATTGTTCC	2520
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	AATTTTGATG TAATTGACAA CTTAATCATT TCACATGAAT TAAAAGGAAA CATAAATGTC	2640
	TOTAL PART GTGTGGGGAC TTACTGCGGG TTTTTAGCCC CCAGTTTAAA GAGTTCAAAA	2700
65	GTGCGCACGA ATGTCACTGT GAAGCTGAGA GTACAAGACA CCTACTTGGA TTGTGGAACC	2760 2820
03	CTGCAGTATC GGGAGGACCC CAGATTCACG GGGTATCGGG TGGAATCCGA GGTGGACACA GAACTGGAAG TGAAAATTCA AAAAGAAAAT GACAACTTCA ATATTTCCAA AAAAGACATT	2880
	GAAATTACTC TCTTCCATGG GGAAAATGGG CAATTAAATT GCAGTTTTGA AAATATTACT	
	AGAAATCAAG ATCTTACCAC CATCCTTTGC AAAATTAAAG GCATCAAGAC TGCAAGCACC	3000
	ATTGCCAACT CTTCTAAGAA AGTTCGGGTC AAGCTGGGAA ACCTGGAGCT CTACGTCGAG	3060
70	CAGGAGTCAG TTCCTTCCAC ATGGTATTTT CTGATTGTGC TCCCTGTCTT GCTAGTGATT	3120
	GTCATTITIG CGGCCGTGGG GGTGACCAGG CACAAATCGA AGGAGCTGAG TCGCAAACAG AGTCAACAAC TAGAATTGCT GGAAAGCGAG CTCCGGAAAG AGATACGTGA CGGCTTTGCT	3240
	GAGCTGCAGA TGGATAAATT GGAAAGCGAG CTCCGGAAAG AGATACTGA CGGCTTGGC GAGCTGCAGA TGGATAAATT GGATGTGGTT GATAGTTTTG GAACTGTTCC CTTCCTTGAC	3300
	TACAAACATT TTGCTCTGAG AACTTTCTTC CCTGAGTCAG GTGGCTTCAC CCACATCTTC	3360
75	ACTGAAGATA TGCATAACAG AGACGCCAAC GACAAGAATG AAAGTCTCAC AGCTTTGGAT	3420
	GCCTAATCT GTAATAAAG CTTTCTTGTT ACTGTCATCC ACACCCTTGA AAAGCAGAAG	3480
	AACTITICTG TGAAGGACAG GTGTCTGTTT GCCTCCTTCC TAACCATTGC ACTGCAAACC	3540
	AGCTGGTCT ACCTGACCAG CATCCTAGAG GTGCTGACCA GGGACTTGAT GGAACAGTGT AGTAACATGC AGCCGAAACT CATGCTGAGA CGCACGGAGT CCGTCGTCGA AAAACTCCTC	3660
80	AGTAACATGC AGCCGAAACT CATGCTGAGA CGCACGGAGT CCGTCGTGA AAAACTCCTC ACAAACTGGA TGTCCGTCTG CCTTTCTGGA TTTCTCCGGG AGACTGTCGG AGAGCCCTTC	3720
-50	TATTTGCTGG TGACGACTCT GAACCAGAAA ATTAACAAGG GTCCCGTGGA TGTAATCACT	3780
	TGCAAAGCCC TGTACACACT TAATGAAGAC TGGCTGTTGT GGCAGGTTCC GGAATTCAGT	3840
	ACTGTGGCAT TARACGTCGT CTTTGARARA ATCCCGGRAR ACGAGRGTGC AGATGTCTGT	3900
	COGAATATTT CAGTCAATGT TCTCGACTGT GACACCATTG GCCAAGCCAA	3960

	TTOTALCELT '	TCTTAACCAA	TITISSTAAA	CCTTATGGAC	TCAGCTTAA	TGAAATTGGT	4020
				GAACTTCTGG			4080
	ATTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCATTGGCC	ACTATGAGAT	ATCAAATGGA	4140
_				AATTTTACTT			4200
5				GAAGCATTCC			4260
	CATCGAGGGA	AGCACAAGTT	CAAAGTAAAA	GAAATGTATC CTTTTTTAGAA	TGACAAAGCT	GCTGTCGACC	4320 4380
				TTTGACTTTT			4440
	AAAAAAATCA	CAGATOCTGA	CCTCCTACAT	ATTTGGAAAA	CAAACAGCCT	TCCTCTTCGC	4500
10				TITGTCTTTG			4560
				GCATTCATGG			4620
				AAGCTTCTCT			4680
	TACAAAGAAG	AAGTAAAATC	TTATTACAAA	GCAATCAGGG	ATTTGCCTCC	ATTGTCATCC	4740
1.5				TCTAAGAAAC			4800
15				ATCGTAAAAT			4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACTCTTGCA	TGTAAAAGTC	4920 4980
				ATGTAAGCAC AATGGCTGCT			5040
				GGCACTGTCT			5100
20		TTAGAAAGCA		0001010101			5121
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			n #: XM_063	570.1			
25	Coding sequ	ience: 170				51	
23	1	11	21	31	41	1	
	ATGCAGAGAA	TOCTTONGO	ACCACCTGAT	GATTGCACAT	GGTCAACTCG	GATTCTTCTT	60
				CGTACTGTTT			120
	CGTGCTCTCT	CAGTCCCTTC	ATCTTCCTAT	TTTCAGGAGC	TGGTGGGCAC	CAGCCAGGAA	180
30	CTGGCTCTCA	CCTTCTGGCA	TTTACTGTCT	ATGTTTGGAT	TCTTCATCGT	GTCCTATGGC	240
	TTTCTCACAG	CATTTGGCAG	GACTCTTTTC	CACTTGGATC	TGCTACAACC	CAACCTTACA	300
	CCTTCACGCT	TTGACAAGTA	CACTGGTCTC	TTCATCTATG	AAATAGAGGG	AGATGGGTTA	360
				ATCCTAGAGG			420
35				ACTGCTGGAG CGCAGTCGCT			480 540
55				AAAGGGCTGA			600
				CGCTGTGCCA			660
				CAGCACCTGG		•	708
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				H predicted			
	Coding seq	uence: 1-93					
	Coding seq	uence: 1-93 11	6 21	31	41	51	
45	1	11 	21 	1	1	1	60
45	1     ATGGAGCCAA	11     GCCACAGCCA	21     ACCCACAATG	   GACATGAAGC	   ACATGCAAGA	GCGTCCAGCT	60 120
45	1   ATGGAGCCAA GCCTCGCCTT	11     GCCACAGCCA   TAAAATGCCA	21     ACCCACAATG   GGACGGCCGC	GACATGAAGC GGCTCCGCTC	ACATGCAAGA AGAGCCCCCT	GCGTCCAGCT CTCGGCTGCT	60 120 180
45	I I ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT	11 	21     ACCCACAATG   GGACGGCCGC   GCTGGGGGCT	   GACATGAAGC	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC	120
	ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGGG GCGGTCGCCC	11 GCCACAGCCA TAAAATGCCA CGCCCGCGCC CCCCGCGAGC	21 	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGCC	120 180 240 300
<b>45</b> <b>50</b>	ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCCCCC TCGCCAGCCC	11	21 	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGGCC AGCTACTGGG	120 180 240 300 360
	1 I ATGGAGCCAA GCCTCGCCTT GGCCCCGCGCT GCCCCCCCGCG TCGCCAGCCC ACACCACCCC ACACCACCCC	11	21	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGGGATCC GGGACGGGCC AGCTACTGGG	120 180 240 300 360 420
	1 I ATGGAGCCAA GCCTGGCTT GGCCCGGGG GCGGTCGCCC TCGCCAGCC ACACCACCCT CACCCCGAGC	11   GCCACAGCCA TAAAATGCCA CGCCCGCGCGC CCCCGCGAGG TAGAAATAG TAGAAATAG TTGAAAGACTC	21   ACCCACAATG GGACGCCCG GCTGGGGCCCCG GCCGGCCCCAG CTCTGACCT CTACCATTGCC	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA GCAGGACCCC TTGTCCAAGG AGGTTCTACC ACTGGCTCTCA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGCGATCC GGGACGGCC AGCTACTGG TCTCACCACT TTTACTGTCT	120 180 240 300 360 420 480
	1 I ATGGAGCCAA GCCTCGCCTT GGCCCGGGCT GCCCCCGCG GCGGTCGCCC TCGCCAGCC ACACCACCCC ATGTTTGGAT	11   GCCACAGCCA TAAAATGCCA CGCCCGCGAGC CCCCGCGAGC TGGGCTCGGC TAGAAAATAA GTGAAAACTA TGGTGGGCAC	21	GACATGAAGC GGCTCCGCTC GGCTCCGCTG GTCACCGGGA CCAGGACCCC TTGTCCAAGG AGGTTCTACA CTGGCTCTCA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA	GCGTCCAGCT CTCGGCTGCT CTCGGCAGC CCCGGCGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC	120 180 240 300 360 420 480 540
50	1 I ATGGAGCCAA GCCTCGCCTT GGCCCGGGGCT GCCCCCCGGG GCGGTCGCCC TCGCCACCCCACC	11   GCCACAGCCA TAAAATGCCA CGCCCGCAGGC CCCCCGCAGGC TAGGAAAATAA GTGAAGACTC TGTGGGCAC TCTTCATCGT	21     ACCCACAATG   GGACGCCCCC   GCTGGGGCCCCC   GCCGCCCCAC   CTCTGACCTC   TACCATTGC   CACCACGAC   CTCTATGCC   CACCATGGC   CACCTTACC	GACATGAAGC GGCTCCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCAGGACCCC TTGTCCAAGG AGGTTCTACCA TTTCTCACAGG CCTTCACGCTCTACAGG CCTTCACGCT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAG CATTTGGCAG	GCGTCCAGCT CCTGGGCAGC CCGGGGATCC GGGACGGGCC AGCTACTGGG TTTACTGTCT GACTCTTTTC CACTGGCCAG	120 180 240 300 360 420 480 540
	ATGGAGCCAA GCCTCGCCTT GCCCCGCGGCT TCGCCAGCCC ACACCACCCC ACACCCCGAGC ATGTTTGATC CACCTCCGAGC	11   GCCACAGCCA TAAAATGCCA CGCCCGGAGC CCCCGGAGC TGGGCTCGGC TGGTGGCAC TGGTGGCAC TCTTCATCGT TGGTCAACCC	21	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC ATGTCCAAGG AGGTTCTACC CTTGTCCAAGG ACTTCTCACGCT GTACTGACGGT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA CATTTGGCAC TTGACAAGTA TCCACTGGAC	GCGTCCAGCT CTCGGCAGC CCGGGGATCC GGGACGGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTACTTTC GACTCTTTTC GACTCGCCAG CCACGGGACTG	120 180 240 300 360 420 480 540
50	1   ATGGAGCCAA GCCTGGCCTT GCCCGGGCT GCCCCCGGG CGGGTGGCCC TCGCCAGCCC ACACCACCT CACCCCGAGC ATGTTTGGAT CACTTGGAT CACTTGGAT TGCATTTGGT	11	21	GACATGAAGC GGCTCCGCTC CTGACTCCTG GTCACCGGGA CCAGGACCCC ATGTCCAAGG AGGTTCTACC CTTGTCCAAGG ACTTCTCACGCT GTACTGACGGT	ACATGCAAGA AGAGCCCCTT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCA CATTTGCAGT TTGACAAGTA TCCACTGGAC ATGGTACCAC	GCGTCCAGCT CTCGGCTGCT CCTGGGCAGC CCGGGGATCC AGCTACTGGG TCTCACCACT TTTTACTGTCT GACTCTTTC CACTGGCCAG CCAGGGACTG TCAAACCCGA	120 180 240 300 360 420 480 540 660
50	I I ATGGAGCCAA GCCTCGCCTT GCCCCCGGGC GCGGTCGCCC CACCCCGAGC ATGTTTGGAT CACTTGGATC CTCCTCGAGC GCGCGGGGGGGGGG	11	21   ACCCACAATG AGGACGCCCC GCGGCCCCC CCGCGCCCCAC CCTGACCTI CTACCATTGC CACCCAGGAA CTCTAACG CCACCTTACC CCACCTTACC CCACCTTACCACTACACACAC	GACATGAAGC GGCTCGCTC CTGACTCCTG GCTCACCGGGA GCAGGACCC TTGTCCAAGG ACGTTCTACC ACTGGCTCTCACGCT GTACTGACCA CTTGCCAAGG ACCTTCACGCT GTACTGACCA AGGGTGGAAA CGGGTGGAAA CGGGTGGAAA	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CTTTTGGCAG TTGACAAGTA TCCACTGGGA ATGGTACCAC ATGGTACCAC ATGGTACCAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	I I ATGGAGCCAA GCCTGGCCTGGGGGGGGGGGGGGGGGGG	11   GCCACAGCCA TAAAATGCCA CAGCCAGCCAGCCCCCCGGAGC CCCCCGGAGC CTGGCTCGGCAG TGGGTCGGCA TCTTCATCT TGCTACAACC CCCAGTTCT CGTACAACC GAGCAGCCCC ACGTAGACAA TGATCATCCAGTTCAGACC	21   ACCCACAATO ACCCACAATO ACCCACAATO ACCCACAATO COGGOCCCCC COGGOCCCAC TACCATTGC TACCATTGC CACCCACACA CTCTAAGCT CTCTAAAGTAT CTCTAAAGTAT CTCTAAAGTAT CTCTAAAGTAT CTCTGAAGC AAGGGCTGAC CACCTTCCCAC	GACATGAAGC GGTCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC TTTCTCACAG CTTCTCACGCT TTTCTCACAG ACGTTCACGCT CTGTACTCACGCT CTGTACTCACGCT TTGCCACGCTGCCT CTTCCCCTGCT TTGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CTTTTGGCAG TTGACAAGTA TCCACTGGGA ATGGTACCAC ATGGTACCAC ATGGTACCAC	GCCCGAGCCC GCGCGAGCCC GCGGGATCC GGGACGGCC AGCTACTGGG TTTTACTGTCT GACTCTTTTC CACTGGCAG CCAGGGACTCC GCCGAGCCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	I I ATGGAGCCAA GCCTGGCCTGGGGGGGGGGGGGGGGGGG	11   GCCACAGCCA TAAAATGCCA CAGCCAGCCAGCCCCCCGGAGC CCCCCGGAGC CTGGCTCGGCAG TGGGTCGGCA TCTTCATCT TGCTACAACC CCCAGTTCT CGTACAACC GAGCAGCCCC ACGTAGACAA TGATCATCCAGTTCAGACC	21   ACCCACAATG AGGACGCCCC GCGGCCCCC CCGCGCCCCAC CCTGACCTI CTACCATTGC CACCCAGGAA CTCTAACG CCACCTTACC CCACCTTACC CCACCTTACCACTACACACAC	GACATGAAGC GGTCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC TTTCTCACAG CTTCTCACGCT TTTCTCACAG ACGTTCACGCT CTGTACTCACGCT CTGTACTCACGCT TTGCCACGCTGCCT CTTCCCCTGCT TTGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CTTTTGGCAG TTGACAAGTA TCCACTGGGA ATGGTACCAC ATGGTACCAC ATGGTACCAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	ATGGAGCCAA GCCTGGCCTT GGCCCGGGG GCGGTGGCCC TCGCCACCCC ACACCACCCT CACCCGAGC ATGTTTGGAT CACTTGGATC CTCCTCGAGC GGCGGAGGAGGGGGCGCGAGGAGCCTTATGTCCTCCACCCCTTGTCGTCCCCCCCC	11	21   ACCCACAATG A GGACGCCCC G GCTGGGGGCT C CGGGGCCCCC C GCCGCCCCAG A CTCTGACCTC C TACCATTGCC C CAGCCTAGGA C CTCTATGC C CACCTTAGC A CTCTATGC C CACCTTGAG A CTCTAGAGG A CTCTGAAGG A CTCTGAAGG A CTCTGAAGG A GCACTTGCAA A GCACTTGCAA A GCACTTGCAA	GACATGAAGC GGTCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC TTTCTCACAG CTTCTCACGCT TTTCTCACAG ACGTTCACGCT CTGTACTCACGCT CTGTACTCACGCT TTGCCACGCTGCCT CTTCCCCTGCT TTGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT	ACATGCAAGA AGAGCCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CTTTTGGCAG TTGACAAGTA TCCACTGGGA ATGGTACCAC ATGGTACCAC ATGGTACCAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	I I ATGGAGCCAA GCCTCGCCTTGGCAGCCC ACACCACCCT ACACCACCCT ACACCACCCT ACACCACCT GCATTTGGAT CACTTGGAT CTCCTCGAGC GCATTTTGGT ACACTCGTGAACACCACCT GCATTTGGT ACACCACCCT ACACCACCCT GCATTTGGT ACACCACCT GCATTTGGT ACACCACCT GCATTGGT	11	21   ACCCACAATG  GAAGGGCGG  GCTGGGGGGCT  CCGCGCCCCC  GCGGGCCCAC  TACCATTGC  TACCATTGC  CAACCTTAC  CTCAAAGTAT  CTCAAAGTAT  CTCAAAGTAT  CTCAAAGTAT  CTCAAAGTAA  CTCAAAGTAA  CTCAAAGTAA  CTCAAAGTAA  CTCAAAGTAA  GCACTTGCCAA  AGGCTGACC  AGGCTGACC  AGGCTGACC  CGCGGAG  GCACCTGGAG  CCGCGCCAA  GCACCTGGAG  CCGCGCCAA  GCACCTGGAG  CCGCGCCAA  CCACCTGGAG  CCGCGCCAA  CCACCTGGAG  CCCCGGAG  CCCCCGGAG  CCCCCGGAG  CCCCCGGAG  CCCCCGGAG  CCCCCCGAC  CCCCCCCCCC	GACATGAAGC GGTCCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC CTTTCTCACAG ACTTCACGCTA CTTCACGCTA CGGGTGGAA CCGGAGATGC CTGGCCTGCT GGTCTCACGCTGCT GGTCTCACGCTGCT GGTCTCACGCTGCT GGTCTACACGCTGCCTGCT GGTCTACACGC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAC CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAC AGGAGCCCAC TGGTACCAC AGGAGCCCAC TCGTCTTCCAC ACCCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	I I ATGGAGCCAA GCCTCGCCTT GCCCCCGGGG GCGGTCGCCC TCGCCAGCCC ACACCACCCT CACCCCGAGC ATGTTTGGAT CTCCTCGAGC GCGCGAGGAGGAGGTCTATGCCTCTCTCTCTCTCTCTCTC	11	21	GACATGAAGC GGTCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC TTTCTCACAG CTTCTCACGCT TTTCTCACAG ACGTTCACGCT CTGTACTCACGCT CTGTACTCACGCT TTGCCACGCTGCCT CTTCCCCTGCT TTGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT GTCATCATGCCTGCT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAC CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAC AGGAGCCCAC TGGTACCAC AGGAGCCCAC TCGTCTTCCAC ACCCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	I I ATGGAGCCAA GCCTCGCCTT GCCCCCGGGG GCGGTCGCCC TCGCCAGCCC ACACCACCCT CACCCCGAGC ATGTTTGGAT CTCCTCGAGC GCGCGAGGAGGAGGTCTATGCCTCTCTCTCTCTCTCTCTC	11   GCCACAGCCA TAAAATGCCA CGCCCGGAGC CCCCGGAGC TGGGGTCGGG TGGGAAAATAA GTGAGAAATAA GTGAGACTCATCGT TCTTCATCGT TCTTCATCGT TCGTACAACC TCGCAGTTCA GGGAGGCCC ACGTAGACAC TGATCATCATCGT GGGAGGGGGGGGGG	21	GACATGAAGC GGTCCGCTC CTGACTCCTG CTGACTCCTG CTGACTCCTG CTGACTCCTG CTTGCCAAGG AGGTTCTACC CTTTCTCACAG ACTTCACGCTA CTTCACGCTA CGGGTGGAA CCGGAGATGC CTGGCCTGCT GGTCTCACGCTGCT GGTCTCACGCTGCT GGTCTCACGCTGCT GGTCTACACGCTGCCTGCT GGTCTACACGC	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCTTAG GGGAGGCAC CATCTGCTAT TGCCCCCACC CCTTCTGGCAC CATTTGGCAG TTGACAAGTA TCCACTGGAA ATGGTACCAC AGGAGCCCAC TGGTACCAC AGGAGCCCAC TCGTCTTCCAC ACCCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC CGGGCATCC CGGGCATCC CGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG TCAAACCCGA GCCCGAGCCC TGCCCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	I HATGGAGCCAA GCCTCGCCTTGGCCCCCGGGGGGGGCGCCCCCGGGGGAGGAGGAGGAGGA	11	21  ACCCACAATG AGGACGCCGG GGACGCCCCC GCGGCCCCAC CCTGACCTC CAGCCAGGAC CTCTGACCTC CAGCCAGGAC CTCTAGCCTC CAGCCAGGAC CTCTAGGCC CACCTTACA ACCCAGGAC ACCTGAGGC CAACCTTGAGCC AGGCCCAGC AGGCCCAGC AGGCCCAGC AGGCCCAGC CAGCCTTGCCAAC AGGCCTGCCAC AGGCCCGGAC CGCCCCACC CGCCCCACC CGCCCCCACC CGCCCCCCCC	GACATGAAGC GGGTCGGTC CTGACTCCTG GGGTCGGTC CTGACTCCTG GCAGGGCC CTGACTCCAGG ACGTTCTACC CTTTCTCACAG ACCTTCACGCT GTACTGACCA CGGGTGGAAA CGGGTGGAAA CGGGTGGAAA CGGGTGGACC CTGGCTGCC GGCTGCAGGTGC GGCTGCAGGTGC GGCTGCAGGTGC GGCTGACCAGGTGC GGCTGACCAGGTGC GGCTGACCAGGTGC GGCTGACCAGGTGC GGCTGACCAGGTGC GGCTGACCAGGTGC GGCTGA SH predictec	ACATGCAAGA AGAGCCCCTC CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCA TTGACAAGTA TCCACTGGGA ATGGTACAAGTA TCCACTGGAC ATGGTACAAGTA TCGTCTTCCT ACCCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TCTCACCACT TTTACTGTCT GACTCTTTC CACTGGCAG CCAGGGACTG TCAAACCCGA GCCGGAGCC CTGCCTCTTC GCCATCCCC	120 180 240 300 360 420 540 660 720 780 840 936
50 55 60	I I ATGGGCAAGC ATGGGCAAGC ATGGTTGGAT CACTTGGAT ACATCCACCT Seq ID No Nucleic AC Coding sec	11   GCCACAGCCA TAAAATGCCA TAAAATGCCA COCCCCGGAGC CCCCCCGGAGC TGGGCTCGGC TGGGCAGC TGTGGCAAC TCTTCATCGT TCTTCATCGT CTCCAGTTCC CGCACAGCCA TGGACAGCCC ACGTAGACAC TGGTAGAAC TGATCATCCC GAGCAGCCCC TGGGAGGAGCC 171 DNA SC CACAGCCC TGGAACACCCC TGAACACCCC TGAACACCC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCTC TTTTCATCT TTTTTCATCT TTTTTCATCT TTTTTCATCT TTTTTCATCT TTTTTTTT	21   ACCCACAATG AGACGCCCCC GCGGGCCCAG CCGGGCCCAG TACCATTACA TACCATTGCA CTCTAAGCTT CTGTCTATGC CAGCCTGAAGCTT CTGTGCTGAAGCT CTGTGCTAAGCT CTGTGCAAGCT AGGCTGACG CAACCTTGCAC CTGTGCCAAG AGGCTGACC CACCTTGCAAG CTGTGCCAAG CTGTGCAAG CTGTGCCAAG CTGTGCCAA	GACATGAAGC GGGTCGGTC CTGACTCCTG GTCACCGGGA GTCACCGGGA GTCACGGGA AGGTTCTACC TTGTCACAG TTGTCACAG TTGTCACAG TTGTCACAG TTGTCACAG TTGTCACAG TTGTCACCA TTGTCACCA TTGTCACCA TTGTCACCA GGGTGGAAA GGGTGGAAA GGGTGGAAA GGGTGGAAA GGACTGA TTGGCCTGCT GTCATCATGC TTGGCCTGCT GTCATCATGC TTGGCCTGCT GTCATCATGC TTGGCCTGCT TTGGCCTG	ACATOCAAGA AGAGCCCCTC CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCACC CCTTCTGGCAC TTGACAAGTA TCCACTGGAA ATGGTACAAGTA TCGTCTTCCT ACCCTTACAC	GCGTCCAGCT CTGGGCAGC CCGGGGAGC CGGGGAGC AGCTACTGGG TTTTACTGTCT CACTGGCCAG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGACTG CCAGGACTG CGCCATCCCC	120 180 240 300 360 420 480 540 660 720 720 780 840 900 936
50 55 60	I I ATGGGAAAGA AAATGGGAAGCA AAATGGGAAGCA GCCTGAGGAGA AAATGGGAAGACAACACCTGAGATGATGATGATGATGATGATGATGATGATGATGATG	11	21   ACCCACAATG A GCACGCCCC GCCGGCCCCC GCCGGCCCAC TACCATTGC TACCATTGC CACCTTACC CACCTA	GACATGAAGC GGGTCGGTC CTGACTCCTG CTGACTCCTG GTCACCGGGA GCAGGGACCCC TTGTCCAAGG A CGGTCTCAC CTGCTCTCA CTGCTCTCA CTGCTCTCA CTGCTCTCAC CTGCTCTCAC CTGCTCTCAC CTGCTCTCAC CTGCTCTCAC CTGCTCTCAC CTGCTCTCAC CTGCTCACAC CTGCACACATCC CTGCACACCC  31   A AAAGCAATCC CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTGCACACCCA CTCCACACCCA CTCCACACCA CTCCACACCCA CTCCACACCA CTCCACACCCA CTCCACACCAC CTCCACACCA CTCCACACCAC CTCCACACCAC CTCCACACCAC CTCCACACCAC CTCCACACCACCAC CTCCACACCACCACCA CTCCACACCACCACCAC CTCCACACCACCACCACCACCACCACCACCACCACCACCA	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGTAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CATTTGGCAC TTGACAAGTA TCCACTGGAC ATGGTACAAGTA TCCACTGGAC ATGGTACCAAGTA TCCACTGGAC ATGGTACCAAGTA TCCACTGGAC ATGGTACCAC TCGTCTTCCCI ACCCTTACAC	GGGTCCAGCT CTGGGCAGC CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGGG TTTACTGTCT GACTCTTTC CACTGGCAGC CCACGGACCC CCGCAGCCCC CTGCCAGCCCC TTACTGTCT CCACTGGCAGCCC CCGCAGCCCC TCACCCCCC  51 CCACTGGCAGCCC CCGCAACCCCC	120 180 240 300 360 420 480 540 660 660 720 720 780 840 900 936
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50 55 60 65	I I ATGGGCAAC AAATGGGCAAC AAATGGGAACCAACA AAATGGGAACCAACACACACACACACACACACACACACAC	11   GCCACAGCCA TAAAATGCCA TAAAATGCCA COCCCGGAGC CCCCGGAGC TGGGCTGGGC TGGGCTGGGC	21   ACCCACAATG A GAACGCCCC C GCCGGCCCCC C GCCGGCCCAC C TACCATTGC C CACCTTACC C C CACCTTACC C CACCTTACC C C CACCTTACC C C CACCTTACC C C C C C C C C C C C C C C C C C C	GACATGAAGC GGCTCGGTC CTGACTCCTG CTGACTCCTG GTCACCGGGA GCAGGGACCCC CTTGTCCAAGG ACGTTCTACC CTTCTCACAG CGTACTCACG TTGCCACGG TGTACTGACCA ACGTGACACCC TGGCTGCAA CGGGAGTGGAA GGGTGGAA GGGTGGAA GGGTGAAA GGACTGA SH predictec  31   AAAAGCAATGC TTCCAACAT TTTTCAAGAA TTTTCAAAAC TTTTCCAAAAC TTTTCCAAAAC TTTTCAAAAC TTTTTCAAAAC TTTTTTTT	ACATGCAAGA AGAGCCCCT CCGAGCCGGG AACGCCGAG GGGAGCGCAC CATCTGCTAT TGCCCCCACC CATTTGCAA TTGCAAGTA TCCACTGGAC ATGGTACAAGTA TCCACTGCAC TGGACAAGTA TCCACTGCAC TGGACAAGTA TCCACTGCAC TGGACAAGTA TCCACTACAC AGAGAACTAC AAGAAACTAC AAAAAACAAG AAAAAACAAG AAAAAACAAG AAAAAACAAG AAAAAACAAG	GCGTCCAGCT CTGGGCAGC CCTGGGCAGC CCGGGGATCC GGGACGGCC AGCTACTGG TTTTACTGTCT GACTCTTTTC CACAGGACCG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACCC CCGCAAACCCCAG CCAAAATTGAC CAAAACCCTAT AGAACCCTAT AGAACCCTAT AGAACCCTAT	120 180 240 300 360 420 480 540 660 720 720 720 730 840 900 936
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50 55 60 65 70	I I ATGGGCCAA GCCCCCGGGG GGGGTGCCCC TCGCGAGCCC ACACCACCCT ACACCACCT TGGATT CACTTGGAT CACTTGGAT GGCGGAGGAGAAACACCACCT ACACCACCCT ACACCACCC ACACCACCACCACCACCACCACCACCACC	11   GCCACAGCCA TAAAATGCCA TAAAATGCCA GCCCCCGGAGC CCCCCCGGAGC CCCCCCGGAGC TGGGCTCGGC TGGGCAGC TGGGCAGC TGTGGCAAC TGTTATCATCT CGTCACATCC GAGCAGCCCC TGGGAGAGCAC TTATTAAAC TTACAACT AACAACT TTACAAACT TTACAACT TTACAAACT TTACAACT TTA	21   ACCCACATO AGGACGCCCC GCGGGCCCAC CCGGGCCCAC CCGGGCCCAC CCGGCCCAC CCGGGCCAC CCGGCCCAC CCGGCCCAC CCGGCCCAC CCGGCCCAC CCGGCCCAC CCACACTTAC CCCAAAGTAT CCCAAAGTAT CCCAAAGTAT CCCAAAGTAT CCCAAAGTAT CCCAAAGTAT CCCAAAGTAT AACCCAAACA CACAAACAA AACCCAAACAA AACCCAAACAA AACCCAAACAA CACAACA	GACATGAAGC GGCTCGGTC CTGACTCCTG GGCTCGGTC CTGACTCCTG GCAGGACCC CTGACTCCAGG ACGTTCTACCC CTGACTCACGC ACGTGCACAC CTGACTCACGC TTGACCACAC ACGTGCACACACACACACACACACACACACACACACACAC	ACATGCAAGA AGAGCCCCCC CCGAGCCGGG AACGCCCAGG GGGAGCGCAG CATTGCTAT TGCCCCCACC CCTTTGGCAG TTGACAAGTA TCCACTGGAA TGCACTACAG ATGTACCAG AGAGCCCAAG AGAGCACAAGG AAAAAACAA AAAAACAA AAAAACAA AAAAGTCAG AAAAGCTATTG AAAAGCAATTA	GCGTCCAGCT CCGGGCATCC CCGGGCATCC GGGACGGCC GGGACGGCC GGGACGGCC GGGACGGCC GGGACTCTTTC GACTACTGGG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCAGGGACTG CCACAGGGCC CCACAGGGCC CCACAGAGGCC CCACAGGCC CCACAGGC CCACAGGCC CCACAGGCC CCACAGGCC CCACAGGCC CCACAGGCC CCACAGGCC CCACAGCC CCACAGGCC CCACAGC	120 180 240 300 360 420 480 660 720 840 900 936 60 120 180 240 300 420 480 660 660 720
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	TTTAGGGCCC	AGGAGAAAGA	ACTTCAAAGG	TATACACAGA	ATCTCAAAGA	TGCAAAGGAT	1200
	TTTGGCATAA	AAAGGACTAT	AGCTTCAAAA	GIGICICITG	GTGCTGTGTA	CTTCTTTATG	1260
5		ATGGACTTGC TCGGGACTGT					1320
•	ATTGGAGCAG	CAGTCCCTCA	CTTTGALACC	TTCCCAATAC	CCCCACCACC	TOCTTTCAT	1380 1440
	ATTTTCCAGG	TTATTGATAA	GAAACCCAGT	ATAGATAACT	TTTCCACAGC	TGGATATAAA	1500
	CCTGAATCCA	TAGAAGGAAC	TGTGGAATTT	AAAAATGTTT	CTTTCAATTA	TCCATCAAGA	1560
10	CCATCTATCA	AGATTCTGAA	AGGTCTGAAT	CTCAGAATTA	AGTCTGGAGA	GACAGTCGCC	1620
10		TCAATGGCAG					1680
		ATGGCTTTAT					1740
	AGTAACAATA	ACCATATTGG TCAAGTATGG	ACCACATGAT	CAAGAGCCTG	TTTTGTTCGG	GACCACCATC	1800
	AGGGAAGCAA	ATGCGTATGA	TTTTATCATG	GAGTTTYCTA	AATTTAAATA	TACATTGGTA	1860 1920
15	GGGGAAAAAG	GAGCTCAAAT	GAGTGGAGGG	CAGAAACAGA	GGATCGCAAT	TGCTCGTGCC	1980
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	CTATCAAGAT	TCTGAAAGGT	CTGAATCTCA	GAATTAAGTC	TGGAGAGACA	GTCGCCTTGG	300
20	TCGGTCTCAA	TGGCAGTGGG	AAGAGTACGG	TAGTCCAGCT	TCTGCAGAGG	TTATATGATC	360
30	CGGATGATGG	CTTTATCATG	GTGGATGAGA	ATGACATCAG	AGCTTTAAAT	GTGCGGCATT	420
	ATCGAGACCA	TATTGGAGTG	GTTAGTCAAG	AGCCTGTTTT	GTTCGGGACC	ACCATCAGTA	480
	ACAATATCAA	GTATGGACGA	GATGATGTGA	CTGATGAAGA	GATGGAGAGA	GCAGCAAGGG	540
	AAGCAAATGC	GTATGATTTT TCAAATGAGT	ATCATGGAGT	TTCCTAATAA	ATTTAATACA	TTGGTAGGGG	600
35	TTCGAAACCC	CAAGATTCTG	ATTETACATC	AACAGAGGAT	TOCCOCTOCAT	TCACAAACCA	660 720
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45	1   GAGAAGCCCT CCCCGGTCCC	11 CTTCCCTTTA CATCCCACCA	21   AAAAAAAAAA AAACCATTTG	AAAAAAGGCT ACAAGCAGGA	[ GCTTCTCGCA CAACGAAGAG	 GAGTGGAAAG GCAGAAGGAT	60 120
45	I GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC	21   AAAAAAAAA AAACCATTTG CCGGGGGACG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG	 GCTTCTCGCA CAACGAAGAG AGAAGTTTCG	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG	120 180
45	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA	21   AAAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC	CAACGAAGAG AGAAGTTTCG TGGTGACCCT	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG	120 180 240
	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCGTGGCA	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC	CAACGAAGAG CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC	120 180 240 300
45 50	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG	11 CTTCCCTTTA CATCCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCGTGGCA CTTGCTGGTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC	120 180 240 300 360
	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCCTACG GTGCTGAGCG	11 CTTCCCTTTA CATCCACCA GCGCGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG	21   AAAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCCGTGGCA CTTGCTGGTG GCGCCTGCTC	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC	GAGTGGAAAG GCAGAAGGAT GCCGGTGCTG GCTGACGCCG CGCCTGGAAC CCTGGGCTAC CCGCGCGAGT	120 180 240 300 360 420
	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACG GTGCTGAGCG TGCCGATCGG GCGCCCCTCA	11 CTTCCCTTTA CATCCCACCA GCGGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CGCTGCGCGG	21 AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG GCCCTGGTG GCGCCTGGTG CCTCCCTGGTG CGTGGCGCTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGGGCTCG ACCGGATGCT TGCACGCAAA CTCGGGGGCG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGC CCTTTTACGA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG CGCCTGGAAC CCTGGGCTAC CCGCGCGCTC GGCGCGCGCGCGCCCC	120 180 240 300 360
50	1 GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGCGGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG GCGCCCTCA ACCGGGAGCG	11	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCTTGC CCCCTGGTG GCGCCTGCTC CTCCCTGGTG GCAGCGCCTG	AAAAAAGGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT TGCACGCAAA CTCGGGGGG TGCCTCGGCC	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGCC TCAGCGCGGC TCAGCGCGGG CCTTTTACGA GCAACCGCAG	GAGTIGGAAAG GCAGAAGGAT GCCGTGCTG GCTGACGGC GCCTTGGAAC CCTGGGCTAC CCGCGCGAGT GCCGCGCTC GCCGCGCCC CTGCGCCCCC CTGCGCCCCC	120 180 240 300 360 420 480
	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCOOGGAGC CTGCCCTACG GTGCTGAGCG TGCCGATCGG GCGCCCCTCA ACCGGGAGCG GAGCTGCCGC	11   CATCCCATTA CATCCCACCA GGGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG CCTGGGTGGC CTGGGTGGC CTGGCTCGC TGGTGCCGTTG	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CTTCGCTGGTG CGCCTGGTC CGTGGCGCTG GCAGCGCCTG CAACCAGGCC	AAAAAAGGCT ACAAGCAGGA ACAGCTCATGG GGCTACGGCC TTCCAGTGCC CCGGCGCTCG ACCGGATGCT TGCACGCAAA CTCGGGGGCG TGCCTCGGCC AAGGCSTCGG	GCTTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT CGTGCAGCGC CGCTCTTCCT GCTCCAGCGC TCAGCGCGC CCTTTTACGA GCAACCGCAG ACGTGCAGGA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGCG GCCTGGAAC CCTGGGCTAC CCGCGGGAGT CGCCGCGGCTC GTGCGCGGCC CTGCGCCGCG	120 180 240 300 360 420 480 540 600
50	1   GAGAAGCCT CCCCGGTCCC CTCGGCCTGT GACCTGCACG GGCGGGGAGC CTGCCCTACA GTGCTGACGG GCGCCCCTCA ACCGGGAGCG GATCTGAAGG	11   CTTCCCTTTA CATCCACCA GCGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT CACGCACGTG GCTGGGGGG CCTGGGTGGC CGGCCTTGGC TGGTGCCGTGC CTGGTGGC CTGGTGCCTTGC CTCAGTCGC	21     AAAAAAAA   AAACCATTTG   CCGGGGGACG   CAGCGCCTTG   CGCCGTGGCG   CTCCCTGGTG   CTCCCTGGTG   CTCCCTGGTG   CAACCAGCCCTG   CAACCAGCCCTG   CAACCAGGCCTG   CAACCAGGCCTG   CATTGGGGGGTGTTGGGGGGGTGTTGGGGGGGTGTGGGGGG	AAAAAAGCT AAAAAAGCT AACAGCAGGA AGGCTACGGC TTCCAGTGCC CCGGGGTCG ACCGGATGCT TGCACGCAAA CTCGGGGGG TGCCTCGGC AAGGCGTCGG TGGATCTTGA	CATTCTCGCA GCATCAGAGA GAAGATTCG GGTGACCCT GGTGACCCC GGTCAGCGC GCTCTCCC TCAGCGC CCTTTTACGA GCAACCGCAG ACGTCGAGAG ACGTCGAGAG TAGCAGTTGT	GAGTIGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC CGCCTGGAAC CCTGGGCTAC CGCGCGAGT CGCCGCGCGCC CTGCGCGCGCC CTGCGCCGCC CTGCCCCGCAGT TATCATT	120 180 240 300 360 420 480 540 600 660 720
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCTGT GACCTGCACG GGCGGGAGC CTGCCCTACA GGCGCCCTCA ACCGGGACG GAGCTGCCGC GAGCTGCAGG GATCTGAAGG	11   CTTCCCTTTA CATCCCACCA GCGGACGCC GCGGACGCC GCACCAC GCATCTTCTC GCCGGCTCTT GCTGGCGG CCTGGGTGGC GGCCTTGGC TGGTGCCGG CTCAGTCCCAC TTGCACCACTT	21 AAAAAAAAA AAACATTIG CCGGGGGACG CAGCGCCTTG CGCCTGGCA CTCCCTGGTG CGCCCTGGTG CGCCCGGTGCC CAACCAGGCC CGTCTTGCCC CACCCGATTCC	I AAAAAAGCT AACAGCAGAAAAAAAAAGCAGAAAAAAAAAGCAGAAAAAA	CAACCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	I GAGTGGAAAG GCAGAAGGAT GCAGGAGGTGCTG GCCTGACGCGC GCCTTGGAAC CCGGGGCTAC CCGCGCGCTC GTGCGCGGCC CTGCGCGGCG CCTCCTGAAG TATCATCATT GCAGCTGAAA	120 180 240 300 360 420 480 540 600 720 780
50	1 GAGAAGCCCT CCCCGGTCCC CTCGGCCTGT GACCTGCACG GGCCGGAGC CTGCCCTACG GTGCTGAGCG TGCGGATCGG GGCCCCTCA ACCGGGAGCG GAGCTGCCGC GATCTGAAGG CTTCTGATTT TTCTGGAAAA	11   CTTCCCTTTA CATCCACCA GCGGACCCC TCAAGCACCA GCATCTTCTC GCTCGTCTT CACGCACGTG GCTGCGCG CCTGGGTGGC CGGCCTTCGC CTGGTCGCATTGGTCCATTGGTCCCAT TTACATCTGT TCTATTTGGA	21     AAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTCCCTGGTG CGCGCCTG CAACCAGGCC GGTGTTGGGC CACCGATGC CACCGATGC	AAAAAAGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATGCT TGCAGGCAAA CTCGGGGGG TGCCTCGGCC TGGATCTTGA CTATCTCCAG CAGATCTTTGA	CAACGAAGAG AGAAGTTTCG CAACGAAGAG AGAAGTTTCG TGGTGACCCT GCTCCAGCGC CCTCTTCCT GCTCCAGCGC CCTTTTACGA GCAACCGCAG ACGTGCAGGA TAGCAGTTGT TTAGTTTTCT TAAGTTAAAGAG	I GAGTGGAAAG GCAGAAGGAT GCCGGAGGGAGCTGACGGGAGCTAC CCCGCGAGGTTC GCCGCGGGGCTC GTGCGCCGCGCC	120 180 240 300 360 420 480 540 600 660 720 780 840
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC GTGCTGACG GGCCCCTCA ACCGGATCG GACCTGCAGC GATCTGAAGG CTTCTGAATT TTCTGGAAAA CCAACTGAAT	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCA GCACCACTC CACCACCATC CACCACCATC GCTGGTGGC GCTGGTGGC GGCCTTCGC TGGTCCCTG TCTACATCTGC TCATCCCCA TTACATCTGT TCTATTTTGGA	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CCGGGGGCAC CTTGCTGGTG CTCCCTGGTG CGTGGGGCTG CAACCAGGCC CACCAGGCCTG CACCCGATGC AACCAGGCCAACAACAACAACAACAACAACAACAACAACA	AAAAAAGCT ACAGCAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGCATGCT TGCACGCAGC TCCCGGGGGGG TGCTTCGGCC AAGGCTCGG CGATCTTGA CTATCTCCAG CAGATCCTTA TGTTTCTTTG	CAACGAGGG CTTCTCGCA CGAGGAGGG AGAAGTTTCG TGGTGACCCT TGGTGACCCT CTCCAGCGC CCTTTTCCT CTCAGCGC CCTTTTAGGA ACGGCGGG ACGGCAGGA ACGGCAGGA ACGGCAGGT TTAGCTATTCT AAACTAAGCA AGGGCTAAGCA	GAGTIGGAAAG GCAGAAGGAT GCCGTGCTG GCTGACGGC CGCCTGGAAC CCTGGGCTAC CGCGCGAGT CGCCGCGCGCT CTGCGCGCCC CTGCGCGCGC CTCCTGAAG TATCATCATT GCAGCTGAAA CACAGAGCAT	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	1   GAGAAGCCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGAGC CTGCCCTACG GTGCTGAGGG GGGCCCCTCA ACCGGGAGGG GATCTGAAGG CTTCTGATT TTCTGGAAAA GCAACTGAAT TATAACACTC AAGGGCCAGT AAGGGCCAGT AAGGGCCAGT AAGGCCAGT AAGGCCAGT AAGGCCAGT AA	11   CTTCCCTTTA CATCCACCA GCGGACCCC TCAAGCACCA GCATCTTCTC GCTGGTCTT CACGCACGTG CGCTGCGCG CGTGCGCGG TGGTCGCC TGGTCCCAT TTACATCTGC TTACATCTGA TTACATCTGA TCTATTTGGA CAGCATAGA CAAGCATAGA CAAGCATGAA CAAGCATGAA CATACAGCAT	21     AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTGCC CTCCCTGGTG CGCCTGCTC CTCCCTGGTG CGAGCGCCTG CAACCAGGCC GGTGTTTGGGC CACCCGATGC CACCGATGC CACCGATGC GAACAGCAGCAG GAATATTAAA AGAGTGGCAG GTTTGCACAAA	AAAAAAGCT ACAAGCAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGG TGCCTCGGCC TGCCTCGGCC TGCATCTTCA CTATCTCCAG CTATCTCCAG CAGATCTTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA	CALCAGAGA CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GAGTGGAAAG GCAGAAGGAT GCCGACGCG GCCTGGACGCG GCCTGGACCCC CCGCAGCT GCCCGCAGCT GCCCGCAGCC CTGCGCCGCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTCCCAAAGAA TTTCAATCCC GACTCAAAGAA TTTCAATCCC GACTCACAGT	120 180 240 300 360 420 480 540 600 660 720 780 840
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGATCG GGGCCTCA ACCGGATCG GACCTGCAGC CATCTGAAGC CTTCTGAAAA CCACCGAATTATAACACTC AAGGCCAGT ATCAGGTCTA ATCAGGTCTA ATCAGGTCTA AAGGCCAGT TATAACACTC AAGGCCAGT ATCAGGTCTA ATCAGGTCTA	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACCACGCACCACCA GCACCACGTG GCCTGGTGGC GGGCCTTCGC TGGTGCCGTG CTCAGTCCCATG TTACATCTGT TCTATTTTGGA ACTACACCATGA ACTACACCAT CTGAAGGAGA ACTACAGCAT TGGAAAAGA CTGAAGGAGAA	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CCGGGGGCAC CTTGCTGGTG CGCCTGCTC CTCCCTGGTG CGACCGCCTG CAACCAGGCC CACCCGATGC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAGCAC ACACGAC ACACGAGCAC ACACGAC ACACGAGCAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC ACACGAC A	I AAAAAAGCT ACAGGACAGAAAAAAAAAGCTTACGGGCTCG ACCGGATGCT TGCAGGAAACTCTGGGGCTCGGCTC	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCT CCGCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC TATCAT GCAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCGT TTCATCTGGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCTGT CTGGCACG GGCGGGGGG CTGCCCTACA GCGCCCCTCA ACCGGGACG GACTGCGG GACTGCGG GATCTGAAGG GATCTGAATT TTCTGGAAAA GCAACTGATT TATAACACT AACAGCAGTA ATAACAGCA	II  CTTCCCTTTA CATCCACCA GCGGACGCC GCGCACCCC GCATCATCTCC GCCTGGTCTT GCTGCGGGGCCTCGC CGGCCTTCGC CGGCCTTCGC TGGTGCCGG CTCAGTCCCA TTACATCTGT TCTATTTGA TGGCAAAAGA ACTACAGCAT CTGAAGGAGA CTTCAAGTACT	21 AAAAAAAAA AAACATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG CGCCTGGTC CGCCGGTGCC CACCGGTGCC CACCGGTGCC CACCGGTGCC CACCGGTGCC ACAGGAGCAG GAATATTAAA AGAGTGGCAG GTTGCACAAA TACGGGGCAAA TACGGTGATTA	AAAAAAGCT ACAAGCAGGA AGGCTCATGG GCTCATGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGCGC AAGGCGTCGG AAGGCGTCGG CTATCTCCAG CTATCTCCAG CAGATCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATGTAACA CCTGTTCTTG GAATGTAACA	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GCCGACGCG GCCTGGACGCG GCCTGGACCCC CCGCAGCT GCCCGCAGCT GCCCGCAGCC CTGCGCCGCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTCCCAAAGAA TTTCAATCCC GACTCAAAGAA TTTCAATCCC GACTCACAGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50	1 GAGAAGCCT CCCCGGTCCC CTGGGCTGT CTGGCACG GGCGGGGGG CTGCCCTACA GCGCCCCTCA ACCGGGACG GACTGCGG GACTGCGG GATCTGAAGG GATCTGAATT TTCTGGAAAA GCAACTGATT TATAACACT AACAGCAGTA ATAACAGCA	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACCACGCACCACCA GCACCACGTG GCCTGGTGGC GGGCCTTCGC TGGTGCCGTG CTCAGTCCCATG TTACATCTGT TCTATTTTGGA ACTACACCATGA ACTACACCAT CTGAAGGAGA ACTACAGCAT TGGAAAAGA CTGAAGGAGAA	21 AAAAAAAAA AAACATTTG CCGGGGGACG CAGCGCCTTG CGCGTGGCA CTTCCTGGTG CGCCTGGTC CGCCGGTGCC CACCGGTGCC CACCGGTGCC CACCGGTGCC CACCGGTGCC ACAGGAGCAG GAATATTAAA AGAGTGGCAG GTTGCACAAA TACGGGGCAAA TACGGTGATTA	AAAAAAGCT ACAAGCAGGA AGGCTCATGG GCTCATGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGCGC AAGGCGTCGG AAGGCGTCGG CTATCTCCAG CTATCTCCAG CAGATCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATGTAACA CCTGTTCTTG GAATGTAACA	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCTC CGCCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC CACAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCAGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT TTCATCTTGGT	120 180 240 300 420 480 540 600 720 780 840 900 1020 1080
50 55	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGC CTGCCCTACA GTGCTGACG GGCCCCTCA ACCGGAGCG GACCTGAGC GATCTGAAGG CTTCTGAATT TTCTGGAAAA CCACCTGAAT TATAACACTC AAGGCCAGT ATAACACTC AAGGCCAGT ATAACACTC ATAACACCA TATACCTTA	II  CTTCCCTTTA CATCCACCA GCGGCACCAC GCACCAC GCACCACT GCCTGGTCTT GCTGGCCGG CCTGGGTGGC CGGCCTTGGC TGGTCCCTG TTACATCTGT TCTACTCTGT TCTACTCTGT TCTACTTGT TCTACTCTGT TCTACTCTGT TCTACTCTGT TCTACACCAT TTACACCAT TTACACCAT TTACACCAT TTACACACAT TTACACCAC TCCTCGCCT TTACACACAC TCCTCCT TTACACACAC TCCTCCT TTACACACAC	21 AAAAAAAAA AAACCATTIG CCGGGGGACG CAGCGCCTTG GCCGTGGCA CTTGCTGGTG GCACGGCCTG CACCCGGTG CACCAGGCC CACCCGATTGC CACCGGATTGC CACCCGATTGC CACCTGATTGC CACCTGATTGCACAAA AGAGTGCACAAA AGAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA ACAGTGCACAAA	AAAAAAGCT ACAAGCAGGA AGGCTCATGG GCTCATGGCC CCGGGGTCG ACCGGATCCT TGCAGGCAAA CTCGGGGCGC AAGGCGTCGG AAGGCGTCGG CTATCTCCAG CTATCTCCAG CAGATCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATGTAACA CCTGTTCTTG GAATGTAACA	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCTC CGCCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC CACAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCAGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT TTCATCTTGGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CTCGGCCTGT CTCGCCACG GGCGGGAGC CTGCCCTACA GGCGCCCTCA ACCGGGACCG GACTGCACG GACTGCACG GACTGCACG ACCGGACCA ACCGGACCG AACTGAAG TATTACACTC AAGGCCAGT ATCAGGTTTA ATAACACTC AATTGCTTTA Seq ID NO:	11 CTTCCCTTTA CATCCCACCA GCGGACGCC TCAAGCACCA GCATCTTCTC GCCTGGTCTT GCTGCGCGG CCTGGGTGGC CGGCCTTGGC TGGTGCCGG CTCAGTCCCAT TACATCTGT TCTATTTGGA TGGCAAAAGA ACTACAGCAT CTGAAGGAGAA ACTACAGCAT TTAAAAAAATA  174 DNA Se	21   MARARARAA AAACCATTTG CCGGGGGACG CAGCGGCTTGCC CTCCCTGGTG CGCGTGCCC CTCCCTGGTG CAACCAGGCC CAACCAGGCC CACCCGATTGC ACAGGAGCAG GAATATTAAA AGAGTGGCAG GTTGCACAAA TACGGTGATT AACATTGGTA TAGACCTTTT AACATTGGTA TQUENCE	I AAAAAAGGCT ACAGGCAGGA AGGCTCATGG GGCTCAGGCC CCGGGGTCG ACCGGATCGT TGCAGGCAAA CTCGGGGGG TGGATCTTGA CTATCTCAG CAGATCCTTA TGTTTTTTT TGTTTTTTTTT TGTTTTTTTT GAATTCAACA CCTGTTCTTG GAATGAGTAG TATCTAGTTATTTTTTTT GAATTCAACA CCTGTTCTTG GAATGAGTAG TTTTTTTTTT	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCTC CGCCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC CACAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCAGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT TTCATCTTGGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCOGGGAGC CTGCCCTACG GTGCTGACG GTGCTGACG GGCCCCTCA ACCGGATCGG GACCTGCAGC GACCTGCAGC GACCTGCAGC TCCTGATTT TTCTGGAAAA GCAACTGAAT TATAACACTC ATAACAGCA TATAGCTTA SEQ ID NO: Nucleic AC	II  CTTCCCTTTA CATCCACCA GCGGCACCAC GCACCAC GCACCACT GCCTGGTCTT GCTGGCCGG CCTGGGTGGC CGGCCTTGGC TGGTCCCTG TTACATCTGT TCTACTCTGT TCTACTCTGT TCTACTTGT TCTACTCTGT TCTACTCTGT TCTACTCTGT TCTACACCAT TTACACCAT TTACACCAT TTACACCAT TTACACACAT TTACACCAC TCCTCGCCT TTACACACAC TCCTCCT TTACACACAC TCCTCCT TTACACACAC	AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG GCCGTGGCA CTTGCTGGTG GCGCCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATTGC CACCGATTGC CACCGATTGC AACAGGAGCAG GAATATTAAA AGAGTGGCAG GTTGCACAAAA TACGGTGATT ATGACCTTTT AACATTGGTA	I AAAAAAGCT ACAGGAGAGAAAAAAAAGCTTGGGGGGTG ACCGGATCT ACCAGGAGAAACTGGGGGGGGGG	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCTC CGCCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC CACAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCAGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT TTCATCTTGGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC CCCGGTCCC GACCGCAGG GGCGGGAGC CTGCCCTCA ACCGGGACG GGCCCCTCA ACCGGGACG GACTGCAGC GACTGAAGC GATCTGAAGC GATCTGAATT TTCTGGAATA TATAACACT AAGAGCCAGT ATAACACT ATAACACC TATTGCTTTA Seq ID NO: Nucleic Ac Coding sequ	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGCTCT TCAAGCACCA GCATCTTCTC GCCGGCTTTT CCACCACGTG GCTGGTCGC GCTGGTCGC CTGGTCGCGG CTCAGTCCCA TGATCCCAT TTACATCTGT TCTATTTGA TGGCAAAAGA ACTACAGCAT CTGAAGGAA CTCAGAGGAT TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11	AAAAAAAAA AAACCATTTG CCGGGGGACG CAGCGCCTTG GCCGTGGCA CTTGCTGGTG GCGCCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATTGC CACCGATTGC CACCGATTGC AACAGGAGCAG GAATATTAAA AGAGTGGCAG GTTGCACAAAA TACGGTGATT ATGACCTTTT AACATTGGTA	I AAAAAAGCT ACAGGAGAGAAAAAAAAGCTTGGGGGGTG ACCGGATCT ACCAGGAGAAACTGGGGGGGGGG	CAACGAAGG CGCTCTCCGCA CGAGGAGGGC CGCTCTTCCT GCTCCAGGGC CCTTTTAGGA GCAACGCAGG ACGTCAGGGC CTTTTAGGA TAGCAGTTGT TTAGTTTTCT AAAGTAAAGC CACTGTATAC GAAAAGAGAA CGCTGTATAC GAAAAGAGAA	GAGTGGAAAG GCAGAAGGAT GGCGGTGCTG GCTGACGGC GCCTGGACGC CCGCGCGCTC CGCCGCGCCC CTGCGCCGCC CTGCGCCGCC CTCTGAAG CATCACAT GCAGAGAC CACAGAGCAT TCCAAAAGAA TTTCAATCCG GACTCACAGT TTCATTCAGT TTCATTCAGT TTCATCTGGT TTCATCTGGT TTCATCTTGGT TTCATCTTGGT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGAGCG CTGCCCTACA GTGCTGAGCG TGCGGATCGG GGGCCCCTCA ACCGGGAGCG GACCTGCAGC GATCTGAAGA CTACTGAATT TTCTGGAAAA GCAACTGAAT ATAACACTC ATCAGGTCTA ATAACACTC TATTGCTTTA ATAACAGCA TATTGCTTTA Seq ID NO: Nucleic Ac Coding seq 1	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCA GCACTTCTCC GCCAGGTCTT CACGCACGTG CCTGGGTGGC GGCCTTCGC TGGTGCCGGG CTCAGTCCCA TTACATCTGT TCTATTTGGA AAGAAAGA CAAGCATGAA TTACAACGAT TTAAAAAATA 174 DNA Sei id Accessio uence: 152.	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CCGGGGGCCTG GCGCTTGCTG CTCCCTGGTG GCGCCTGCTG CCACCCGGTGCA ACACGACCC CACCCGATTGC CACCCGATTG CACCCGATTG CACCCGATTG CACCCGATTG CACCCGATTG ACAGTGCCA ACAGGACAG GAATATTAAA AGAGTGCCAG GTTTGCACAAA TACGGTGGTT AACATTGGTA TGCGTATTTAACCTTTT AACATTGGTA  1 #: NM_032 .2422 21	AAAAAAGGCT ACAAGGAGGA AGGCTCATGG GGCTACGGCC CCGGCGCTCG ACCGGATCCT TGCAGGCAAA CTCGGGGGCG TGCCTCGGCC TGCATCTTTGA CTATCTCCAG CAGATCCTTA TGTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG GAATGAGTAG TTTTT  211.5	CAACGAAGA AGAAGTTTCC CAACGAAGAAGAGAGAGTTTCC TGGTGCACGCC CGCTCTTCCT GCTCCAGGGC CCTTTTACGA GCAACCGCAG CACTGTCAGGAC CTTTTACGA ACGTCAGGA TAGCAGTTGT TTAGTTTTCT AAACTAAAGC ACACTGTATAC CAAAAGAAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GCCGGACGCG GCCTGGACGCC CCGCGCAGT GCCGCCGCC CTGCGCCCCC CTGCGCCCCC CTGCGCCCCC CTGCGCCCCC CTCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140
50 55 60 65	1   GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CTGGCGCGGGGGGGG	11 CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCATCTTCTC GCCGGTCGT GCTGGCGGG CCTGGGTGGC GGCCTTGGC TGGTCCCTG TGTTCCCTG TGTACATCTGT TCTAATTTGGA ACTACAGCAT TTAAAAAATA 174 DNA Seidi ACCESSIO uence: 152. 11	21   MARARARAA AACCATTTG CCGGGGACG CAGCGCCTTG CGCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG CGTGGCGCTGCTC CACCCGATGC CACCCGATGCC CACCCGATGC ACACGGACCA ACAGGACCAG ATACTACAA AGAGTGGCACAA AGAGTGGCACAAA AGAGTGGCACAA ATACATTGGACAAA  QUENCE 1 #! NM_032 .2422 21   GAGGCGGATA	AAAAAAGGCCCCC	CONTINUES OF THE PROPERTY OF T	GAGTGGAAAG GCAGAAGGAT GCOGGTGCTG GCTGACGCC CCTGGGCTAC CCGCGCGCTC GTGCGCGCC CTGCGCGCC CTCCTGAAG TATCATCATT GCAGCTGAAA CACAGAGCAT TCCAAAAGAA TTCAATATCCG GACTCACAGT TTCATCTGGT GGGAGGGAGC	120 180 240 300 360 420 480 540 660 720 780 900 900 1020 1080 1140 1175
50 55 60 65	1 GAGAAGCCT CCCCGGTCCC CTCGCCTGT CCCCGGTCCC CTCGCCCTCA GGCGGGGGG GGCCCCTCA ACCGGGACG GGCGCCCTCA ACCGGGACG GATCTGAAGG GATCTGAAGA CAACTGAAT TATAACACT AATGAACAGCA TATTGCTTTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTCGGGGG GGCTCGGGGG CCGTTAGCGC CCGTTAGCGCC CCGTTAGCGCC CCGTTAGCGCC CCGTTAGCGCC	11   CTTCCCTTTA CATCCACCA GCGGACGCC TCAAGCACCA GCATCTTCTC GCCGGTCTTT CACCACGTG GCTGGCCGG CCTGGTGGC CGGCCTTGGC TGGTGCCGG CTCAGTCCCA TACATCTGT TCTATTTGGA TGGCAAAAGA ACTACAGCAT TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11   CCCGCGGGCCGG TGCTCCCCCG	21   MARARARAA AAACCATTTG CCGGGGGACG CAGCGGCTTG CGCGTGGCA CTTGCTGGTG CGCCTGGTC CTCCCTGGTG CGCGTGCCC CACCCGATGC AACCAGGCC GGTGTTGGGC CACCCGATGC ACAGGAGCAG GATTATTARA AGAGTGGCAG TTGCACAAA TACGGTGATT AACATTGGTA  Quence n #: NM_032 .2422 21   GAGGCGGATAC GAGGCGCCCCC	AAAAAAGGCCCCGGGAAAAAAAAAGGCCCGGAAAAAAAA	CATCTCTCGCA CAACGAAGAG AGAAGTTTCG TGGTGACCCT GCTCCAGCGC GCTCTACCT GCTCCAGCGC CCTTTTACGA GCAACCCAGCA TAGCAGCAGCA TAGCAGTTTTT TAGTTTTTC TAAGTAAAGC AACTGTATAAA CAACTGTATAAAA AAAAAAAAAA	GAGTGGAAAG GCAGAAGGAT GCCGACGCC GCCTGGACC CCTGGGCTAC CCGCCGCGAGT GCCGCCGCGC CTGCGCCGCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCACAAA CACAAAAGAA TTCAATAT CCAAAAAGAA TTCAATCCG GACTCACAGT TTCATCTGGT TCATCTGGT TCATCTCGT TCATCTCGG	120 180 240 300 360 420 480 540 660 720 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGCG GGGCCCTCA ACCGGAAGGG GAGCTGCAGC TCTGGATAT TTTTGGAAAA GCAACTGAAT TATAACACTC AACAGGCAGT AACAGGCAT AATAACAGCA TATTGCTTA ATAACAGCA CTGCTGATT TTCTGTAAA GCACTGAAT ATAACAGTC ACCGCTGAGGGGGGGGGG	11 CTTCCCTTTA CATCCCACCA GCACCACCA GCACCACCA GCACACTC CACCACAGG CATCTTCTC CACCACAGG CGCTGGTGGC GGGCCTTGGC TGGGCGGG CTCAGTGCCGG CTCAGTCCCA TTACATCTGT TCTATTTGGA AAGAAAGA CTCCTGAGGGAG TTAAAAAATA 174 DNA Se 101 ACCESSIO uence: 152. 11   CCGCGGGCGG TGGTCCCCCCC TCGCTCCCCCC TCGCTCCCCCC TCAGTCTTCCCCCC TCAGTCTTCCACTGT TCAGTTTTAAAAATA TTAAAAATA TTAACACTT TTAACACT	21   AAAAAAAAA AAACCATTTG CCGGGGGACG CCGGGGGCCTTG GCCGTGGCG CTTGCTGGTG GCGCCTGGTG GCAGCGCCTG CAACCAGGCC CACCCGATGC ACAGGGCTG GCAGCGCTG CAACCAGGCC ACAGGACAG GTTGCACAAA AGAGTGGCAG GTTGCACAAA AGAGTGGCAG TACCGTTTT AACATTGGTA TUBENCE n #: NM_032 .2422 21   GAGGCGGATA GGAGCGGATA CGGCGCCCCC TTGAAGTCAC	AAAAAAGCCCCCCACACGACCACACCCCCGCACCACCACC	CAACGAGGGCCCCCACACACACACACACACACACACACA	GAGTGGAAAG GCAGAAGGAT GCCGGAGTGCTG GCTGACGGCG GCCTGGACGCC CCGCGGAGT GCCGCGCGCC CTGCGCCGCC CTGCGCCGCC CTGCGCCGCC CTGCGCCGCC CTGCGCCGCC CTGCAAAAGAA TATCAATAT GCAGCTGAAA TATCAATACCG GACTCACAGT TTCAATCCG TGTTTTGAAT  51   GGGAGGGAGC CTCCATCTGG CCACCCTCTT	120 180 240 300 360 420 480 540 660 720 780 840 960 1080 1140 1175
50 55 60 65	1   GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11   CATTCCCTTTA CATCCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCACCACGG GCACCACGG GCACCACGG GCACCACGG GCACCACGG GCGCCTTCGC GGGCCTTCGC TGGTCCCTGG TCTACATCTGT TCTAATTTCGA ACTACACCAT TTAAAAAATA ACTACAGCAT TTAAAAAATA  174 DNA Sei did Accessio uence: 152. 11   CCGCCGGCCGG TCCGCGCGCCG TCCGCTGCTCC TCACTCTCACC TCACTCTCCCC TCACTCTCACC TCACTCCTCACC TCACTCTCACC TCACCTCTCACC TCACCTCTCAC TCACTCTCAC TCACCTCTCAC TCACCTCAC TCACCTCTCAC TCAC	21   MARARARAA AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG GCAGCGCTTG CAACCAGGCCTG AACCAGGCCTG AACCAGGCCA CACCGATGC AACAGGACAA AGAGTGGCAAA AGAGTGGCAAA AGAGTGGCAAAA ATAGACTGTA AACATTGGTA  Quence   #: NM_032 .2422 21   GAGGCGGATA GAGGGCGGATA GGGGGGGATA CGGGGCGCCCCC TTGGAGTCCCCCCC TTGGAGTCCACAAA CGGGCCCCCC TTGGAGTATA CGGCCCCCCC TTGGAGTCAC TTGGAGTCACA CGCCAGCCCCCC CCGGGGATA CGGCCCCCCC TTGGAGTCAC TTGGAGTCAC CCCAGCCCCCC CGCGCCCCCC CGCGCCCCCCC CGCGCCCCCC	AAAAAAGGCTAAGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	COLCACCACAGE  AGAGGAGGA  AGAAGTTTCG  TGGTGACCCT  TGGTGACCCT  CGTCCAGCGC  CCTCTCCT  GCTCCAGCGC  CCTTTTACGA  ACGTGCAGGA  ACGTGCAGGA  ACGTGCAGGA  ACGTGCAGGA  ACGTGCAGGA  ACGTGCAGGA  ACGTTTTTCT  AAAGTAAAGC  AGGGCTCGCA  ACTTTTATAC  GAAAAGAGAA  AAAAAAAAAT  41     AGGGCGCCCC  ACTGTCCCCC  ACTGTCCCCC  ACCCCACCAG  CCCCCACCAG  CCCCCACCAG  CCCCACCAGC  CCCCCACCAG  CCACAGTCAC  CAAGGTCACC  CAAAGGCACAC  ACCCCACCAGC  ACCCCACCAGC  CCCCCACCAG  CCCCACCAGC  CCCCACCAGC  CCCCCACCAG  CCCCACCAGC  CCCCACCAGC  CCCCACCAGC  CCCCACCACCAG  CCCACAGTCAC  CAAGGTCAC  CACAGTCAC	GAGTGGAAAG GCAGAAGGAT GCOGGTGCTG GCTGACGCCC CCTGGGCTAC CCCGCGCGCTC GTGCGCGCC CTCCTGAAG CACCACCACT TCAAAAGAA TTCAATAT TCAACAGT TTCATCATGT TTCATCATGT TTCATCATGT TTCATCATGT TTCATCATGT TTCATCATGT TTCATCATGT TTCATCATGT TCATCATGT TCATCATCT TCATCATGT TCATCATCT TTCATCATCT TTCATCATCATC TTCATCATCATCATC TTCATCATCATCATC TTCATCATCATCATC TTCATCATCATCATC TTCATCATCATCATC TTCATCATCATCATCATC TTCATCATCATCATCATC TTCATCATCATCATCATCATC TTCATCATCATCATCATCATCATCATCATCATCATCATCA	120 180 240 300 360 420 480 540 660 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTCGGGCCTGT GACCTGCACG GGCGGGAGG GGCGCCCTCA ACCGGATCGG GAGCTGCCGG GAGCTGCCGG GACTTGAGG TTCTGAATA TATAACACTC AACAGCCAT ATAACAGTCA ATAACAGCCA TATTGCTTA Seq ID NO: Nucleic Ac Coding seq 1 GGCTGGGGGG GGCTTAGGGC TATCTTGCCT TATGTTCTTG TATTTTTGCGCC TATGTTCCTT	11 CATCCCTTTA CATCCCACCA GCACCTCCACCA GCACACTCCCC GCACACTCCCCCCCCCC	21  AAAAAAAAA  AAACCATTTG CCGGGGGGCG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCGCTGCCC CTCCCTGGTG CAACCAGCCC CAACCAGCCC AACCAGCCC AACCAGCCC AACAGCAGCAG CACCAGATTAAA AGAGTGGCAG GAATATTAAA AGAGTGGCAG TTGCACAAA TACGGTGATT ATGACCTTTT AACATTGTA  QUENCE  1  GAGGCGGATA CGGCGCCCCC TTGAAGTCAC CACACCCCCC CACACCCCCCC CACACAGCCCCC CAGAGAGCAA	AAAAAAGGCTCAGCCCGGCAGGAGGA	CACCACAGE  41  AGGGGGCCCCCACAGGCCCCACAGGCCCCACAGGCCCCCACAGGCCCCCGCCCCCC	GAGTGGAAAG GCAGAAGGAT GCCGACGCC GCCTGGACGCC CCTGGGCTAC CCGCCGCGCTC GTGCGCCGCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCACGCC CTCCCCAAAAGAA TTCAATAT CCAAAAAGAA TTCAATCCC GACTCAAACCC TTCCTCGCCCC CTCCCCCCC CTCCCCCCCC CTCCCCCCCC	120 180 240 300 360 420 480 540 960 1020 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CTGGGCCGGGGGGGG	11   CATTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCATCTTCTC GCCGGTCTT GCTGGGGGG CCTGGGTGGC GGCCTTGGC GGCCTTGGC TGGTCCTGG TGGTCCGCG TCAGTCCTGA TTACATCTGT TCTAATTTGGA ACTACAGCAT TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11   CCGCGGGCGG TCGCGGGCGG TCGGCTTGGC TCGGCGTGGC TCGGCGTGGC TCGGCGGCGG TCGGCGGCGGCGG TCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21   MARARARAA AACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATGC ACACGATGC ACACGAGCA AGAGTGGCAA AGAGTGGCAA  QUENCE   MACATTGGTA  QUENCE   GAGGGCGGATA GGAGGCGGATA CGGGGCCCCC CAGAGGCCCCC CAGAGGCCAA TGTGTAATGAA TGTGATGATCAA CGCCCCCC CAGAGAGCAA TGTGTGATGAA TGTGCCTTT	AAAAAAGCCTA ACAGCACGG ACAGCCCCGG AAAAAAAGCCTA ACAGCACGAAA ACGCTCATGG ACCGCATCGT TCCAGTGCC ACCGCATCGT TCCAGCCAAA CTCGGGGCTGG ACGCGTCGG ACGCCTGGATCTTA TCTTTCTTTG CAAATTTCAT TATGTCAACA CCTGTTCTTG AAAAAGCCCCC CCAGCCCCGG CAGCCCCGG CAGCCCCGG CCAGCCCGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCCGGG CCAGCGGGGGGGG	COCCACAGAGC CACAGGAGCA CACAGGAGCA CATCCACAC CATCCACAC CACACAC	GAGTGGAAAG GCAGAAGGAT GCAGACGCC CCTGGACCCC CCTGGACCCC CCTGGACCCC CTGCGCCTC CTGCGCCTC CTGCCCGCC CTCCTGAAC CCTCCTGAAC CACAGAGCAT TCCAAAAGAA TTCAATATCCG GACTCACAGT TTCATCTGT TGTTTTGAAT  51    GGGAGGGAGC CCTCCATCTGC CCACCCTCTT TGGGCACCACACTCCA AGGTGCTGCA ACGTGCTCA ACGACCCCCACACCCCCACACGCCCACACGCCCCCATCACACCCCCACCCCCACCCCACCCCCACCCCCACCCCCACCCC	120 180 240 300 360 420 480 540 660 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTCGGGCCTG GACCTGCACG GGCOGGAGC CTGCCGATCGG GGCCCTCA ACCGGATCGG GACCTGCAGG GACCTGCAGG GACCTGCAGG GACCTGCAGG CTTCTGATTT TTCTGGAAAA GCAACTGAAT ATAACACTC AACAGGCCAGT ATCAGGTCTA Seq ID NO: Nucleic Ac Coding seq 1   GGCTCGGGGGG GGCTTGGGGG TATCTTGCCT TATGTTTCTTGCC TATGTTTCTTG TAAGGTCCTGC TATGTTCCTTG TAAGGTCCTGC TAGGCCAGT TAGGCCAGT TAGGCCAGT TAGGCCCAGT TAGGCCCAGGCCAGG	11   CATTCCCTTTA CATCCCACCA GCATCTCTCC TCAAGCACCA GCATCTTCTC GCTGGTGTT CACGCACGTG GCTGGTGTCT CACGCACGTG CGGGGGGCGCGGCGC	21  AAAAAAAAA  AAACCATTTG CCGGGGGCGC CAGGGCCTTG GCGCTGGCA CTTGCTGGTG GCGCTGCCA CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCCGATTG AACATTAAA AGAGTGATT ATGACCTTTT AACATTGTA  QUENCE n #: NM_032 .2422 21 GAGGGCGGATA GAGGCGGATA CGCCACCCC CCCAGCCCCC CAGAGAGCAA TGTGAAGCATTAAA AGAGTGCATA AACATTGTAA AACATTTT AACATTT AACATTTT AACATTT AACATT	AAAAAAGGCTAGGGAGAGAGAGAGAGAGAGAGAGAGAGAG	GCTTCTCGCA GCTTCTCGCA CAAGGAGGG GAAAGTTTCG TGGTGACCCT GCTCCAGCGG GCTCTTCCT GCTCCAGCGG GCTACCGCGG CCTATCGG GCAACCGCAG AAGTATCT TTAGTTTTCT TAGTATTTCT TAGATAAGC AACTGTATAC CAACAGCAG CAACCGCAG GAAAAGAAAA	GAGTGGAAAG GCAGAAGGAT GCCGGCGCGC CCCGCGCGAGT GCCGCGCGCC CTGCGCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCC	120 180 240 300 360 420 480 540 660 780 900 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CCCGGTCCC CCCGGTCCC CTGGGCCTGT GACCTGCACG GGCGGGAGGC GGCGGATCGG GGCGCCTCA ACCGGGAGGG GGCCCCTCA ACCGGAGCG GACCTGAAGC CATCTGAATT TTCTGAAAAA CCACTGAAT ATAACACTC AAGGCCAGT ATCAGTCTA ATAACACCC TATCGCTTA CCGTTAGCGC CCGTTAGCGC CCGTTAGCGCC TTTGGCCCAGACGCAACGCA	11 CTTCCCTTTA CATCCACCA GCACCACCA GCACCACCA GCACACTC GCACACACTG GCACGACGAC GCACACTTCCC GCTGGTGGCGGG CGGCCTTCGC TGGTGCCTG TGGTGCCTG TCTAATTTGGA ACTACTCTT TCTAATCTGT TCTAATCTGA TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11   CCGCCGGCCGG TCAGCTGGCCTGG TCTGGTGTGCCTGGCTGGCCTGGC	21  AAAAAAAAA  AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGGCA CTTGCTGGTG GCAGCGCCTG GCAGCGCCTG CAACCAGGCC CACCCGATGC ACACGGACCA GATTTAAA AGAGTGCAG TACGGAGCAG TACGAGCAC Quence  ##: NM_032 21    GAGGCGGTA GAGGCGATA CGGCACCCC CAGAGAGCAA TGTGTAATAA AAGCTGCCTT TGAGAGACAA TGTGTAATAA AAGCTGCCTT TGGAGAAATGT GGGGAATTCAG	AAAAAAGGCT ACAGCAGGA AGGCTCATGG GGCTACGGCC CCGGGGTCG TGCACGGCCCA AGGCGTCGG TGCACCGCCCA AGGCGTCGG TGGATCTTA TGTTCTTTC CAAATTTCTTTG CAAATTTCAT TATGTAACA TTTTTTTTT CAAATTCAT TTTTTTTT CAAATTCAT TTTTTTTT	CACACACAGAG  CACACAGAGC  CAACGAGAGG  AGAAGTTTCG  TGGTGCAGGC  GGTCCAGGGC  GCTCTTCCT  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TCAGCGCGGC  TAGCTATAC  AAGTAAAGC  ACTGTATAC  AAAAAAAAAT   41    AGGGCGCCCGG  ACTGTCACGG  ACTGTCACGG  ACTGTCACGGC  CACACGCCCCGGC  ACCACACAGAGC  ACCACAGAGC  ACCACAGAGC  CACACAGAGC  CACACAGAC  CACACAGAGC  CACACAGAGC  CACACAGAGC  CACACAGAGC  CACACAGAC  CACACACA	GAGTGGAAAG GCAGAAGGAT GCAGACGCG GCCTGGACC CCTGGGCTAC CCGCGCGCTC GTGCGCGCC CTCCTGAAG TATCATCATT GCAGCTGAA CACAGAGCAT TCCAAAAGAA TTCAAACAG TTCATCATT TCATCATCATT TCATCATCATT TCATCATCATT TCATCATCATCATCATCATCATCATCATCATCATCATCAT	120 180 240 300 360 420 480 540 660 780 960 1020 1080 1140 1175
50 55 60 65 70	1   GAGAAGCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCAGC GACCTCAACGGAACGC GGGGAGCC GACCTGAACCGGAACCGAACC	11   CATTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACCACGG GCATCTTCTC GCCGGTCTT GCTGGGGGG CCTGGGTGGC GGCCTTGGC GGCCTTGGC TGGTCCTGG TGGTCCGCG TCAATCCCA TTACATCTGT TCTAATTTGGA ACTACAGCAT TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11   CCGCCGGCCG TCGCGGCCT TCGGGCACT TCGGGCACT TCGGCGCGC TCGGCGCT TCGGCCTTCGC TCGGCCTTCGC TCGGCCTTCGC TCGGCCTTCGC TCCCCCGCGCCC TCTCACCCC TCCCCCGCCCC TCTCTGCC TCTCACCC TCTCTGCC TCTCACCC TCTCACCC TCTCACCC TCTCACCC TCTCACCC TCTCACCC TCTCACCC TCTCACCC TCCCCCCGCCC TCTCACCC TCTCACCC TCTCCCCCCC TCCCCCCCC	21   MANAMAMA AACCATTTG CCGGGGACG CAGGGCCTTG GCGGTGGCA CTTGCTGGTG GCGCTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATGC AACCAGGCC CACCGATGC AACAGGCCGG CACCGATGC AACAGGACAA AGAGTGGCAA AGAGTGGCAA TAGACTTTT AACATTGGTA  Quence   #1 MM_032 _21	AAAAAAGCCTA ACAGCACGG ACAGCCCCGG CAAAAAAGCCCCCCCGG AAAAAGCCCCGG AAAAAAGCCCCCCGG AAAAAAGCCCCGG AAAAAAGCCCCCGG AAAAAAGCCCC	COCCACAGAGA  AGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GAGTGGAAAG GCAGAAGGAT GCAGACGCC CCTCGGACCCC CCTCGGACCCC CTGCGCCCCC CTGCGCCCCC CTGCGCCCCC CTGCGCCCCC CTGCACACC CCTCCTGAAC CACACACC CACACCCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	120 180 240 300 420 480 600 660 780 840 900 900 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCT CCCCGGTCCC CTGGGGCTGT GACCTGCACG GGCGGGAGCG GGCGGAGCG GGGCCCTCA ACCGGAGCG GACCTGCAGC GACCTGCAGC GACCTGCAGC GACCTGCAGC GACCTGCAGC GACCTGCAGC CATCTGAAAG CTACTGAATT TTCTGAAAA CCACTGAAT ATAACACTC AACAGCCAGT ATCAGTCTA ATAACAGCA TATTGCTTA  Seq ID NO: Nucleic Ac Coding seq 1   GGCTGGGGGG GGCCTTGGCGC TACTTGCCC TACTTGCCC TAGGCCCAG CCAGGCCAG CCAGGCCAG GCCCCAGGGC GCCCCAGGCC GCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCAGGCC GCCCAGGCC GCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCAGGCC GCCCCAGGCC GCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCAGGCC GCCCCAGGCC GCCCCAGGC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGCC GCCCCAGGC GCCCAGGC GCCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGGC GCCCAGC GCCCA	11   CATTCCCTTTA CATCCCACCA GCATCTCCCCCCCCCCC	21  AAAAAAAAA  AACCATTTG CCGGGGGACG CCTGGCGGCTTGGGC GCGCTGGCG GCGCCTGCTG GCGCGCTGGCG GCGCCTGCC GCGGCCTGCC GCGGCCTGCC CACCCGATGC AACCGGACC CACCCGATTG ACATTGACAAAA TACGTGATT AACATTGTA ACATTGTA CCGCGCCCCC CCAGGCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGGCGCCCCC CCAGGCGCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGGCCCCC CCAGGCCCCCC CCAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CAGGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCAGCCCCCC CCCAGCCCCCC CCAGCCCCCC CCCAGCCCCCC CCCAGCCCCC CCCAGCCCCCC CCCAGCCCCCCC CCCAGCCCCCC CCCAGCCCCC CCCAGCCCCCC CCCACCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCAGCCCCCC CCCACCCCCCC CCCACCCCCCC CCCACCCCCC	AAAAAAGGCTAGGGAGAGAGAGAGAGAGAGAGAGAGAGAG	GCTTCTCGCA GCTTCTCGCA CAAGGAAGAG AGAAGTTTCG TGGTGACCCT GCTCCAGGGC GCTCTACGCG CCTCAGGGC CCTCTCAGGGC CCTTTTAGGA ACGTGCAGGA CAACCGCAG CAACCGCAG CAACCGCAG CAACCGCAG CAACTGCAC CAACTGCAC AGGGGCCCCG ATCCAGGAG ACTGTCCCACCAG ACCAGTCCC ACGGCCCCTGG ATCCAGGAG ACTGTCTCCA ACTGTCTCCCA ACTCTCAGAAG ACTGTCTCCCA ACTCTCTGCCA ACTCTCTGCCA ACTCTTCTCCAA ACTGTCTCCCA ACTCTTCTCCAA ACTGTCTCCCA ACTCTTCTCCCA ACTCTTCTCCCA ACTCTTCTCCCA ACTCTTCTCCCA ACTCTTCTCCCA ACTCTTCTCCAA ACTGTTCTCCCA ATCCTTGCCA ATCCTTTGCCA	GAGTGGAAAG GCAGTAGGAC GCAGAAGGAT GCCGGAGCGC GCCTGGACC CCGCGCGAGT GCCGCGCGC CTGCCCGCGC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCC	120 180 240 300 360 420 480 540 660 720 780 960 1080 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCCGG	11 CTTCCCTTTA CATCCACCA GCATCTCCC GCACACCA GCATCTTCCC GCACACCA GCATCTTCTC CACCACGTG GCTGGTGGC GGGCTTGGCGGGG CGGCCTTCGC TGGTGCCTG TCTAATCTGT TCTAATCTGT TCTAATCTGT TCTAATCTGT TTAAAAAATA  174 DNA Sei did ACCEBBio ouence: 152. 11   CCGCGGGGCGG TCAGCTGGC TGGGCTTCG CTGGTTGGC CTGGTTGGC CTGGTTGGC CTGGTGGCC CTGGTGGCC CTGGCTTCG CTGGGCACCG CTGGGCACCG CTGGGCACCG CCGCCGGCGC CCGCCGCGCGC CCGCCGCCGC CTGGCCCCCGCGCC CTGGCCCCCC CTGCACCACG CTGCCCCCCC CTGCTCCACC CTGCTCCACC CTGCTCCCCC CTGCGCCCC CTGCGCCCC CCGCCCCC CTGCTCCACC CTGCTCCACC CTGCTCCACC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCCCCCC CTGCCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCC CTCCCCCC CTCCCCCC CTCCCCCC CTCCCCCC	21  AAAAAAAAA  AAACCATTTG CCGGGGACG CAGCGCCTTG GCCGTGCTC CTCCCTGGTG GCAGCGCCTG CAGCGCCTG CAGCGCCTG CAGCGCCTG CAGCGCTGC CACCGGATGC ACACGGACCA GAATATTAAA AGAGTGGCAG ACAGTGCA ACAGTGCA ACAGTGCAAA AGAGTGCAGACA Quence 1 #: NM_032 21    GAGGCGGATA CGGCGCCCCC CAGAGAGCAA ATGTTGATA AAGCTTCTTT TGAACAATTGTA CGGCCCCCC CAGAGAGCAA ATGTTGATA AAGCTGCCTT TGGACAATTGTA AAGCTGCCTT TGGACAATTGTAAC AAGCTGCCTT TGGACAATTGTAAC AAGCTGCCTT TGGACAATTGTAAC AAGCTGCCTT TGGACAATTGTAACA AAGCTGCCTT TGGACAATTGTAACA AAGCTGCCTT TGGACAATTGTAACA AAGGACAATTGTGGCAATCGCCCCCC CAGAGAGCAA AAGCTGCCTT TGGACAATTGTAACA AAGGACAATTGTGGCAAATCGTGCCTA AAGGAGGCCCAA AAGGAGGCCCCAA AAGGAGGCCCAA AAGGAGGCCCAA AAGGAGGCCCAA AAGGAGGCCCAA AAGGAGGCCCCAA AAGGAGGCCCAA AAGGAGGCCCACAC AAGGAGGCCAAA AAGGAGGCCCACCCCCAACACCCCCCAACACCCCCCAACACCCCCC	AAAAAAGGCT ACAGCAGGA AGGCTCATGG GGCTACGGCC CCGGGGTCG TGCACGGCCC AAGGCATCTT TGCACGCAAA CTCGGGGCTGG TGGATCTGA CTATCTCCAG CAAATTCATT TATTCTTTC GAATTTCATT GAATTACAT CCTGTTCTTG CAAATTTCAT TATGTCAAC CCTGTTCTTG AAAAAGGCCCC CCAGCCCCCG CCCCAGGGGAG CCAAGGGAG CCAAGGGAG CCAAGGGAG CCAAGGGAG CCAAGGGAG CCAAGGCAC CCCTGCCCCC CCACCCCCC CCCCCCCCCC	GCTTCTCGCA GCTTCTCGCA GCAGGAGGGG GGTGCAGGGC GGTCTGCCG TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TCAGCGGGC TTAGCTAGCA ACGTCCAGCA ACGTCAGCA ACGTTTCT AAATAAAGA AAAAAAAAA  41   AGGGCGCCCG TCAGCAGGA ACTGTCAGGA ACGTCACCACAG ACGTCACCACAG ACGCCCTGG ACCACAGGAC ACCACAGGAC ACCACAGGAC ACCACAGGAC ACCACAGGAC ACCTCCACAG	GAGTGGAAAG GCAGGAGGAT GCAGGAGGAT GCAGGAGGAC CCTGGGCTAC CCGCGCGCTC GTGCGCGCC CTCCTGAAG TATCATCATT GCAGGAGAT TCCAAAAGAA TTCAAACAG TTTCATCATT TCATCTTGAT TCCATCAGG GCACCACAGGCC CCCCCTCTTGAAC CACAGGAGCAC CCACCACTTTGAA CACAGGGAC CCACCTCTTTGAA AGAAGGAGCAC CCACAGTGCC CCACCTCTT TGGGCACCAC AGGTGCTGCA CCACAGTGCC AGTACGCCA GCTCCTTTGGA ACGTAGGGGT ATGCCCTTCG GTGCCAAGGAG CTCCCTTCGG GTGCCAAGCA GCTCCCTCGG GTGCCAAGCA GCTCCCAGGGT ATGCCCTTCGG GTGCCAAGGGGT ATGCCCTTCGG GTGCCAAGGGGT ATGCCCTTCGG GTGCCAAGGGGT ATGCCCTTCGG GTGCCAAGCA GCTGCCAGGGT ATGCCCTTCGG GTGCCAAGGGGT GTGCCAAGGGGT GGCGCAGGGGGGGGGG	120 180 240 300 420 480 540 660 720 780 840 960 1020 1140 1175
50 55 60 65 70	1 GAGAAGCCCT CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGTCCC CCCCGGCGCGGGGGGGG	11   CTTCCCTTTA CATCCACCA GCGGACGCC GCGGACGCC GCACGACGAC GCATCTTCTC GCCGGTCTT GCTGGGGGG CCTGGGTGGCGG CCTGGTGGCGG CTCAGTCCCAC TTACATCTGT TCTATTTGGA ACTACAGCAT TTAAAAAATA  174 DNA Se id Accessio uence: 152. 11   CCGCCGGCGC TCGCGGCGT TCGGGCTTGC TCAGTTTCAAACACAT TTAAAAATA  CTAAGGATA TTAAAAATA  CTGAAGGACA TCCTGAGTT TTAAAAATA  CTGAAGGACA TCCTGAGTT TCAATGCCT TCAGTGTCGCCC TCGCTGCCCCC TCGCGCCCC CGCCGCCCC CGCCGCCCC CCCCCCCC	21  AAAAAAAAA  AAACCATTTG CCGGGGACG CAGGGCCTTG GCCGTGCTC CTCCCTGGTG GCAGCGCCTG CAACCAGGCC CACCGATGC AAACCAGGCA GGTGTTGGCC CACCGATGC AAACAGGCAG GAATATTAAA AACATTGGTA TAGACCTTT AACATTGGTA  QUENCE	AAAAAAGGCTA ACAAGCAGAA AGGCTCATGG GGCTACGGCC CCGGGGCTCG ACCGGATCGT TGCAGGCAA CTCGGGGCTCG ACCGGATCGT TGCAGCCCAA AGGCGTCGG TGGATCTTA TGTTTTTTTT CTTTTTTTTTT	CATTTCTCGCA CAGGAGGGCCACTAGGAGGAGGAGAGAGAGGAGAG	GAGTGGAAAG GCAGTAGGAC GCAGAAGGAT GCCGGAGCGC GCCTGGACC CCGCGCGAGT GCCGCGCGC CTGCCCGCGC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCCC CTCCCCCC	120 180 240 300 360 420 480 540 660 720 780 960 1080 1140 1175

	CCCTAAGTCT	AGGCTGAAGA	GCCTGACGAA	TAAGAACTCC	TTCTGGATCC	ACCAGGTCAC	900
	CTGCCTGGGG	ACAGAGCCCC	ACATGGCCAA	CTGCCAGGTG	CAGGTGGCTC	CAGCCCGGGG	960
	CAAGCTGCGG	CCAGCCTGCC	CAGGTGGCAT	GCATGCTGTG	GTCAGCTGTG	TGGCAGGGCC	1020
5	TCACTTCCGC	CCACCGAAGA	CAAAGCCACA	ACGCAAAGGG	TCCTGGGCAG	AGGAGCCGAG	1080
)	GCTGCGCCTG	CCCTCCCGGG	CCCAGGTGGG	CGAGGGCCGG	GTGGAAGTGC	TCATGAACCG	1140
	CCAGTGGGGC	ACCUTCTGTG	ACCACAGGTG	GAACCTCATC	TCTGCCAGTG	TOGTGTGTCG	1200
	TCAGCTGGGC	TITGGCTCTG	CTCGGGAGGC	CCTCTTTGGG	GCCCGGCTGG	GCCAAGGGCT	1260
					GAGCGGACCC		1320
10	CCCTGCCCTG	GAAGGGTCCC	AGAATGGTTG	CCAACATGAG	AATGCTGCTG	CTGTCAGGTG	1380
10	CAATGICCCT	AACATGGGCT	TTCAGAATCA	GGTGCGCTTG	GCTGGTGGGC	GTATCCCTGA	1440
	CACTCAAAAC	TIGGAGGIGC	AGGTGGAGGT	GAACGGGGTC	CCACGCTGGG	GGAGCGTGTG	1500
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	COTCATCACT	CCCTACAAGG	CCTCACCCAC	CIGGICGGG	CTGCAGCAGT	CCCAGGAGGT	1620
15	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CACTGCTCCC	POSCHOOCHE	WONGC LOCKE	GCTGGAGTCT	CCTCCATCCA	1680 1740
	CAGTGCACCA	GACCTGCTGA	TCAACCCCCA	CCTACTCCAC	GAGACGGCCT	ACTIOCATOON	1800
	COGCCCGCTC	AGCCAGCTGT	ATTGTGCCCA	CCACCACAAC	TGCCTCTCCA	ACTITIONNON	1860
	TCACATGGAC	TGGCCCTACG	GATACCGCCG	CTATTGGG	TTCTCCACAC	AGATCTACAA	1920
					AGCTGGGTTT		1980
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	AGGACTGCAG	CGGCGCTACG	CATGTGCCAA	CTTTGGAGAA	CAGGGAGTGA	CTGTAGGCTG	2160
	CTGGGACACC	TACCGGCATG	<b>ACATTGATTG</b>	CCAGTGGGTG	GATATCACAG	ATGTGGGCCC	2220
26	CGGGAATTAT	ATCTTCCAGG	TGATTGTGAA	CCCCCACTAT	GAAGTGGCAG	AGTCAGATTT	2280
25						GGCTGCACAA	2340
	CTGCCACACA	GGGAATTCAT	ACCCAGCCAA	TGCAGAACTC	TCCCTGGAGC	AGGAACAGCG	2400
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	AGATACCTCA	GCTTATTGGA	GCCATGCCCT	TCACAGAGTC	CCAACTCAGA	GGAAAAGGGC	2520
30	CAGTGCCAAG	GGGCACCAAG	AACCTGCTCA	GGAAGCCTTT	TGATGGCAAG	ATCACCAATC	2580
30	CAGATGGTAT	TGCTCCCTCA	GGATGGCTCT	GGGCCTGCCC	CTAAGGGCCT	GTGGCCTATG	2640
	CONTRACTO	CCCAGGCTTT	GCTCAGCTGA	GCTCCTCTTC	TGTAAGGAAA	CCCAGTCATC	2700
					TGGAGGAGTA	GGATGGACȚA	2760
	GACCABASTA	CACACCACCT	ACTOTTACCT	CTCTCCTACC	AGCTCAAAGC	TAGGACAGAG	2820 2880
35					TCCTTTCTTC		2940
						TTACCACACA	3000
	CATGGGTGTT	TCTATTATCC	TTGGAAGCAC	AGACCTCGGG	CATCCCCTTA	TTGCCTGATG	3060
	GGCCAACACC	AACAGTTACG	GAGTGCTTGA	GAAGGGGCAA	GTTTCACAGA	AATGGCCAGA	3120
	TAGGGCCTTC	CTACAGAGCA	GCAAGAGTAG	GCCAAGCAGA	AAGACTGCTG	AGGTAACACG	3180
40					TGGACCATTT		3240
	CAGTCTGCTC	TCTCTCAGGA	TCACCACGCA	TCTCAGGATT	GGTCTAAACT	TCAAGTCTCA	3300
	ACCAAGTGTC	TGAAGTGAAC	TTTGCATTGA	ATAAATTTTT	GCCATGGAAA	GAACATCAAA	3360
	CAAGCCACTC	ATCTCTACAG	AGATAAGAAA	ACAAGTTTGG	CAGAGCAAGA	GACAGAAGAC	3420
15	CGTGGAGAAA	TCAGAAGGGG	GAACAGTCAG	TTTAGTTAAG	GATGGAACCT	GGGAAAGGCC	3480
45	ACCATTCCTG	CTTGATGGGG	CTCTGATTTG	CTCTTGCTCA	AGTGGAATAA	AACCCCATGG	3540
	TCTTCTTGAC	ATGATTCTTG	ATCTTTTCTC	CACTGAGACA	CACTTAAGTG	ATGATCCTTA	3600
	CAGGACTGAC	ACCCTAATGC	CAATAAAAGT	TGCTCATTAT	GGACTGCTAC	алалалала	3660
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55		CGGGCCTCT		GGGAACTCGG	TEGGAGGGGG	CAACATTGTT	60
	TCAAGTTGGC	CAAATTGACA	AGAGCGAGAG	GTATACTGCG	TTCCATCCCG	ACCCGGGGCC	120
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60	ACAAGTTGAC	GGGAGAGGTG	GTGGCGCTTA	AGAAAATCCG	CCTGGACACT	GAGACTGAGG	360
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						ACCCATGAGG	720
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70	ATGAGGTGGT	GTCGCCACCA	CTTACTTCTA	TCCGGAICTI	Chrocorroca	TTCCCC ACT	900
	GGGCCCCGCA	AGATTTTACT	AAAGTTGTAG	*ACCIONITA	TOMOCUMOT	TTCCCCAAGT	960 1020
	TATOGCAAAT	GCTGCACTAC	GACCCTAACA	AGCGCATTTC	CCCCAACCCA	GCCCTGGCTC	1020
	ACCUTTUTE	CCAGGATGTG	ACCAAGCCAG	TACCCCATCT	TOGACTOTO	TAGCCTTCTT	1140
7.	GAAGCCCCCA	GCCCTAATCT	CACCCTCTCC	TCCAGTGTCC	GCTTGACCAG	GCTTGGCCTT	1200
75	GGGCTATTTG	GACTCAGGTG	GGCCCTCTGA	ACTTGCCTTA	AACACTCACC	TTCTAGTCTT	1260
	GGCCAGCCAA	CTCTGGGAAT	ACAGGGGTGA	AAGGGGGGAA	CCAGTGAAAA	TGAAAGGAAG	1320
	TTTCAGTATT	AGATGCACTT	AAGTTAGCCT	CCACCACCCT	TTCCCCCTTC	TCTTAGTTAT	1380
	TGCTGAAGAG	GGTTGGTATA	AAAATAATTT	TAAAAAAGCC	TTCCTACACG	TTAGATTTGC	1440
90	CGTACCAATC	TCTGAATGCC	CCATAATTAT	TATTTCCAGT	GTTTGGGATG	ACCAGGATCC	1500
80	CAAGCCTCCT	GCTGCCACAA	TGTTTATAAA	GGCCAAATGA	TACCOCCCCCC	TANCTTOCTO	1560
	CTTTTGAGAA	CCAAGTAAAA	CAAAACCACT	GGGAGGAGTC	TATTTTAAAC	AATTCCCTTG	1620
	AAAAAATAGA	TCCAATCAGT	TTATACCCTA	GTTAGTGTTT	TGCCTCACCT	AATAGGCTGG	1680
	GAGACTGAAG	ACTCAGCCCCG	GGTGGGGGTTG	CAGAAAAATG	ATTGGCCCCA	GTCCCCTTGT	1740
	GAGACTGAAG	ACTCAGCCCCG	GGTGGGGGTTG	CAGAAAAATG	ATTGGCCCCA	GTCCCCTTGT GTGCTTCATT	1740 1800

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5	GGATGAACAA TTATATTTAT ATTTCAGGTT ATATCCAATA GTAGAGTTGG CTTTTTTTTT	2100
		2160
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10	THOUSE THE PROPERTY P	
	Seq ID NO: 176 DNA Sequence	
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15	1 11 21 31 41 51	
	GGAAGCAGGG CGGGGCCTCT GGTGGCGGTC GGGAACTCGG TGGGAGGCGG CAACATTGTT	60
		120
		180
20		240 300
20		360
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		480
25		540
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	TGACTCGCCG GGCCCTATTC CCTGGAGATT CTGAGATTGA CCAGCTCTTC CGGATCTTTC	780
20		840
30		900 960
	***************************************	1020
		1080
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		1260
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	ATCCCATTTT CCTCTGACGT CCACCTCCTA CCCCATAGGA GTTAGAAGTT AGGGTTTAGG	1860
	CATCATTTTG AGAATGCTGA CACTTTTTCA GGGCTGTGAT TGAGTGAGGG CATGGGTAAA	1920
	AATATTTCTT TAAAAGAAGG ATGAACAATT ATATTTATAT TTCAGGTTAT ATCCAATAGT AGAGTTGGCT TTTTTTTTTT TTTTTTTGGT CATAGTGGGT GGATTTGTTG CCATGTGCAC	1980 2040
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	AAAAA	2226
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65	GAGGAGAGCA GCTGCCACAC GGAGGATGAC TTGACTGATG CAAGGGAAGC TGGCTTCCAG GTCAAGGCCT ACACTTTCAG TGAACCCTTC CACCTGATTG TGTCCTATGA CTGGCTGATC	300 360
03	CTCCAAGGTC CAGCCAAGCC AGTTTTTGAA GGGGACCTGC TGGTTCTGCG CTGCCAGGCC	420
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	GCTGCCCGCC TCCTCTTCTC CTTCTACAAG GATGGAAGGA TAGTGCAAAG CAGGGGGCTC	780
	TCCTCAGAAT TCCAGATCCC CACAGCTTCA GAAGATCACT CCGGGTCATA CTGGTGTGAG	840
75	GCAGCCACTG AGGACAACCA AGTTTGGAAA CAGAGCCCCC AGCTAGAGAT CAGAGTGCAG	900
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	TIGIGIATIC TCTCTTAACA CAACAGAATT CIGCTGTCTA GATCAGGAAT TTCTATCTGT	1440
	TATATCGACC AGAATGTTGT GATTTAAAGA GAACTAATGG AAGTGGATTG AATACAGCAG	1500

	TCTCAACTGG G GTCATTATAC T	TGGGGGGTT (	GGGGATGGT (	GGATGTGTG :	TGCTACTGGC	ATCCAGTAAA	1560 1620
	TAGAAGCCAG G						1680 1740
5	CTAGGTGTTG G						1800
,	CATTCAGCTA 1	TOTTACTOR (	TATACCAGTC '	TTAGCTGGT	GCTATGGTCT	GTTCTTTAGT	1860
	TCTAGTTTGT A	TCCCCTCAA	AAGCCATTAT	GTTGAAATCC '	TAATCCCCAA	GGTGATGGCA	1920
	TTAAGAAGTG G	GCCTTTGGG A	AAGTGATTAG	ATCAGGAGTG	CAGAGCCCTC	ATGATTAGGA	1980
10	TTAGTGCCCT T	AAAAATTTAT	GCCCCAGAG	AGCTAACTCA	CCCTTCCACC	ATATGAGGAC	2040 2100
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	TGTAAAAAAA			Chincinio			2181
	10110-0001						
16	Seq ID NO: 1						
15	Nucleic Acid			46.1			
				31	41	51	
	Ī	i	ŀ	1	1	1	
20	GCTCCGGCCA (	CCCCCCCCTCC	AGAGCGCGCG	AGGTTCGGGG	AGCTCCGCCA	GGCTGCTGGT	60
20	ACCTGCGTCC	GCCCGGCGAG	CAGGACAGGC	TGCTTTGGTT	TGTGACCTCC	AGGCAGGACG	120 180
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~-	GGCATTGGGA	ATCTCGTGAC	ATTTGGCCAC	AGCCTGAGCA	AGACCTGTTC	CCCGGCCTGC	360
25	CCCATCCCAG	AAGGCGTCAA	TGTTGGTGTG	GCTTCCATGG	GCATCAGCTG	CTGCCAGAGC	420
	TTTCTGTGCA GCCGGGCTGC						480 540
	CCCTGTCCCC	CONTCCCCA	GCTCAGGAAG	GAAAGCCCAG	CCCTTTCTGG	ATCCCACAGT	600
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35	CCTCAGTCCC	TGTAGCCCCC	TGCCCTGGCA	CAGCTGCATG	CACTTCAAGG	GCAGCCTTTG	1020
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	Tecce						1143
40	Seq ID NO:	179 DNA Sec	quence				
	Nucleic Aci	d Accession	n #: XM_113	526.2			
	Coding sequ						
	1	11	21 	31 	41 1	51 i	
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55	GAGGCGTGAGG	CCACCGCAA	CAGGAGCIC	CAGCTGGAGG	GCAACAGGC	TCAGGAGCGG TGTCAGCAG	660
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60	CAACACAAAA	AATGCCAGGA	CCAGATTAN	GATCTGGAG	AGAAGCTGT	C CAGCCAAGAA C CCTGCAAGAG	
00	CAGGATGCAG	CGATTGTGAA	GAACATGAAG	TCTGAGCTG	G TACGGCTCC	C TAGGCTGGAA	1020
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	GGGCTGCTCC	AGGAAGAGCT	GGAAGGGCTY	CAGAGGAAG	C TGGGGGGCCC	A GGAGAAGATG	1140 1200
65	CAGGAGACGC	TOGETTOGCTT	CARGCTGGAG	AACGAGAGG	DAADAYYYY A	A GCTGCAAAGC A CCTTTCCAGA	
05	TTCGTGGTTG	AGCTGCAGC/	GAGGGAGCT"	r gccttgaag	G ACAAGAACA	G CGCCGTCACC	1320
	AGCAGCGCCC	GGGGGCTGG	GAAGGCCAG	CAGCAGCTG	C AGGAGGAGC	T CCGGCAGGTC	1380
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70						C CATCCTGGGG G GCGCATGCGG	
, 0						A GGCTCAGCTG	
	TCGCAGGCCC	* TGGAGGAGC*	r GGGAGGCCA	G AAACAAAGA	G CAGACATGO	T GGAGATGGAG	1680
	CTGAAGATGC	TGAAGTCTC	A GTCCAGCTC	T GCCGAACAG	A GCTTCCTGT	T CTCCAGGGAG	1740
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,,	CAGGGAAAAGA	CCAAACTCC	H GGCACAGCT	C CTGAACCCC	A CCAGTGTO	G TGACTATGAC C CAGGCAGCGC	
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	GCCATGGAGA	GAGGAGGCA	C CGTCCCAGC	C GACCTTGAG	CTGCCGCCG	C GAGTCTGCCA	2040
øΛ	TCGTCCAAGG	AGGTGGCAG	A GCTGAAGAA	G CAGGTGGAG	A GTGCCGAGC	T GAAGAACCAG	2100
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	GAGCACCCAC	GCGACTGCC	T CATCTTCAA	G GCCACCAGO	C CCTCGGGTT	C CAAGATGCAG	2280
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	GTGGCGTAGC C	TGCAGGCTC	GGGGGCATAG	CCGGAGCCAC	TCTGCTTGGC (	TGACCTGCA	2460 2520
	GGTCCCCTGC C CAGCAGCATG A	CTCACAGCC	ACAGGCTGGG	CTACCTCCCC	CTTCTCCTC	CCCACAGGCAG	2580
	CACCCTCTCC A	CGTGCAGAC	CCCTGGGAC	CCGGAGCCTG	GTGTGTGGGC (	STOGGCCACC	2640
5	AGCCTGGGTT C	CTCACCTTG	TGAAATAAAA	TCTTCTCCCC	TAG		2683
	Seq ID NO: 1						
	Nucleic Acid		_	73.1		•	
10	Coding seque			31	41	51	
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	GCGACGTCCC C	CCCCCCCTC	GGTCCGCATC	CTGCGCGCTG	CCGCTGCCTG	CGACCTTCTC	300
	GGCTGCCTGG C	STATOGTGAT	CCGGTCCACC	GIGIGGITAG	CATTCCCCAAA	CCCCACTCCC	360 420
	AGCGTCTCGG A	ATATGAACCA	CACGGAAATT	TTCTCCTCC	TETTTTECTA	TGCAGTGGAT	480
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	GCGTGGGGCC 1	TGGCCACCCT	GCTCTGTGTG	GAGGGAGCCG	CCATGCTCTA	CTACCCTTCC	600
	GTGTCCAGGT (	GTGAGCGGGG	CCTGGACCAC	GCCATCCCCC	ACTATGTCAC	CATGTACCTG	660
	CCCCTGCTGC 1	<b>IGGTTCTCGT</b>	GGCGAACCCC	ATCCTGTTCC	AAAAGACAGT	GACTGCAGTG	720
0.0	GCCTCTTTAC 1	TTAAAGGAAG	ACAAGGCATT	TACACGGAGA	ACGAGAGGAG	GATGGGAGCC	780
25	GTGATCAAGA '	TCCGATTTTT	CAAAATCATG	CTGGTTTTAA	TTATTTGTTG	GTTGTCGAAT	840
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	TTGAAACCTG CCCCAGGGAT	TCAGAACTGC	AGCCAAGACC	TACCCCTCCA	CACCATCCAC	CCTGGGTTTT	1020
	CACTCTCCCA	CCAACCACAT	CAGTGGGAA	TCACTGACCA	CCTCGGCTGC	TGAGGGGGCT	1080
30	CACCCATCCC	CACTGATGCC	CCATGAAAAC	CCTGCTTCCG	GGAAGGTGTC	TCAAGTGGGT	1140
	GGGCAGACTT	CTGACGAAGC	CCTGAGCATG	CTGTCTGAAG	GTTCTGATGC	CAGCACAATT	1200
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	CATGGAGACC	TATGAAGGGG	ATGTGCTGGG	GGTCCAGACC	CCATATTCCT	CAGACTCAAC	1320
25	AATTCTTGTT	CTTTAGAACT	GTGTTCTCAC	CTTCCCAACA	CTGCACTGCC	GAAGTGTAGC	
35	GGCCCCCAAA	CCTTGCTCTC	ATCACCAGCT	AGAGCTTCTT	CCCGAAGGGC	ACCACTCTAC	1440 1500
	GGAGAAAGGG	TTCATGCACA	CACGIGIGAG	CTTTTCTCAC	CCCCCTCCAG GCTGGCTGTA	TOTOACTOA	1560
	AAGGTCCACA					701017010101	1607
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40	Seq ID NO:	181 DNA Se	quence				
			n.#:NM_139	317.1			
	Coding sequ	ence 174	1070				
	coerus sed-	Circo. Z.d.	. 10 / 0				
		11	21	31	41	51	
15	1	11	21 	1	1	1	60
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45	1     CCCTGGGATA   CCAGGGTGGG	11 CTCCCCTCCC CCCCGGGGGT	21     AGGGTGTCTG   CAGGAGCTCG	   GTGGCAGGCC   AGAAGGGCCA	   TGTGCCTATC   GCTGGGCATA	CCTGCTGTCC TTCTGAGATT	120
45	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC	11 CTCCCCTCCC CCCGGGGGT CCCCATTTCT	21 	   GTGGCAGGCC   AGAAGGGCCA   TGGTCAGAGC	TGTGCCTATC GCTGGGCATA CAGTGTTCCC	CCTGCTGTCC TTCTGAGATT TCCATGGGAC	
	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG	11 CTCCCCTCCC CCCCGGGGT CCCCATTCT TGCCAAGTGC	21 	   GTGGCAGGCC   AGAAGGGCCA   TGGTCAGAGC   GACCACAGCC	 TGTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGG	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGGTG	120 180
45 50	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG	11  - CTCCCCTCCC CCCCGGGGT CCCCATTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAC	21	GTGGCAGGCCA AGAAGGGCCA TGGTCAGAGCA GACCACAGCCA GCTCTCTGGG GGCAGATCCT	 TGTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG CGGCCCCTGA	120 180 240 300 360
	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA	11 	21	GTGGCAGGCCAGAGGCCAGAGGCAGAGGCAGAGGCCACAGGCCAGAGCCAGGCCAGAGCCCAGAGCCAGCCCTGGCGGCAGACCCTGCCACCCTGGCGCAGACCCTGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGGCCACCCTGCACCCTGCACCCTGCACCCTGCACCCTGCACCCTGCACCCTGCACCCTGCACCCTGCACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCCTACCACC	TGTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCTGTC GGGCCAGCTG	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG CGGCCCCTGA GCCTTCCCCG	120 180 240 300 360 420
	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC	11  - CTCCCCTCCC CCCCGGGGT CCCCATTTCT TGCCAGGTG GCAGGAGGG AGCCTGGGA AGCCTGGGA TGAGGAGTTC	21	GTGGCAGGCCA AGAAGGGCCA TGGTCAGAGC GACCACAGGCG GGCAGATCCT CCACCTTGTC CCTTCTATGA	TGTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGC GAGCCACTGC CAGGGCACTGC CAGGGGGCCT CTGGCCGCTG	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCCGTG CTAGGCCTTGA GCCTTCCCCG ACTGCTGAGG	120 180 240 300 360 420 480
	1	11  -  -  -  - 	21	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA GACCACAGCC GCTCTCTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAC	TGTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCTGTC GGGCCAGCTG CAGGGGGCCCT ACTGGCCCTGC AGGCCATCAG	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGTG CTAGGCCTGG CGGCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA	120 180 240 300 360 420 480 540
50	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCACCCGA GGTGCTTCTT	11 CTCCCCTCCC CCCCGGGGT CCCATTTCT TGCCAGTGC GCAGGACGC AGCCTGGGAC AGAGGAGTTC GCTGCTGGCC CTGCTATGGC	21	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA GGACACAGCC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCTTCTATGC TCTTCTACACAC GCTGGAAGCC	TGTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCACTGC GGGCCAGCTG CAGGGGGCCT CTGGCCGCTG AGGCCATCAG CGGGCACTAG CGGGGACGACGACGACGACGACGACGACGACGACGACGAC	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGTG CTAGGCCTGG CGGCCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA CCCTGGACCG	120 180 240 300 360 420 480 540 600
	1 CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ACACCTGCAG ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCCGA GGTGCTTCTT AGCATGCCAA	11  -   CTCCCTCCC CCCCGGGGT CCCCATTCT TGCCAGTGG GCAGGAGGGG GCAGGAGGAGGAG TGAGGAGTTC GCTGCTGGGT CTGCTATGGG GTGGTTCCCC	21	GTEGCAGGCCA AGAAGGCCAA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GCCACATCTC CCTTCTATGA TCTTCCACAC GCTGGAAGCC TCCTGCTCCCC	I TGTGCCTATC GCTGGCATA CAGTCTTCCC GAGCCACTGG CAGCCACTGG CAGCCACTGTC CAGGGGCACT CTGGCCGCTG AGGCCATCA GGGCACTA GGGCACTA GGGCACTA GTCAAAAAGGA	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGTG CTAGGCCTGA GCCTTCCCCG ACTGCTGACG GACAAGGTGA CCCTGGACGG AGAGACTTTG	120 180 240 300 360 420 480 540 600
50	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTAAAGACAG   ATGGTCCCAC   CACACTGCAG   CAGAGGAGGA   CCAGAGGAGGA   GCATGGGTTCTT   AGCATGCCAA   AGCATGCCAA   AGCATGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11 	21   AGGGTGTCTG CAGGAGCTCC GCTGCAACCC CTGCACCGTG TGTGGACCC CACGTGGATG GGCCCGGGG GGCTGCAGG GGCTGCAGG AGCTTCAGG AGCTGTCAGG CACTCCAGG CACTCCAGG CACTCCAGG CACTCCAGG CACTCCAGG CACTCCAGG CACTCCCAGG CACTCCCCAGG CACTCCCAGG CACTCCAGG CACTCCCAGG CACTCCAGG CACTCCCAGG CACTCCCAGG CACTCCCAGG CACTCCCAGG CACTCCCAGG CACTCCAGG CACTCCCAGG CACTCCAGG CACTCCCAGG CACTCCCAGG CACTCCAGG CACTCAGG CACTCCAGG	GETGGAGGCCA AGAAGGCCAA TGGTCAGAGC GACCACAGCC GCTCTCTGGG GCCACATCT CCTTCTATGA TCTTCCACAC GCTGGAAGCC TCCTGCTCCC TCCTGCTCCC TGCTGGGCTC	I TGTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG GGGCAGCTG CAGGGGGCCT CAGGCGACTAC GGGCACTAC GGGCACTACAC GGCCACCACCAC CAGGGACCACCACCACCACCACCACCACCACCACCACCAC	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCAGCCGGTG CTAGGCCTGG CGCCCTGA GCCTTCCCCG ACTGCTGAGG GACAAGGTGA CCCTGGACGG AGAGACTTTG TGGGAAGAAC	120 180 240 300 360 420 480 540 600
50	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTANAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   CCATGGGCTC   TGCCACCCGA   AGCATGCTCTT   AGCATGCCCAA   TCCACAGTGT   CGAGAGAGCG   CACCCAGGAG	11	21	GTGGCAGGCCA TGGTCAGAGG TGGTCAGAGG GACCACAGGCC GCTCTCTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG GCTGGAAGGCC TGCTGGAGGCC TCCTGCTGCCCC TCCTGCTCCC CCCTCCTCCCCC CCCCCGCCT CCCCAGGGCCC CCCAGGAGGCC	TOTGCCTATC GCTGGGCATA CAGTGTTCCC GCTGGGCATA CAGCCACTGG GAGCCACTGG CAGCCACTGTC CAGCCACTGTC ACTGGCCGCTG AGGCCATCAA CCTGGCACCACCC GTCAAAAGGA CTGGGACCAC TTGGGACCCC TGGGACCCC AGGACGACCCC TGGGACCCC TGGGACCCC AGGACGACCCC TGGGACCCC	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG CTAGGCCTGA GCCTTCCCCG ACTCTCCCG GACAAGGTGA CCTGGACGG GACAAGGTGA TGGGAGGACAA GAGACTTTC TGGGAGGACAA AGTCCACCA AGTCCACCCA	120 180 240 300 360 420 480 540 600 660 720
50	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   GGCACCCGA   GGTGCTTCTT   AGCATGCCAA   TCCACAGAGTGT   CCGAAGACGC   CACCCAGGAG   AGGCCCAGAGAGAGACGC   AGGCCCAGAGA	11	21	GTGGCAGGCCA TGGTCAGAGC AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCCCTCTGGG GCCAGATCCT CCACCTTGTC CCACCTTGTCACAC GCTGGAAGCC TCCTGCACCC TCCTGCTCCC TCCTGCCCC CCCCAGGAGCC CCCCAGGAGCC	I TOTGCCTATC GCTGGCATA CAGTGTCCC GGCCACTGT GGCCACTGT GGCCAGCGC GGCCAGCTGT CAGGGGCCT AGGCCATCAG GCCAGCAGCGC CTGGGACAAAGGA CCTGGACCCG TGGGACCCG TGGGACCCG TGGGACCCG TGGGACCCG CTGGGACCCG CTGGACCCC TGGGACCCG CTGGACCCG CTGGACCCG	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GCACCCTGA GCTTCCCCG ACTGCTGACG GACAAGGTGA CCTGGACGG AGAGACTTT TGGGAAGAAC GAGTGCCCA AGTCCAGCCG GAGCGCCCCA	120 180 240 300 360 420 480 540 600 720 780 840 900
50	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   TGCCACCCGA   AGGATTGTT   AGCATGCCAA   TCCACAGTGT   TCGCAACAGTGT   CGGAACACC   CACCCGGAG   AGGCCCAGAG   TGCGCCGGCT	11  CTCCCTCCC CCCCGGGGT CCCCATTTCT GCCAAGTGG GCAGGAGGGC GGAGGAGGAGTT GAGGAGGAGTT GCTGCTGGCT GCTGCTATGGG GTGGTTCCCC GCAGGAGGAC AGCCCTGTT AGAGGTCCA GGCGTGGTGG GCAGGAGGAC	21	GTGGCAGGCCA AGAAGGGCCA AGAAGGGCCA TGGTCAGAGG GGCACACGCC GCTCTTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGGCTC TCCTGGGCTC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC AGGTGGGCTA AGGTGTGGCTA	TGTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG CAGGGGCACTG CAGGGGCACTG CAGGGGCACTG CTGGCCGCTG AGGCACGAC GTCAAAAGGA CTGGGACCAC TGGGACCAC TGGGACCAC TGGGACCAC GTCAAAAGGA CTGGGACCAC TGGGACCAC	CCTGCTGTCC CTTCTGAGATT TCCATGGAC GCACCCGTG GCACCCGTG GGCCCTGA ACTGCTGAGG GACAAGATG ACCTTGAGG AGAGACATT TGGGAAGAAC AGTGCAACA AGTCAAC AGTCCAGCG GAGCTGCCCA AGTCCAGCG GAGCTGCCCC GAGCGCCAGC GAGCTGCCATCG GAGCTGCCATCG GAGCTGCCATCG GTGTCCATCG	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50	1     CCCTGGGATA   CCAGGGTGGG   GGCCAATCAGC   CTAAAGACAG   ATGGTCCCAC   CAGAGGAGGA   CCATGGAG   CAGAGGAGGA   GCATGGGCTC   TGCCACCCGA   GGTGCTTCTT   AGCATGCCAA   TCCACAGTGT   CGGAACAGCC   CACCCAGGAG   AGGCCCAGGAG   TGCGCCGGCT   TCTTTGTGCCC	11 CTCCCTCCC CCCCGGGGT CCCCATTCT TGCCAAGTGC GCAGGAGCGC AGACGAGGAG AGACGAGGAG AGACGAGGAG AGACGAGAGAG AGACGAGGAGAG AGACGAGGAGAGAG AGCCCTGTC GCAGGAGAG AGACGAGGAG AGACGAGGAG GCAGGAGGAG GCAGGAGGAG GTGCGCCCAGTGTGCC GCAGGAGGAG	21	GTGGCAGGCCA GAGAAGGGCCA TGGTCAGAGG GACCACAGGCC GCTCTCTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGCTGCAGGCC TCCTGGAGGCC TCCTGCTGCCT TCCTGCTCCC TCCTGCAGGCC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCTGAGTGTGCC GCTGAGGTGCCT	TOTGCCTATC GCTGGGCATA CAGTGTTCCC GGCCACTGTC GGCCACCTGTC CAGGCCACTGA CAGGCCACTGA CAGGCGCACT CAGGGGCACTA CCTGGCACCGCTG GGCACGACGAC GGCAAAAGGA CCTGGGACCGC CAGGGACGACCCC CAGGGACGACCCCCCC CCCCGGCACCACCCCCCCC	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG CTAGGCCTGA GCCTTCCCCG ACTCTCAGG GACAAGGTGA CCCTGGACGG GACAAGGTGA CCGGAGGACAA GAGGACTTTC TGGGAAGAAC GAGTGCCCA AGTCCACGC GAGGGCAGC GTGTCCATCG CAGCTGTGCC CAGCTGTCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 1020
50	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   GGCACCCGA   GGTGCTTCTT   AGCATGCCAA   ACCCAGGAG   CGAAGACGC   CACCCAGGAG   AGGCCCAGAG   TGCGGCGCCT   TCTTTCTGCAG   CCATCTGCAG	11	21	GTGGCAGGCCA TGGTCAGAGC TGGTCAGAGC GACCACAGCC GCTCTCTGGG GCCAGATCCT CCACCTTGTC CCACCTTGTC TCTTCCACAC GCTGGAGGCC TCCTGGAGGCC TCCTGCAGCC TCCTGCAGCC CCCAGGAGCC CCCAGGAGCC CCCCAGGAGCC CCCAGGAGCC CCCAGGAGCC CCCAGGAGCC CTGAGTGTCCC TGGCTGCCC TGCTGCCCC TGCTGCCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCC TGCTGCCCCCCCC	I TOTGCCTATC GCTGGCATA CAGTGTCCC GGGCCATGC GGGCCAGCG GGGCCAGCG CAGGGCACTA CAGGCCATCAG CAGGCACTACAG CAGCCCGCCCTAG CCCCCGCCCTAG CCCCCCCCCC	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTGA GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC AGGTGCCCA AGTCCACGCG GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020
50	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTAAAGACAG   ATGGTCCCAC   ATGGTCCCAC   ACACTGCAG   ACACTGCAG   ACACTGCAG   ACACTGCAG   ACACTGCAG   GGTGCTTCTT   AGCATGCCAC   AGCATGCGAG   AGGCCCAAGA   AGGCCCAAGA   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   AGGCCCAGGAG   ATGGCCGGCCCCACTGCAGAG   ATGGCCGGCCCCCACTGCAGAG   ATGGCCGGCCCC	11  CTCCCTCCC CCCCGGGGT CCCCATTICT TGCCAAGTGG GCAGGAGGGG AGCCTGGGA AGAGGAGGAG TGAGGAGGAT TGAGGAGTTC GCTGCTGGCT GCTGCTTGCT AGAGCTCCTGCT AGAGCTCCAG AGCCCCTGTT AGAGGTCCAA AGCCCCCGTT AGAGGTCCAA AGCCCCCCGTT AGAGGTCAAA AGCCCCCCGTT AGAGGAGGAA AGCCCCCCGTT AGAGGAGGAA AGCCCCCCGTT AGAGGAGGAA AGCCCCCCGTT AGAGGAGGAA AGCCCCCGTT AGAGGAGGAA AGCCCCCGTT AGGTGGGCCAA	21   AGGGTGTCTG CAGGAGCTCC CTGCACCGTG CTGCACCGC CTGCACCGGG CTGCACCGGG GCCCCGGGG GCCCCCAGG GCCCCCAGG GCCCCCCGG GCCCCCCCG GCCCCCCGG GCCCCCC	GTGGCAGGCCA AGAAGGGCCA AGAAGGGCCA TGGTCAGAGC GACCACAGCC GCTCTTGGG GCCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGGCTC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGCC TCCTGGCTC CCCAGGAGCC CCCCAGGAGCC CCCAGGAGCC C	TITITECTATE GETGGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG CAGGGGCACTA CTGGCGCGCTG AGGCCACTGG GTCAAAAGGA CTGGGACCAC GTCAAAAGGA CTGGACCAC AGGACGAC CAGGGACGAC CAGGGACGAC CCGGGCCCC CCCCGGCCCC CCCCGGCCCC CCCCGGCCCC CCCTGCCCCC	CCTGCTGTCC CTTGTGAGATT TCCATGGAC GCACCCGTG GCACCCGTG GGCCCTGA ACTGCTGAGG GACAAGATG ACCTTGCAGG AGAGACATTT TGGGAAGAAC AGTGCACA AGTCCAGCG GAGCTGCCCA AGTCCAGCG GAGCTGCCCC GAGCTGCCCC CGGCTGTCCATCG CACGTGTCCC TTCTGGACTG CCCAGGTGCC CCCAGGTGCCC TTCTGGACTG TTCTGGACTG TTCTGGACTG TTCTGGACTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTAAAGACAG   ATGGTCCCAC   CAGAGGAGGA   CAGAGGAGGA   CAGAGGAGGA   GCATGGGCT   GGCACCCGA   GGTGCTTCTT   AGCATGCTG   CGGAAGACGC   CACCAGGAG   TGGGCCCAGAG   TGGGCCGGCT   TCTTTGTGCC   CCATCTGCAG   ATGGCCGGCT   TGTTGTGGCG   CTTCTTGGGCG   CTTCTTGGGCGGCT   CTTTTCTGGGCGGCT   CTTTTCTTGGGCGGCT   CTTTCTTGGGCGGCT   CTTTTCTTGGGCGGCT   CTTTTCTTGGGCGGCT   CTTTTCTTGGGCGGCT   CTTTTCTTGGGCGGCT   CTTTTCTTGGGCGCTCT   CTTTTCTTGGGCGCGCT   CTTTTCTTGGGCGCTCT   CTTTTCTTGGGCGCTCT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGGCTCT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGGCTCT   CTTTTCTTGGGCGGCTCT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTCTTGGGCGCGCTT   CTTTTTTGGGCGCGCTT   CTTTTTTGGGCCGCTT   CTTTTTTTGGCCGCCTCT   CTTTTTTTGGCCGCCTCT   CTTTTTTTTGGCCTCT   CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	11	21	TOTAL CONTROL OF THE	TOTGCCTATC GCTGGGCATA CCAGTGTTCCC GGTGGGCATA CCAGTGTTCCC GGGCCAGCTG CGGCCCGCTG CGGGCCATCA CCTGGCCGCTG CGGGCACTACA CCTGGCACCGCTG CGGGACCAC CCGGGACCAC CCGGGACCAC CCGGGACCAC CCGGGACCAC CCGGGACCAC CCGGGACCAC CCGGGACCAC CCCGGCCTG CCCCGGCCTG CCTGTCCTAC CCGGCCTGCCCC CCGGCCTGCCCCCCCCCC	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GCACCCTGA GCCTTCCCCG ACTCTCCCG GACAGGAGA CCTGGACGG GACAAGGTGA CCTGGACGG GAGAGAAC GAGCTGCCCA GAGCGCAGC GAGGGCAGC GAGGGCAGC TCTCCATCG CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCCTGAT CCTGACTG CAGCCCTGAT	120 180 240 300 360 420 480 600 660 720 780 840 900 960 1020
50	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   TGCAACCCGA   AGCATCCCAA   AGCATCCCAA   AGCACCAGAG   AGGCCCAGAG   AGGCCCAGAG   AGGCCCAGAG   ATGGCCGCC   CCATCTGCAG   ATGGCCGCC   TCTTTCTGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGCCCGACCA	11	21	GTGGCAGGCCA AGAAGGCCA AGAAGGCCA AGAAGGCCA AGAAGCC GCTCTCTGGG GCAGATCCT CCTTCTATGA TCTTCACACA GCTGGAAGCC TCCTGCTGGCT CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCCTGCTCC CCCAGGAGCC TCCTGCTCC CCCCAGGAGCC TCCCTGCTCC CCCCAGGAGCC AGGTCCATC AGGCCCTTGCCT AGGCCCTTGCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCTTGCCT	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTCAGG GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC GAGTGCCCAG GAGTGCCCAG GAGCGCAGC GAGCGCAGC GAGCGCAGC GCCAGGTGCC CCAGCTGCCC GCCAGGTGCC TTCTGGACTG CAGCCTGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   TGCAACCCGA   AGCATCCCAA   AGCATCCCAA   AGCACCAGAG   AGGCCCAGAG   AGGCCCAGAG   AGGCCCAGAG   ATGGCCGCC   CCATCTGCAG   ATGGCCGCC   TCTTTCTGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGGCCGCCC   TCTTCTCAGC   ATGCCCGACCA	11	21	GTGGCAGGCCA AGAAGGCCA AGAAGGCCA AGAAGGCCA AGAAGCC GCTCTCTGGG GCAGATCCT CCTTCTATGA TCTTCACACA GCTGGAAGCC TCCTGCTGGCT CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCCTGCTCC CCCAGGAGCC TCCTGCTCC CCCCAGGAGCC TCCCTGCTCC CCCCAGGAGCC AGGTCCATC AGGCCCTTGCCT AGGCCCTTGCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCTTGCCT	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GCACCCTGA GCCTTCCCCG ACTCTCCCG GACAGGAGA CCTGGACGG GACAAGGTGA CCTGGACGG GAGAGAAC GAGCTGCCCA GAGCGCAGC GAGGGCAGC GAGGGCAGC TCTCCATCG CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCTGTCCC CAGCCTGAT CCTGACTG CAGCCCTGAT	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1260
50 55 60	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   GGCACCCAGGA   GCATGCCAA   ATCCACAGAG   ATGCATCCAA   ATGCATCCAA   ATGGCCCAGAG   ATGGCCCAGAG   ATGGCCCAGAG   ATGGCCGACCA   CTATTCTGCCC   CCATTTCCAGC   ATGGCCGCCCACCACCACCACCACCACCACCACCACCACCAC	11  CTCCCTCCC CCCCGGGGT CCCCATTCT TGCCAAGTGC GCAGGAGCGC GCAGGAGGAG AGAGGAGGAG AGAGGAGGAG AGAGGAGGA	21	GTGGCAGGCCA AGAAGGCCA AGAAGGCCA AGAAGGCCA AGAAGCC GCTCTCTGGG GCAGATCCT CCTTCTATGA TCTTCACACA GCTGGAAGCC TCCTGCTGGCT CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC TCCTGCTCC CCCAGGAGCC TCCTGCTCC CCCCAGGAGCC TCCCTGCTCC CCCCAGGAGCC AGGTCCATC AGGCCCTTGCCT AGGCCCTTGCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCT AGGCCCTTGCCT	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTCAGG GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC GAGTGCCCAG GAGTGCCCAG GAGCGCAGC GAGCGCAGC GAGCGCAGC GCCAGGTGCC CCAGCTGCCC GCCAGGTGCC TTCTGGACTG CAGCCTGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60 65	I CCCTGGGATA CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCCGA ACGATGCTTCTT AGCATGCCAA TCCACAGTGT CCGCAACAGAG AGGCCCAGAG AGGCCCAGAG AGGCCCAGAG AGGCCCAGAG TCCTTTTGTGCC CCATCTGCAG ATGCCCGACA CTGTACCTGT CA Seq ID NO:	11  CTCCCTCCC CCCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGCGC AGCCTGGGAG AGCCTGGGAC CTGCTATGCC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC GCAGGAGGAC TGCGCCCAGGC CCGCCCAGGC CCGCCCAGGC CCGCCCAGGA	21   AGGGTGTCTG   AGGGTGTCTG   CAGGAGCTCC   CTGCACCGTG   TGTGGACCCC   CAGGTGGATG   GGCGCCGGGG   CGTCTGCCGG   CGTCTCCCAGG   AGCCTCCCAGG   GCCCTCCCAGG   GCCCTCCCAGG   GCCCTCCCAGG   AGGACTGCAGCCGCC   CTGGACTGCG   ATGCACAGCCGCC   CTGGTCTGTC   CTGGTCTGTC   CTGACAGCCGCC   CTGGTCGGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCC	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GGCACACGC GCTCTTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGGCTC CCCAGGAGC CCCAGGAGC CCCAGGAGC TCCTGGCTC CCCAGGAGC TCCTGGCTC CCCAGGAGC	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTCAGG GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC GAGTGCCCAG GAGTGCCCAG GAGCGCAGC GAGCGCAGC GAGCGCAGC GCCAGGTGCC CCAGCTGCCC GCCAGGTGCC TTCTGGACTG CAGCCTGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60	I CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC CAGAGGAGGA CAGAGGAGGA GCATGGGCT GGCACCCGA GGTGCTTCTT AGCATGCTG CGGAAGACGC CACCAGGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TCCTTGCAG ATGCCGGCC TCTTTCTGGC TCCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic Ac	11	21	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GGCACACGC GCTCTTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGGCTC CCCAGGAGC CCCAGGAGC CCCAGGAGC TCCTGGCTC CCCAGGAGC TCCTGGCTC CCCAGGAGC	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTCAGG GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC GAGTGCCCAG GAGTGCCCAG GAGCGCAGC GAGCGCAGC GAGCGCAGC GCCAGGTGCC CCAGCTGCCC GCCAGGTGCC TTCTGGACTG CAGCCTGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60 65	I CCCTGGGATA CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC AGCATGCCTA AGCATCCCAG ATGCACCAGAG CCACGAGGCTT CTTATGCCCAA ATGGCCCAGAG ATGGCCCAGAG ATGGCCCAGAG ATGGCCAGAG ATGGCCCAGAG ATGGCCCAGAG ATGGCCCAGCA CTGTTCTGGC CCATCTCCAG ATGGCCGCC TCCTCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq	11  CTCCCCTCCC CCCCGGGGT CCCCATTCT TGCCAAGTGC GCAGGAGCGC GCAGGAGGAG AGAGGAGGAG AGAGGAGGAG AGAGGAGGA	21   AGGGTGTCTG   AGGGTGTCTG   CAGGASCTCC   CTGCACCGTG   TGTGGACCCC   CAGGTGGATG   GGCGCGGGG   GGTCTGGCT   GGCCCGCGGG   GGCCTGCAGA   AGGCTGCAGA   AGGACGTGCA   GGCCCCTCCC   GGTCTGAAGGT   GGTCTGAGG   GGTCTTGAG   GGTCTTGAG   AGGACGTGC   CAGAGTGGG   CAGAGTGGG   CAGAGTGGG   CTGAATAGAI   CTGAATAG	GTGGCAGGCCA AGAAGGCCA AGAAGGCCA AGAAGGCCA AGGACACAGCC GCTCTTGGG GCAGAATCCT CCTTCTATGA TCTTCACACA GCTGGAAGCC TCCTGGCTC CCCCAGGAGC CCCCAGGAGC CCCCAGGAGC CCCCAGGAGC CCCCAGGAGC CCCCAGGAGC AAGGTGGCCT TCCCTGCCTC CCCCAGGAGC AAGGTGCCAT AAGGCCTTGCCAAAAGTGCCAAAAAAAGTGCA	TITITCCTIGG  TITITCCTIGG  TITITCCTIGG  TITITCCCTIGG  TITIT	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCAGCCGTG GCAGCCGTG GCCTCCCC ACTGCTGAGG GCCTTCCCC ACTGCTGAGG GAGAGACTTTG TGGGAAGAG GAGGCCCCA AGTCCAGCG GAGCGCCAGC GAGCCCAGC GAGCCAGC GAGCAGC GAGCCAGC G	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60 65	I CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC CAGAGGAGGA CAGAGGAGGA GCATGGGCT GGCACCCGA GGTGCTTCTT AGCATGCTG CGGAAGACGC CACCAGGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TCCTTGCAG ATGCCGGCC TCTTTCTGGC TCCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic Ac	11	21   AGGGTGTCTG   AGGGTGTCTG   CAGGAGCTCC   CTGCACCGTG   TGTGGACCCC   CTGCACCGGG   GGTGCAGGGG   GGTCTGCGGGT   GGCCTCCAGG   AGGCTGCAGG   AGGCTGCAGG   AGGCTGCAGG   AGGACTGCGGG   TCTGAAGG   GTTCTTGAG   AGGACTGCG   TGTGAGGGG   TGCAGAGGGG   TGCAGAAGGG   TGCAGAAGGG   TGCAGAAGGG   TGCAGAAGGG   TGCAGAAGG   TGCAGA	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GGCACACGC GCTCTTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG TCCTGGCTC CCCAGGAGC CCCAGGAGC CCCAGGAGC TCCTGGCTC CCCAGGAGC TCCTGGCTC CCCAGGAGC	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG CAGCCCACTGG CAGCCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CTGGCACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CTGGGACGAC CAGCGATGTG GGACCGCCC CCCCGCCTG CCCCGCCTG CCTGCCTGCCTG CCCCGCCTGCTG CCTGCCTG	CCTGCTGTCC TTCTGAGATT TCCATGGAG GCACCCGTG GCACCCGTG GCCTCTCAGG GCTTCCCCG GACAAGGTGA CCTGGAGGG AGAGACTTTC TGGGAAGAAC GAGTGCCCAG GAGTGCCCAG GAGCGCAGC GAGCGCAGC GAGCGCAGC GCCAGGTGCC CCAGCTGCCC GCCAGGTGCC TTCTGGACTG CAGCCTGAC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60 65 70	1	11	21	GTGGCAGGCCA TGGTCAGAGG TGGTCAGAGG GACACAGGCC GCTCTCTGGG GGCAGATCCT CCTTCTATGA TCTTCCACAG GCTGGAGGCC TCCTGGCAGGCC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC CCCAGGAGGC AGCCAGGAGGC AGCCAGGAGCC AGCCAGGAGGC AGCCAGGAGGC AATAAAGTGGC AATAAAGTGGC 2151.2	TOTGCCTATC GCTGGCATA CAGTGTCCC GCTGGCATA CAGCCATGG GAGCCATGG GAGCCATGG GAGCCATGA CAGGCGCT CAGGGGCATCA GGGCATCAA CAGGGGCATCA GGCATCAA CAGGGACGAC CAGGACGAC CAGGACGAC CAGGACGAC CAGGACGAC CAGGACGGGCT CAGGACGGGCT CAGGACGGGCT CAGGACGGGCT CAGGACGGGCT CAGGACGGGCT CAGGACTGAC TAGGACGGGCT CAGCACTGAC TAGGACGGGCT CAGCACTGAC TAGGACGGGCT CAGCACTGAC TAGGACGGGCT CAGCACTGAC TAGGACTGAC TAGGACCAC TAGGACTGAC TAGGACTAC TAGGACTAC TAGGACTAC TAGGACTAC TAGGACTAC TAGGACTAC TAGGACTAC T	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GCACCCGTG GCCCCTGA GCCTTCCCCG ACTCTCCCG GACAAGGTGA CCCTGGACGG GACAAGGTGA CAGGCACTGC GAGGCAGAC GAGGCAGC GAGGCGCAGC GTGCCCCG GCAGGTGCC TTCTGGACTG CAGCTGTCCATCG GCAGGTGCC TTCTGGACTG CAGCTGTCCAC GAGCGCAGC TTCTGGACTG CAGCCTTGAT CAGCCCTGAT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1200 1200 1320
50 55 60 65	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   ACACCTGCAG   CAGAGGAGGA   GCATGGGTTC   TGCACCCGA   ATGCACCCAGAG   ATGCACCAGAGA   AGGCCCAGAG   AGGCCCAGAG   ATGCGGCGGCT   TCTTTGTGCC   CCATCTGCAG   ATGCCCGACCA   CTGTACCTGT   CA   Seq ID NO:   Nucleic Ac   Coding Beq   1   CCCTGGGATA	11	21   AGGGTGTCTG   AGGGTGTCTG   CAGGASCTCC   CTGCACCGTG   TGTGGACCCC   CTGCACCGTG   GGTGCAGGCG   GGTCCGGGG   GGTCTGGCGT   GGCCCCTCCC   GGCCCCCCGGG   GGCCTCCAGA   AGGCTGTCAGT   GGCCCTCCCGGG   TGTGAAGGG   ATGCCAGAGG   TGTGAGGGG   TGGAGAAGGG   TGGAGAAGGA   TGGAAAGGA   TGGAAAGA   TGGAAAGGA   TGGAAAGA   TGGAAAGA   TGGAAAGA   TGGAAAGA   TGGAAAGA   TGGAAAGGA   TGGAAAGGA	GTGGCAGGCCA AGAAGGCCA AGAAGGCCA AGGACACAGCC GCTCTCTGGG GGCAGATCCT TCTTCCACAG TCTTCCACAG TCCTGGCCT CCCAGGAGCC TCCTGGCTG CCCAGGAGCC TCCTGGCTG TCCTGGCCTG TCCTGGCCTGCCC TCGTGTGCCTG TCCTGGCCCTGCCC TCGTGTGCCTG TCCTGGCCCTGCCC TCGTGGCCAGGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCCAGGCC TCGTGGCAGGCC TCGTGGCAGGCC TCGTGCAGGCCAGGC	TITITECTIAN  GATGGCATA  CASTGTTCCC  GAGCCACTOS  GAGCCACTOS  GAGCCACTOS  GAGCCACTOS  CAGGCCACTOS  CAGGCCACTOS  CAGGCCACTOS  CAGGGGCACGAC  CAGGCCACCAG  CAGGACGAC  CAGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGGACGAC  CAGGACTOS  CAGGCACTOS  CAG	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCAGCCGTG GCAGCCGTG GCCTCCCC ACTGCTGAGG GCCTTCCCC ACTGCTGAGG GAGAGACTTTG TGGGAAGAG GAGGCCCCA AGTCCAGCG GAGCGCCAGC GAGCCCAGC GAGCCAGC GAGCAGC GAGCCAGC G	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1240 1320 1322
50 55 60 65 70	I CCCTGGGATA CCAGGGTGGG GGCCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC AGCATGCAGC CACACCAGGA ATGCACCAGA ATGCACCAGA ATGCACCAGAA ATGCACCAGAA ATGCACCAGAA ATGCACCAGAA ATGCACCAGAA ATGCACCAGAA ATGCACCAGCA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq I CCCTGGGATA CCAGGGTGGG	11	21	GTGGCAGGCC AGAAGGCCA AGAAGGCCA AGAAGGCCA AGAAGCACACACC GCTCTTGGG GCAGATCT CTTCTATGA TCTTCACACA CCTCTGCTC CCCCAGGAGCC AGGTGCCAC AGGTGCCAC AGGCCCACACACCC AATAAAGTGCA ATAAAGTGCA AGGCCCTTGCC AATAAAGTGCA AGGCCCTTGCCC AATAAAGTGCA AGGCCCTTGCCCC AATAAAGTGCA AGGCCCTTGCCCCCCCAGAGGCC AATAAAGTGCA AGGCCCTTGCCCCCCCCAGAGGCCCCCCCCAGAGGCCCCCCCC	TOTGCCTATC GCTGGCATA CAGTGTTCCC GGGCACTGC GGGCCACTGG CAGCCCACTGG CAGCCCACTGC CAGCCCACTGC CAGCCCACTGC CAGCGCACTGC CAGCGCACTGC CAGCGCACTGC CAGCGACGACGAC CAGCGACGACGACGACGACGACGACGACGACGACGACGAC	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG CCTAGCCTGA GCCTTCCCCG ACTCTCAGG GACACGTGA CCTGGACGG GACAAGGTGA CCTGGACGG GAGAGATTC GAGAGATTC GAGAGACAC GAGCTGCCC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCGCAGC GAGCTCCATC GAGCTTCCATCG GAGCGCAGC GAGCTCCACC GAGCTGCCC GAGCTGCCC GAGCTGCCC GAGCTGCCC GAGCTGCCC TTCTGGACTG CAGCCCTGAT GATGCCTTAA GATGCCTTAA CATCTGAGATT CTCATGGAGTT CTCATGGAGT CTCATGGAGTT CTCATGGAGT CTCATGGAGAT CTCATGGAGT CTCATGAGGAGT CTCATGGAGT CTCATGAGGAGT CTCATGAGGA	120 180 240 300 360 420 480 540 660 720 780 840 960 1020 1320 1322 1322
50 55 60 65 70	I CCCTGGGATA CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC TGCCACCCGA GGTGCTTCTT AGCATCCCAA TCCACAGAGA AGCCCCAGAG AGGCCCAGAG TGCGGCGGCT TCTTTGTGCC CATCTTGCAG ATGGCCGACA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq I CCCTGGGATA CCAGGGTGGG GGCATCAGGGGG GCCATCAGGAGA CCCTGGGACA CTGTACCTGT CA Seq ID NO: Nucleic Ac Coding seq CCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11	21   AGGGTGTCTG   AGGGTGTCTG   CAGGAGCTCC   CTGCACCGTG   TGTGGACCCC   CTGCACCGTG   GGTGCAGGCG   GGTGCAGGCG   GGTCCCGGGG   GGTCTGGCGT   GGCCCTCCGGGG   GGCCTCCAGG   AGGCTGTCAGG   AGGACGTGCG   TGTGAAGGG   ATGCAGAGG   TGCAGAAGGG   TGCAGAGGG   TGCAGAAGGG   TGCACGT   TCCAGAGGC   TGCACGC   TGCACCG   TCCACCG   TCCACACCG   TCCACACCG   TGCACCG   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCCC   TCCACACCG   TCCACCCC   TCCACACCG   TCCACCCCC   TCCACACCG   TCCACCCCCC   TCCACCCCCCCCCCCC   TCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GTGGCAGGCC AGAAGGCCA AGAAGGCCA TGGTCAGAGC GACCACAGCC GACCACAGCC GACCACAGCC GACCACAGCC GACCACAGCC CCTCTTGGC CCTCTTATAR TCTTCCACAG CCCAGGAGCC TCCTGGCTC CCCAGGAGCC CCCAGGAGCC CCCAGGAGCC CCCAGGAGCC CCCAGGAGCC CAGGAGCC CCCAGGAGCC CCCAGGAGCC CAGGAGCC CCCAGGAGCC CCCCAGGAGCC CCCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGC CCCCAGGAGCC CCCCAGGAGC CCCCAGGAGCC CCCCCAGGAGCC CCCCAGGAGCC	TITITECTION  GAGGACTAT  GAGGCATTA  GAGGCACTOT  GAGCCACTOT  GAGCCACTOT  GAGCCACTOT  CAGGCACTA  CAGGCACTA  CAGGCACTA  GAGCCACTA  GAGCCACTA  GAGCCACTA  GAGCCACTA  GAGCACTA  GAGCACTA  GAGCACTA  CAGGACCA  CAGGACTA  CAGGACTA  CAGGACTA  CAGGACTA  CAGGACTA  CAGCACTA  CAGCACTA  TACCCACTA  TACCCACTA  TACCCACTA  TACCCACTA  TACCACTA  TACCACTA  TACCACTA  CAGCACTA  TACCACTA  CAGCACTA  TACCACTA  CAGCACTA  CA	CCTGCTGTCC CCTGCTGTCC CTTGCTGAGATT TCCATGGAGC GCAGCCCTGG GCGCCCTGG ACTGCTGAGG ACTGCTGAGG ACAGCTGAGG AGAGACTTTG TGGGAAGAAG AGAGCTGA AGTCCACCG GAGCTGCCCA AGTCCACCG GAGCTGCCCC TTCTGGACG GCAGCCGAGG CGCAGCCTGAC AGTCACCCG TTCTGGACTG CAGCCTGAT AGGTACCCAG  51   CCTGCTGTCC TTCTGGACT CTTCTGAGATT CCTGCTGTCC TTCTGGACTG CATCTCTGAGTGC CAGCCCTGAT CCTGCTGTCC CAGCCCTGCAT CCTGCTGTCC CAGCCCTGCC CCTGCTGTCC CAGCCCGTGC CCTGCTGCCC CCTGCTGCC CCTGCTGCCC CCTGCTGCCC CCTGCTGCCC CCTGCTGCCC CCTGCCCCC CCTGCTGCC CCTGCCCCC CCTGCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCCC	120 180 240 300 360 420 480 540 660 720 900 960 1020 1080 1140 1260 1320 1322
50 55 60 65 70	1     CCCTGGGATA   CCAGGGTGGG   GGCCATCAGC   CTAAAGACAG   ATGGTCCCAC   CAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	21	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACACAGCC GCTCTTGGG GGCAGATCT CCTTCTAGG TCTTCCACAC GCTGGCTC TCCTGGCT CCCAGGAGCC CCCAGGAGC CCCAGGACC CCCAGGAGC CCCAGGACC CCCAGGAGC CCCAGGACC CCCAGGAGC CCCAGGACC CCCCAGGACC CCCCCAGGACC CCCCAGGACC CCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCCC CCCCAGC CCCCCAGC CCCCCAGC CCCCCAGC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCCC	TITITECTATE GAGGACATA CAGGACATA CAGGACATA CAGGACACTA GAGCCATATC GAGCCACTATC CAGGACACTA CAGGACTATC CAGCACTACTA CAGGACTATA CAGGACCATTA CAGGACCACTAC CAGCACCTATA CAGGACCACTAC CAGCACCTATA CAGGACCACTAC CAGCACCTATA CAGGACCACTAC CAGCACCTATA CAGGACCACTAC CAGCCCCTATA CAGGACCACTAC CAGCCCCTATA CAGGACCACTAC CAGCCCCTATA CAGGACCACTAC CAGCCCCTATA CAGGACCACTAC CAGCCCCTATA CAGGACCACTAC CAGCCCCTATA CAGCCCCTATA CAGCCCCTATA CAGCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCTATA CAGCCCCCCCCCC	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCACCCGTG GCGCCCTGA GCCTTCCCCG GCCCCTGAGGCGACGACGACGACGACGACGACGACGACGACGACGA	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1320 1322
50 55 60 65 70	I CCCTGGGATA CCAGGGTGGG GGCATCAGC CTAAAGACAG ATGGTCCCAC ACACCTGCAG CAGAGGAGGA GCATGGGCTC AGCATGCAG CCAGAGGAGGA TCCACAGAG TCGACAGAGC CCACCAGGAG AGGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGAG TGCGCCCAGCA CTGTTCTCGGC TCCCCGACCA CTGTACCTGT CA Seq ID NO: Nucleic AC CCding seq I CCCTGGGATA CCAGGTGGG CTAAAGACAG ATGGTCCCA ATGGTCCCA ACACCTGCAG ACACCTGCAG ACACCTGCAG ACACCTGCAG ACACCTGCAG	11	21	GTGGCAGGCC AGAAGGCCA AGAAGGCCA AGAAGGCCA AGAAGCCC AGACACACC GCTCTTGGG GCAGATCT CTCTTCACAC AGCTGTCCC CCCCAGAGCC CCCCAGAGCC CCCCAGAGCC CCCCAGAGCC AAGGCACCT CCCCCAGAGCC CCCCAGAGCC CCCCAGAGCC CCCCAGAGCC AAGGCACCT CCCCCAGAGCC CCCCAGAGCC CCCCCAGAGCC CCCCAGAGCC CCCCCAGAGCC CCCCCCC CCCCCAGGCC CCCCCCC CCCCCCCC	TOTGCCTATC GCTGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGC CAGCCACTGC CAGCCACTGC CAGCCACTGC CAGCCACTGC CAGCGACGAC CAGCGACGAC CAGCGACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGAC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACGACC CAGCCACCACC CAGCCACCACCACCACC CAGCCACCACCACCACCACCACCACCACCACCACCACCAC	CCTGCTGTCC CTTGTGAGATT TCCATGGAGC GCAGCCGGGG GCAGCCGGGG ACTGCTGAGG ACTGCTGAGG ACTGCTGAGG AGAGACTTTG TGGGAAGAAAA GGAGCTGCCCA AGTCCAGCG GAGCGCGGG GAGCGCAGC GAGCGCAGC CTGCTGACG AGAGCTGCCC TTCGGAAGAAAA CAGGGAAGAAAA CAGGGAAGAAC AGTCAGCCG CAGCCTGAT CAGCCTGAT CAGCCTGAT CAGCCTGAT CAGCCTGAT CTCAGCAT CTCAGCAT CTCAGCAT CTCAGCAT CTCAGCATGC CTAGGCCTGG CCTAGGCCTGG CCAGGCCGGGG CCAGGCGGGGG CCTAGGCCTGG CCAGGCCGGGG CCAGGCCGGGG CCAGGCCGGGG CCAGGCCGGGG CCAGGCCGGGG CCAGGCCCGGGG CCAGGCCCGGGGGGG CCAGGCCCGGGG CCAGGCCCGGGG CCAGGCCCGGGG CCAGGCCCGGGG CCAGGCCCGGGGGGGG	120 180 240 300 360 420 480 540 660 720 780 840 1020 1140 1260 1320 1322
50 55 60 65 70	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   ACACCTGCAG   CAGAGGAGGA   GCATGGGTTCT   AGCATCCCAA   ACACCTGCAGAG   ACACCAGGAG   ACACCAGGAG   AGGCCCAGAG   AGGCCCAGAG   ATGGGCGGCT   TCTTTGTGCC   CCATCTTGCAG   ATGGCCGGCC   CCTTTCTGGGC   CCACTGTACCTGT   CA   Seq ID NO:   Nucleic Ac   Coding Beq   1   CCCTGGGATA   CCAGGGTGGG   GGCCATCAGAGACAC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAGAC   ACACCTGCAGAC   ACACCTGCAGAC   ACACCTGCAGAC   ACACCTGCAGAC   ACACCTGCAGAC   ACACCTGCAGAC   CAGAGGAGGAGGAC   CCAAGGAGGAGGAC   CCAAGGAGGAGGAC   CCAAGGAGGAGGAC   ACACCTGCAAG   CAGAGGAGGAGACAC   CACCTGCAAGACACC   CACCTCCAAGACACC   CACCTCCAAGACACC   CACCTCCAAGACACC   CACCTCCAAGACACC   CACCTCCAAGACACC   CACCTCCAACC   CACCTCA	11  CTCCCCTCCC CCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGGGG GCAGGAGGGGGGGGGG	21   AGGGTGTCTG   AGGGTGTCTG   CAGGASCTCC   CTGCAACCCC   CTGCACCGTG   TGTGGACCCC   CTGCACCGTG   GGCGCCGGGG   GGTCTGCCGT   GGCCTCCAGA   AGGCTGTCAGA   AGGCTGTCAGA   AGGACTGCAG   TGTGAAGGG   TGTGAAGGG   TGTGAAGGG   TGGAAGAGGG   TGGAAGAGG   TGGAAGG   TGGAAGAGG   TGGAAGAGG   TGGAAGAGG   TGGAAGAGG   TGGAAGAGG   TGGAAGG   TGGAAGAGG   T	GTGGCAGGCC AGAAGGGCCA AGAAGGGCCA AGAAGGGCCA AGGACACAGCC GGCCACTGTC CCACCTTGTC CCACCTGTC CCACCTGTC CCACCAGGAGC TCCTGCTCCC CCACGAGGC CCCACGAGGC CCCACGAGGC CCCACGAGGC CCCAGGAGCC CCCACCACGC CCCACCACGC CCCACCACGC CCCACCTCC CCCCCC AGAAGGCC CCCCTCCTGGCC CCCCTCCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCTTCTGGCC CCCCCTTGCC CCCCCTTCTGGCC CCCCCTTCTGGCC CCCCCTTGCC CCCCCTTCTGGCC CCCCCTTGCC CCCCCTCCTGGCC CCCCCTTCTGGCC CCCCCTTGCT CCCCCCCTCCTCC CCCCCTTCTCTGCC CCCCCTTCTCTGGCC CCCCCTTCTCTGCC CCCCTTCTCTGCC CCCCTTCTCTGC CCCCTTCTCTCTC	TITTCCTOC C GAGCCACTO C CAGGGCATA C CAGTGTTCCC GAGCCACTOG GAGCCACTOG C CAGGGCACTA C CAGGCCACTOG C CAGGGCACTA C CTGGCCACTOG C CAGGGCACTA C CTGGCCACTA C CAGGGCACTA C CAGGGCACTA C CAGGGCACTA C CAGGCACTA C CAGGCACTA C CAGGCACTA C CAGGCACTA C CAGGCCTATA A CCTGGCCATA A CCTGGGCATA C CAGGCCACTA C CAGGCCCACTA C C C CAGGCCCACTA C C CAGGCCCACTA C C C CAGGCCCACTA C C C CAGGCCCACTA C C C C C C C C C C C C C C C C C C C	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GGCACCCTGA ACTGCTGAGG ACTGCTGAGG ACTGCTGAGG ACAGCTGAGG AGAGACTTTG TGGGAAGAAC AGTCACCCG AGTCCACCG AGTCACCCG AGTCACCCC TTCTGAGATG AGTCACCCG TTCTGAGTG AGGTACCCAG ATTCTGAGATT CCTGAGTCC TTCTGAGATT CTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGTT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGCTGG CCGCCCCTGA TTCTGGGCTGG CCGCCCCTGA TTCTGGGCTGG CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TCCCCGCCCCTGA TCCCCCCCCTGA TCCCCCCCCCC	120 180 240 300 420 480 540 660 720 1080 1140 1200 1320 1322 60 120 130 300 360 420
50 55 60 65 70	1	11	21	GTGGCAGGCC AGAAGGGCCA TGGTCAGAGC GACACAGCC GCCACTTGTC GCGCAGAGCC TCCTGCAGAGCC TCCTGCAGAGCC TCCTGCAGAGCC TCCTGCAGAGCC TCCTGCAGAGCC TCCTGCTGCC TCCTGCTGCC TCCTGCTGCC TGCCAGGAGCC TCCTGCTGCC TGCCAGGAGCC TCCTGCTGCC TGCCAGGAGCC TCCTGCCTGC TCCTGCCC TGCCAGGAGCC TGCCAGGAGCC TGCCAGGAGCC TGCTAGGCACTTGC AAAAAAGTGGC AAAAAAGTGGC CTGCTCAGGCC TGGTCAGGCC TGGTCAGGC TGGTCAGGCC TGG	TITTGCCTATC GGTGGGCATA CGAGCCACTGG GGGCCAGCTG CGAGCCACTGG GGGCCAGCTG CGAGCCACTGG GGCCAGCTG CGAGCCACTGG GGCCAGCTG CGAGCCACTGG GGCCAGCTG AGGACGAC GGCAGACGAC CGAGCACTGAC CCAGGGACGAC CCAGGACGAC CCAGGACTGAC CTGGCCTACT CAGGACTGAC CTGGCCTACT CAGGACTGAC CTGGCCTACT CAGGACTGAC CTGGGCCAGCTGC CAGGCCACTACC CGAGCCACTACC CGAGCCACTACC CGAGCCACTACC CGAGCCACTACC CGAGCCACTACC CGAGCCACTACC CGAGCCACTACC CAGGGGGCCC CCAGGGGGCCC CCAGGGGCCCC CCAGCGCCCCC CCAGCCCCCCC CCAGCCCCCCC CCAGCCCCCCCC	CCTGCTGTCC TTCTGAGATT TCCATGGGAC GCACCCGTGA GCCTTCCCCG GACGCCCTGA GCCTTCCCCG AGCCTTCAGG AGAGACATT TGGGAAGAG AGAGACTTT TGGGAAGAG AGAGCCACG AGTCCAGCG GAGCGCAGC CAGCTGCCCA CAGCTGCCCA CAGCTGCCCA TTCTGAGAT CAGCTGCCAG CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CAGCCCTGAT CTCATGGACT CCTGCCCCG CCTGCTGTCC CCTGCTGTCC CCTGCTGTCC CCTGCTGCCG CCTGCCCTGAT CCTGGCCCTGAT CCTGCCCCGG CCTGCCCCGG CCTGCCCCGG CCTGACCCGG CCTGCCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGCCCCGG CCTGACCCCGG CCTGCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCGG CCTGACCCCG CCTGCCCCG CCTGCCCCG CCTGCCCCG CCTGCCCCG CCTGCCCCG CCTGCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCG CCTGCCCCCC CCTGCCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCCC CCTGCCCCCCCC	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1320 1322
50 55 60 65 70	1     CCCTGGGATA   CCAGGGTGGG   GGCATCAGC   CTAAAGACAG   ATGGTCCCAC   ACACCTGCAG   CAGAGGAGGA   GCATGGGCTC   GGCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11  CTCCCCTCCC CCCGGGGGT CCCCATTTCT TGCCAAGTGC GCAGGAGGCG GCAGGAGGAGCA AGAGGAGGAG AGAGGAGGAG AGCCTGTATGGC CTGCTATGGC GCAGGAGAGCA AGCCCCGTT AGAGGTCCAC AGCTGGGAGAGCA AGCCCCCGT AGGTGGCCA  182 DNA S AGCCCCGTT AGGTGGCT  182 DNA S AGCCCCGGGGAGAC  182 DNA S AGCCCCGGGGAGAC  182 DNA S AGCCCCGGGGAGAC  164 ACCCGGGGGC CCCCCCAGGAGGCC CCCCCCAGGAGGCC CCCCCCAGGAGGCC CCCCCCGGGGAGACC CCCCCGGGGAGACC CCCCGGGGAGAGCA AGAGGAGGAGT CCCCATTTC CCCCGGGGGA AGGGGAGGAC CTGAGGAGGAC CTGAGGAGGAC CTGAGGAGGAC CTGAGGAGGAC CTGAGGGAGGAC CTGAGGGAGT CTGAGGGAGGAC CTGAGGGAC CTGAGGGACT CTGCCCTCCC CCCCCTCCC CCCCCTCCC CCCCCTCCC CCCCCTCCC CCCCCTCCC CCCCCTCC CCCCCC	21	GTGGCAGGCC AGAAGGCCA AGAAGGCCA AGAAGGCCA AGGACACAGCC GCTCTTGGG GCAGATCT CTTCTATGA TCTTCACAG AGCTGGCTG CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC CCCCAGGAGCC AAGGTGTGCA AAGGTGCCAGAGC AAGGCCCAGAGCC CCCCAGGAGCC CCCCTGCC CCCCAGGAGCC CCCCTTGCAGGC CAGGAGCC CAGGAGGCC CAGGAGGCC CAGGAGGCC CAGGAGGCC CAGGAGGCC CAGGAGGCC CTGCTCAGGG CGCCCTTGT CCTTCTATG CGCCCTTCTATG CGCCACTTGT TCCTCCACA TCCTTCAAGG CGCCACTTGT TCCTCCACA TCCTTCCACA TCCTTCTATG TCCTCCACA TCCTTCCACA TCCTTCTATG TCCTTCAAGG TCCTTCTATG TCCTTCAACG TCCTTCTAATG TCCTTCAACG TCCTTCAACG TCCTTCTTAATG TCCTTCAACG TCCTTCTTCAACG TCCTTCTTCAACG TCCTTCAACG TCCTTCTTCAACG TCCTTCTAATG TCCTTCAACG TCCTTCTTCAACG T	TOTTGCCTATC GCTGGGCATA CAGTGTTCCC GAGCCACTGG GAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCCACTGG CAGCGACGAC CAGCGACGAC CAGCGACGAC CAGCGACGAC CAGCGACGAC CAGCGACGAC CAGCCACGAC CAGCCACCAC CAGGCCACCAC CAGCCCACCAC CAGCCACCAC CAGCCCACCAC CAGCCCACCAC CAGCCCACCAC CACCACCAC CACCACCACCAC CACCACCA	CCTGCTGTCC TTCTGAGATT TCCATGGAC GCACCCGTG GGCACCCTGA ACTGCTGAGG ACTGCTGAGG ACTGCTGAGG ACAGCTGAGG AGAGACTTTG TGGGAAGAAC AGTCACCCG AGTCCACCG AGTCACCCG AGTCACCCC TTCTGAGATG AGTCACCCG TTCTGAGTG AGGTACCCAG ATTCTGAGATT CCTGAGTCC TTCTGAGATT CTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGTT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGATT TTCTGAGCTGG CCGCCCCTGA TTCTGGGCTGG CCGCCCCTGA TTCTGGGCTGG CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TTCTGGGCTGC CCGCCCCTGA TCCCCGCCCCTGA TCCCCCCCCTGA TCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 1020 1020 1140 1200 1320 1322

	TCCACAGTGT CGGAAGACGC	AGCCCCTGTG	GCCCCTCCG	TCCCTGCCTC	TGGGTACCCT	GAGCTGCCCA	720 780 840
	CACCCAGGAG CGCAGCTGCG	GCGGCTGCAG	CACCACAGIG CACCACAGAGA	CGTGCAAGGT	GTGCCTGGAC	CGCGCCGTGT	900
5	CCATCGTCTT	TGTGCCGTGC	GGCCACCTGG	TCTGTGCTGA	GTGTGCCCCC	GCCTGCAGC	960
•	TGTGCCCCAT	CTGCAGAGCC	CCCGTCCGCA	GCCGCGTGCG	CACCTTCCTG	TCCTAGGCCA	1020
	CGTGCCATGG	CCGGCCAGGT	GGGCTGCAGA	GTGGGCTCCC	TGCCCCTCTC	TGCCTGTTCT	1080
	GGACTGTGTT CCTGATTCCC	CTGGGCCTGC	TGAGGATGGC	AGAGCTGGTG	TCCATCCAGC	ACTGACCAGC	1140 1200
10	GCTTAACTGT	ACCTGTTTCG	ATGCTTCTGA	ATAGAAATAA	AGTGGGTTTT	CCCTGGAGGT	1260
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						TGCTGCCACA	60 120
20						CATGGGCAGC TTCGCAGTAC	180
						GCTGCTGAGG	240
						CAAGAGCGAA	300
						AGATTACACG	360 420
25						GTCCACACCC TGCAGTGAGG	480
						CTCCCCGGAG	540
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						CAGCCTGCCC	660
30						GGACCCACA GGACAGCAAC	720 780
50						CCACTCGAAC	840
						GTGCAGCATC	900
						GCAGCGCAGC	960
35						GCGCTGCAGG	1020 1080
"						CTCGCAGAAG GGAGAAGCGG	1140
						GACCAAGCTC	1200
	AGGTCCTACG	AGAGGGAGAA	GACCAGCTTC	GCCCCCCCCCC	TGGAGGAGAC	CCAGTGGGAG	1260
40						GTCCCAGACG	1320
40						GGACACGCGG	1380 1440
						GCCGGAGCTG	1500
	CTGCGGGAGA	AGGTGAACCT	GCTGGAGCAG	GAGCTGCAGG	AGCTGCGGG	CCAGGCCGCC	1560
45						GCAGCGGGAG	1620
47						GATGTCCTCG	1680 1740
						GGAGAAGGCC	1800
						CCTGGAAGGG	1860
50						CTGGGAAGGC TGCTCAGCAA	1920 1980
50						CCGAGGGGAG	2040
						TGCAGCCCAC	2100
						GTCTGTCTGC	2160
55						CTCCCCCTCC	2220 2280
55						ATGACCAGAA	2340
	GCCTTGGAAC	CAGCCCCATC	AGAACCTGAG	CTATTTTCCT	CTGGCCGCAG	AGGTGTAGGG	2400
	GTGGAATGAG	CCGCGGGGA	GCTGGCTTT	AAACCTCAGG	GCTGTCCCA	CCCCGGCAAG	2460
60						CACAGCCAGA CAGCCCCTGG	2520 2580
00						GGACAGCCAG	2640
						CCTGGGCTGG	2700
						CCAGGCACCC	2760
65						TITGCTTGAT	2820 2880
03						CCTCCTCTGC	2940
						T GAGTTCTGGG	3000
						A AGCAGGACGA	3060
70						T CCCTCCACCT	3120 3180
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	TAGAGAGAG	TAAAAGGTG	G AGTTTCTCT	G TICTITICGT	T CAGGGATTT	TTAATTTTTA T	3300
	TTATGAGAC	A GGGTCTTGC	T CTGTCCCCC	A GGCTGGAGT	G CAGTGGCAT	G ATCATAGCTC	
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						A GCCCTTCCCT	3900
	GAGTGCGGG	C TGAGGCCAG	A GTCACCTTT	T CTGTGGCTG	G CTCTACCTT	C CTGTCCCTGA	3960
	GGTTAAACG	G TGCCCATCC	T GCCATCCTC	A AACGACAGA	G GAGCTTTTC	T GGAATTTCAA	4020

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	ACCATTGCTC TTAGTCCCAA GCTAGGCTTA AACCTGGAAT CTACAAGCCA AAAGTCCCTC	4080 4140
	CCTGCCTGAG GGCAGTACCC TCCATTGGGC ACAGTCCAGA CCCAAGTCAA AGATGCCCCA TTCCTTGGGC CTCAGCCCTC AGTTCCTTCA TTTCCACCAG GCCGTGCCTT GTTTGAGTTT	4200
	TTCCTCCCAG TGAGACTGCC CCACGGAGAC AGAGGAAAGG GCTGGCTCCC CCTCCCCAGG	4260
5	CTGGAGACCC CCCCCAACTC CAGGAAAGAG CAGTCAGAGT CCAGTGCTCT GCCTCAGACG	4320
_	TTGCCTGAGA AGAAGTGGCT GCCACACCCA GGGGAAGGCC CTGAGGCGGA GGCTGTGCTC	4380
	CGCCATGGTG TCCCGGTACC TTCCATACAC AGAGGAGTGC AGCCTTCTCC ATATCTCCAT	4440
	GGCCCTGTCC CAGGCCGGCC CAGATGTGTC CCCCCAGGC CTTGTCCTAC GTCCAAGGTG	4500
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25	TIGTGGCAAT TITATGTTTT TATTTATGAA TAAAGAATGC CATTTCTCAC GCCCTCTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	5492
23	ANDIANUAR KARAMANA ANAMANANA M	
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	CTTCCTGGTG CTTGAGGCCG TGGCGGGGGC CCTGGTGGTG GCCCTCTGGG GCCCGCTGCA	600

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	GOGCTTCCTC CTCGACCAAG TCCAGCTCGG GCTGAGGTGC TGCGGAGGTG CCTCCTACCA	120
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5		900 960
	COOCCOCCO CICCOCCOCO COCOCOCOCOCOCOCOCOC	1050
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••	CENTERCITIC CONCORNOR CONCUTRATI TOCCTOGGC TTCGGGTGAC TTCGCCGCAG	1260
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40	AIGGCAGCCC	WAY! IOCKON	NOGCK 100CA	TICALIONAG	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
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60	TOAGATGTOG TGACTCATGT GAAGTGGTGT CATAGGAATG AAGGACTGTG GGCGCTGGGT TCAAATTCCA GTTCTATGCA CCACTCCAGG TAGGGATACC CATGGGGGCA GCTGTGCCTG	2220
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	GTTTCAGTGA GCCCAGATCG CGACACTGCA CTCCAGCCTG GGCAACAGAG TGACACTCTG	2580
	ΤΟΤΟΝΑΝΑΝ ΤΑΝΝΑΤΑΝΑΝ ΤΑΝΝΑΤΑΝΑΝ ΤΑΝΝΑΤΑΝΑΝ ΤΑΝΝΑΤΑΝΑΝ ΑΝΝΑΝΑΝΑΝΑ	2640
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	TOGTGTCATT GI	ACATCCTGG C	AGGTGATTT I	GACCCCCAT C	CCTTTGCCA C	ACCUTATOR	660 720
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	CCTGGTGAAA G	TGGTGGGGC '	TGTATGGCTT (	CATGCTCAGC A	ATATOGCOIC (	ACTCACCCT	960 1020
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	1	11 	21 	1	ì.	Ĩ.	
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	CACATGGGTG	CTCCTTCAC	r GGTTAACTAA	CAGTATATT	COCTGTTTC	CTCTCCAACC TCCACAGTGC	1440
	CTAATAATAC	TGTGGAACT	A GGTTTTAATA	AATTTTTAA	r TGATGTTGT	ntgggcagga	1500
65	<b>ፕሮ</b> ርርር ልልርር ልር	ACCATTGTC	T CAGAGCAGGT	CCTGGCTCT	r TCCTGGCTAG	CTCCATGTTGG	1560
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Seq ID NO: 198 DNA Sequence

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35	LAHAPQPGPG	IGGDAHFDED	CRWTNNPREY	COCTORACTOS	GHSLGLSHST KI.TFDAITTI	DIGALMYPSY RGEVMFFKDR	240 300
	FYMRTNPFYP	EVELNFISVE	WPOLPNGLEA	. AYEFADRDEV	RFFKGNKYWA	VQGQNVLHGY	360
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	GFPKQIAEDI	PGIDSKIDA	FEEFGFFYFI	TGSSQLEFDE	NAKKVTHTL	K SNSWLNC	
	Co= 10 NO.	. 303 Broke	in Formence				
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65						D ITETSINGHG D RGPPGRPGLP	480
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	Protein Accession #: XP_057014 1 11 21 31 41 51	
	1 11 21 31 41 51	
10	MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA	60
	CUPCRICERG ANGIPCTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL	120
		180
	GSPENSIN INCIDENCE CONTOURS WITH THE CONTOURS WI	240
15	LPK	
13	Seq ID NO: 204 Protein sequence	
	Protein Accession #: Eos sequence	
	1 11 21 31 41 51	
20	MPGTKLTRTG APADYRVILK TSQEDELDVP DDISVRVMSS QSVLVSWVDP VLEKQKKVVA	60
20	SPOYTURYRE KGELARWDYK OLANRRVLIE NLIPDTVYEF AVRISQGERD GKWSTSVFQK	120
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	ASPAHHASTO GTSHRPSLPA SLNDNDLVDS DEDERAVGSL HPKGAFAQPR PALSPSKQSP	540
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	PARPPAARSO OHPSVPRRMT PGRAPEQQPP PPVATSQHHP GPQSRDAGRS PSQPRLSLTQ	900
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	MONEWAY PAROCATAL GAGAGGENICO GAGAGGENICA COM COLLEGE CONTROL	1080
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		1320
		1380 1440
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00	MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI	60
80	LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGGFREEFV SIDHLLPDDK	120 180
	TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEEGFREEFV SIDNLFFDUK VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH	240
	LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR	300
	LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLANAA	360

	VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF GIGCAEVNKP GVYTRVTSPL DMIHEQMERD LKT	420
5	Seq ID NO: 207 Protein Sequence Protein Accession #: CACO3433.2	
	1 11 21 31 41 51	
10	LWWEOKHCWL LKTHWTLDKY GVQADAKLLP TPQHKMLRLR LPNLKMVRLR VSFSAVVFKA	60 120 180 240 300 360
15	SLLEDITDIP KLADNIKLPR PKKLIPKAFK QYMPIFKOTS IAYFRIKELE GEPLEKINI. RGCEVVPDVN VAGRKFGIKL LIPVADGMUE MYLRCDHENQ YAQMMAACML ASKGKTMADS SYQPEVLNIL SFLRMKNINS ASQVASSLEN MDMNPECPVS PRCAKKHKSK QLAARILEAH QNVAQMPLVE AKLRFIQAMQ SLPEFGLTYY LVRFKGSKKD DILGVSYNKL IKIDAATGIP VTTMRFTNIK QMNVNMETRQ VVIEFDQNVP TAFTCLSADC KIVHEYIGGY IFLSTRSKDQ	420 480 540 600 660
20	NETLDEDLPH KLTGGQD	677
20	Seq ID NO: 208 Protein Sequence Protein Accession #: NP_114433.1 1 11 21 31 41 51	
25		
25	MASRSMRLLL LLSCLAKTOV LODIIMRPSC APGMFYHKSN CYGYFRILRN WSDAELECOS YGNGAHLASI LSLKEASTIA EYISGYGRSQ PIWIGLHDDQ KRQQWQWIDG AMYLYRSWSG KSMGGNKHCA BMSSNNNFLT WSSNECNKRQ HPLCKYRP	60 120 158
30	Seq ID NO: 209 Protein Sequence	
30	Protein Accession #: XP_051860.2 1 11 21 31 41 51	
35	MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPHNPGH DQDHHVHIGQ GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTHIL IDNGGELHAG SALCPFQGNP TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHGQKKLS WTFLNKTLHP GGMAEGGYFF ERSWGRIGVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAVPDGR ILSVAVNDEG	60 120 180 240
	SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF	300
	KLFQTEHGEY FNVSLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVRPK LTVTIDTNVN	360 420
40	STILNLEDNY QSWKPGDTLY IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGE	480
	EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKP ALGFKAAHLE	540 600
	GTELKHMGQQ LVGQYP1HFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI KDVVGYNSLG HCPFTEDGPE ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI	660
4.5	PKPRODCNAV STPWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP	720
45	LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPPLSII SARYSPHQDA DPLKPREPAI	780 840
	IRHFIAYKNO DHGAWLRGGD VWLDSCRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG ESGNVGTEMM DNRIWGPGGL DHSGRTLPIG QNFPIRGIQL YDGPINIQNC TFRKFVALEG	900
	RHTSALAFRL NNAWQSCPHN NVTGIAFEDV PITSRVFFGE PGPWFNQLDM DGDKTSVFHD	960
50	VDGSVSEYPG SYLTKNDNWL VRHPDCINVP DWRGAICSGC YAQMYIQAYK TSNLRMKIIK	1020 1080
50	NDFPSHPLYL EGALTRSTHY QQYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDSGLLFL	1140
	KLKAONEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKFTERAV VDVPMPKKLF	1200
	GSQLKTKDHP LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE	1260 1320
55	QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L	1361
	Seq ID NO: 210 Protein Sequence Protein Accession #: NP_036244.1	
	1 11 21 31 41 51	
60	MSQVKSSYSY DAPSDFINFS SLDDEGDTQN IDSWFEEKAN LENKLIGKNG TGGLFQGKTP	60
	LRKANLOQAI VTPLKPVDNT YYKEAEKENL VEQSIPSNAC SSLEVEAAIS RKTPAQPQRR	120
	SLRLSAGKOL EQKEKHHVKM KAKRCATPVI IDEILPSKKM KVSNNKKKPE EEGSAHQDTA	180
65	EKNASSPEKA KORHTVPCMP PAKQKFLKST EEQELEKSMK MQQEVVEMRK KNEEFKKLAL AGIGQPVKKS VSQVTKSVDF HFRTDERIKQ HPKNQEEYKE VNFTSELRKH PSSPARVTKG	240 300
05	CTIVKPPNLS QGKKRTPDET VSTYVPLAQQ VEDFHKRTPN RYHLRSKKDD INLLPSKSSV	360
	TKICRDPOTP VLOTKHRARA VTCKSTAELE AEELEKLQQY KFKARELDPR ILEGGPILPK	420
	KPPVKPPTEP IGFDLEIEKR IQERESKKKT EDEHFEFHSR PCPTKILEDV VGVPEKKVLP ITVPKSPAPA LKNRIRMPTK EDEEEDEPVV IKAQPVPHYG VPFKPQIPEA RTVEICPFSF	480 540
70	DSRDKERQLQ KEKKIKELQK GEVPKFKALP LPHFDTINLP EKKVKNVTQI EPFCLETDRR	600
	GALKAQTWKH QLEEELRQQK EAACFKARPN TVISQEPFVP KKEKKSVAEG LSGSLVQEPF	660 720
	QLATEKRAKE RQELEKRMAE VEAQKAQQLE EARLQEEEQK KEELARLRRE LVHKANPIRK YQGLEIKSSD QPLTVPVSPK FSTRFHC	747
75		
75	Seq ID NO: 211 Protein Sequence	
	Protein Accession #: NP_065169.1 1 11 21 31 41 51	
80.	MSRRKQAKPQ HINSEEDQGE QQPQQQTPEF ADAAPAAPAA GELGAPVNHP GNDEVASEDE ATVKRLRREE THVCEKCCAE FFSISEFLEH KKNCTKNPPV LIMNDSEGPV PSEDFSGAVL	60 120
<b>60</b> ·	SHOPTSPGSK DCHRENGGSS EDMKEKPDAE SVVYLKTETA LPPTPQDISY LAKGKVANTN	180
	VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQQLQQIQ LTEQIRIQVN	240
	MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP	300 360
	SATSSLSPGL APPTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK	200

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	GKPPNISAVD V	KPKDEAALY I	KHKCKYCSKV	FGTDSSLQIH	LRSHTGERPF V	VCSVCGHRFT	420
	TKGNLKVHPH R TSVGLPQNLS S	HPQVKANPQ I	LFAEFQDKVA	AGNG I PYALS	VPDPIDEPSL :	SLDSKPVLVT PRAGGEOGSG	480 540
	TPEPGSETLK L	QQLVENIDK I	ATTOPNECLI	CHRVLSCQSS	LKMHYRTHTG	ERPFQCKICG	600
5	RAFSTKGNLK T	HLGVHRTNT	SIKTQHSCP1	COKKETNAVM	LOCH I RATING	GQIPNTPLPE	660 720
	NPCDPTGSEP M TLGFAMMASL D	DAPGKVGPAP	FNLQROGSRE	NGSVESDGLT	NDSSSLMGDQ	EYQSRSPDIL	780
	ETTSPQALSP A	unsqaes i ks	KSPDAGSKAE	SSENSRTEME	GRSSLPSTFI :	Rapptyvkvė	840
10	VPGTPVGPST L	SPGMTPLLA SNLKVHYMTH	AQPRRQAKQH GANNNSARRG	GCTRCGKNFS RKLAIENTMA	LLGTDGKRVS	EIFPKEILAP	900 960
••	SVNVDPVVWN (	)YTSHLNGGL	AVKTNEISVI	QSGGVPTLPV			1020
	SGI SADVEKP	SATDGVPKHQ	FPHFLEENKI	AVS			1053
1.5	Seq ID NO: 2						
15	Protein Acce		P_005092 21	31	41	51	
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	MGWDLTVKML A ASQGLGPGST V	AGNEFOVSLS	SSMSVSELKA	QITQKIGVHA	POORLAVHPS	GVALQDRVPL	60 120
20	LPWLTPEGKP					V30223VQ2D	165
	C ID 110	Deep - 4 -					
	Seq ID NO: 3			•			
25	1	11	21	31	41	51	
23	 MIILIYLPLL	l Lwedtogwgf	KDGI FHNSIW	I LERAAGVYHR	I EARSGKYKLT	YAEAKAVCEF	60
	EGGHLATYKO	LEAARKIGFH	VCAAGWNAKG	RVGYPIVKPG	PNCGPGKTG1	IDYGIRLNRS	120
	ERWDAYCYNP : DLEDDPGCLA						180 240
30	QIKYVAMDPV						
	Seq ID NO:	214 Protein	sequence				
	Protein Acc	ession #: 1	NP_009046.1			<b></b>	
35	1	11 	21 	31 	41	51 	
					EARSGKYKLT		60
					PNXXFGKTGI CYWHIRLKYG		120 180
40	DLEDDPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDELPDDI IS	TGNVMTLKFL		240
40	QIKYVAMDPV	SKSSQGKNTS	TTSTGNKNFL	AGRFSHL			
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45	Ī	Ī	Ĩ	Ī	ı	1	
						LLGSKILKPR SVAQVKAMIE	60 120
			DGKMMADYGI			•	165
50	Sea ID NO:	216 Protei	n Semience				
		ession #:	NP_002349.1				
	1	11	21 I	31 i	41	51 !	
						LTLLVTTDLE	60
55						KDDSAPREKS GPQFITNSEE	120 180
		HKVNSMVAYK					205
	Sea in No.	217 Protei	n semence				
60		cession #:	NP_001889.1				
	1	11	21 	31 	41 	51 [	
	MAQYLSTLLL	LLATLAVALA	WSPKEEDRI	PGGIYNADL	N DEWVQRALHE	AISEYNKATK	60
65		RSLVKSRCQE		RTICTKSQP	N LDTCAFHEQE	ELQKKQLCSF	120
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		218 Protest cession #:	in sequence NP_009162.	ı	~		
70	1	11	21	31	41	51	
70	( MDKLKCPSFP	KCREKEKVS	) A SSENFHVGE	i N Denodrgnw	I S KKSDYLLSMI	   GYAVGLGNVW	60
	RFPYLTYSNG	GGAFLIPYA:	MLALAGLPL	F FLECSLGQF	A SLGPVSVWR	LPLFQGVGIT	120
						THOMVSTVNK TGVIVWYLA	180 240
75	LCLLLAWLIV	GAALFKGIK	S SGKVVYFTA	L FPYVVLLIL	L VRGATLEGAS	S KGISYYIGAQ	300
						CLTNCLTSVF	360 420
	LDSQFASIET	ITTTIQDLF	P KVMKKMRVP	I TLGCCLVLF	L LGLVCVTQA	3 IYWVHLIDKF	480 540
80						F VITPILLIAI B NIFQRLISCC	600
•			D MVDPKKEAD				
	Seq ID NO:	219 Prote	in sequence				
			NP_006389.				

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	1	1	21 	1	ĺ	1	
	MAPNASCLCV	HVRSEEWDLM	TFDANPYDSV	KKIKEHVRSK	TKVPVQDQVL	LLGSKILKPR	60
5	RSLSSYGIDK	EKTIHLTLKV	VKPSDEELPL	FLVESGDEAK	RHLLQVRRSS	SVAQVKAMIE	120
د	TKTGIIPETQ	IVTCNGKRLE	DGKMMADYGI	KKGNLLLLAS	ICIGG		
	Seq ID NO:	220 Proteir	sequence				
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10	1	11	21	31 	41 	51 I	
10	MKANYSAEER	FLLLGPSDWP	SLOPVLFALV		NSALVLLAVR	DPRLHTPMYY	60
	FLCHLALVDA	<b>GFTTSVVPPL</b>	LANLRGPALW	LPRSHCTAQL	CASLALGSAE	CVLLAVMALD	120
	RAAAVCRPLR	YAGLVSPRLC	RTLASASWLS	GLTNSVAQTA	LLAERPLCAP	RLLDHFICEL	180 240
15	CCSHCTAVCI.	DGDTTENQMF FYGSAIYTYL	OPAGRYNOAR	GKFVSLFYTV	VIPALNPLIY	TLRNKKVKGA	300
	ARRLLRSLGR		dragaria.	•			
	Sea ID NO:	221 Protei	n Seguence				
20		cession #: 1					
	1	11	21	31	41	51	
	   MDPPTEKLLS	RTRARRENLQ	RKMAERPTAA	I PRSMTHAKRA	ROPLSEASNO	OPLSGGEEKS	60
						DTISDSVAVP	120
25						FSPMPSEEKA	180
						GTACLSKFSS VKATSPVKST	240 300
	TSITDAKSCE	GONPELLPKT	PISPLKTGVS	KPIVKSTLSQ	TVPSKGELSR	EICLQSQSKD	360
30		KPFLERFGER					420
30						STPLKKHQGV SLKVTSDPKV	480 540
	EQKIEVIRE	EMSVDDDDIN	SSKVINDLPS	DVLEEGELD	i eksqeemdqa	LAESSEEQED	600
	aln i ssmsli	. APLAQTVGVV	SPESLVSTP	LELKDTSRSD	ESPKPGKFQF	TRVPRAESGD	660
35	SLGSEDRDLI	. YSIDAYRSQR	INCOUPER	C QVIVRKEDVI	F SKLDEKNNAF F RILLIATGKE	PCQVNIKQKM	720 780
55	KNEGPORKNI	( ASPQSEFMPS	KGSVTLSEIF	LPLKADEVCS	TVQKPDAAN	YYLIILKAGA	840
	ENMVATPLA:	S TSNSLNGDAL	. TFTTTFTLQI	VSNDFEINI	E VYSLVQKKDI	SGLDKKKKTS	900
	KSKAITPKR	L LTSITTKSNI	HSSVMASPGO	LSAVRTSNF	A LVGSYTLSLS	S SVGNTKFVLD G GNCISYWTYP	960 1020
40	DDEKRKNPI	RINLANCTS	QIEPANREF	ARRNTFELIT	VRPQREDDRI	TLVSQCRDTL	1080
	CVTKNWLSA	TKEERDLWM	KTMÖATADII	R LWQPDACYKI	P IGKP		1124
	Sec ID NO	: 222 Protei	in Semience				
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45	1	11	21	31	41	51	
		 		C ABALLICEA	e vuerement	 E TRVILVQEAG	60
	KOEELTKAL	K DIKVGPVKMI	E SVEEFEGLD	S PEFENVFVV	T DEQUEVEND	L YKADCRVIGP	120
	PVVLNCSQK	G EPLPFSCRP	L YCTSMMILV	L CPTGFRKKE	E LVRLVTLVH	H MGGVIRKDFN	180
50						D FRNEFKVPPF	240 300
						L PFEPSKKLYV R RLKETLAQLS	360
	RDTDVSPFP	P RKRPSAEHS	L SIGSLLDIS	N TPESSINYG	D TPKSCTKSS	K SSTPVPSKQS	420
55	ARWQVAKEL	Y OTESNYVNI	L ATIIQLFQV	P LEEEGQRGG	P ILAPEEIKT	I FGSIPDIFDV I IKCEKQKPRF	480 540
33	HAFLKINOA	K PECGROSLV	E LLIRPVORL	P SVALLLNDL	K KHTADENPD	K STLEKAIGSL	600
	KEVMTHINE	D KRKTEAQKQ	I FDVVYEVDG	C PANLLSSHR	S LVQRVETIS	L GEHPCDRGEQ	660
	VTLFLFNDC	L EIARKRHKV	I GTFRSPHGQ	T RPPASLKHI	H LMPLSQIKK	V LDIRETEDCH E NLIYTADPES	720 780
60	FEVNTKDME	S TLSRASRAI	K KTSKKVTRA	P SPSKTPKRA	L RRALMTSHG	S VEGRSPSSND	840
• •		T SSLAGIPSP					883
	Com ID NO	: 223 Prote	in Semience				
		ccession #:					
65	1	11	21	31	41	51	
	   MDCDAFDVE	 EV LYTIGTGSY	C PONTERY	D CKILVMKEI	D YGSMTEAER	(O MLVSEVNLLR	60
						E EFVLRVMTQL	120
70	TLALKECHI	R SDGGHTVLH	IR DLKPANVFI	D CKONVKLGI	OF GLARILNHI	T SFAKTFVGTP	
70						RE GKFRRIPYRY OL GEPEKSQDSS	
						EN LLIONYSLLKE	
	RKFLSLASI	NP ELLNLPSS	I KKKVHPSGI	ES KENIMRSEI	NS ESQLTSKSI	KC KDLKKRLHAA	420
75	QLRAQALS	DI EKNYQLKSI	Q ILGMR				445
13	Seg ID N	): 224 Prote	in Secuence	<b>a</b>			
		Accession #:	Eos seque	nce			
	1	11	21	31	41	51 !	
80	DISYENEN'	YN SSWIPGSH:	I IV SPSLLLNIJ	NN GOLLPLOIA	QG PLNSWIPP	FS GILQQQQQAQ	60
	I PGLSQFS	LS ALDQFAGLI	LP NQIPLTGE	AS FAQGAQAG	QV DPLQLQTP:	PQ TQPGPSHVMP	120
						IP FYAQFGYIPQ	
		GQ QQLAYDPQ! AV DQTITPEL!			NE MINTRADS	AG VFMPSTSPKP	271

5	Protein Acc 1     RGKEHRSRMV LNNGQLLPLQ	225 Protein ession #: e 11   QIFLFRSRSK LQGPLNSWIP GQVDPLQLQT	os sequence 21       IYHTKMKIII   PFSGILQQQQ	31     LLGFLGATLS   QAQIPGLSQF	SLSALDQFAG	LLPNQIPLTG	60 120 180
10	QPQQTVPRSP	QQTRQQQYEE QKEAINFRHD	QIPFYAQFGY	IPQLAEPAIS	QCQQQLAFDP	QLGTAPEIAV	240 300 304
15	Protein Acc	226 Proteir cession #: A 11	IP_003970.1 21 	31 	41 	51 	
20	RRKMLPTQFL KLVRGRKPLS LTYVLFLMAL DDTILSSALA	NGLKSKYYRL PLLGVLGIFG LLVILGLAVG TFLMSSFTFC ANGWVFLLAY ETGDTLYAPY	LTFAPIIGLD FSLVQDVIAI GSFTGWKRHG VSPEFWLLTK	GSTGPTRPFL EYIVLTMNRT AHIYLTMLLS QRNPMDYPVE	FGILPSICPS NVNVPSELSA IAIWVAWITL DAFCKPQLVK	CLLAHAVSLT PRRNEDFVLL LMLPDFDRRW KSYGVENRAY	60 120 180 240 300 357
25		227 Protein		•			
	1	11	21	31 1	41 	51 I	
30	EHLRDGISAR QVINELRNTS KSLEQELASP	VDFPFQPYKC KIAERAQGEL YRPKVCVLGS ILDIEDLVKS EAHNVEKMCE	FPDRALSSWG REQLCIHPEV GSKHRVCPYY	NAAAAAGDPI KKQESNHLQI LSRNLKQQAD	ACYTDIPKII HLCRKKVASR IIFMPYNYLL	Yasrthsqlt Schfynnvee Daksrrahni	60 120 180 240 300
35	ADSPSPGLNM TKGCILDSLD YKVHIHPDAG TLAPVSSFAL	ELEDIAKLKM QIIQHLAGRA HRRTAQRSDA EMQIPFPVCL	ILLRLEGAID GVFTNTAGLQ WSTTAARKRG ENPHIIDKHQ	AVELPGDDSG KLADIIQIVF KVLSYWCFSP IWVGVVPRGP	VTKPGSYIFE SVDPSEGSPG GHSMHELVRQ DGAQLSSAFD	LFAEAQITFQ SPAGLGALQS GVRSLILTSG RRFSEECLSS	360 420 480 540
40	TISAYYARVA QFLDEMKGQG RAQLPSWVRP GPFFSTRKAK SEQRAGSPGE	VVPYGLLIFF APGSTGATFL GAGGQFLSGQ HVRVYDNFGH SLDLHVPSLK EQAHSCSTLS	AVCRGKASEG EWYRQQASRA VIRDVAQFFR QRSSGSPAAG LLSEKRPAEE	LDFSDTNGRG VNQAIGRVIR VAERTMPAPA DPESSLCVEY PRGGRKKIRL	VIVTGLPYPP HRQDYGAVPL PRATAPSVRG EQEPVPARQR VSHPEEPVAG	RMDPRVVLKM CDHRFAFADA EDAVSEAKSP PRGLLAALEH AQTDRAKLFM	600 660 720 780 840 900
45	KQQFEEVCIQ HLNQGRPHLS AALTAYKQDD PGMEPPGPQE	ERLAVPPVLT	EHSIPRRQRA SQPQWGSGVP ALTTAKPEDF HRAPQPGPSR	QPVLDPTGRT RAGKQGQHAV PLLHRFSMFV SEKTGKTQSK	APDPKLTVST SAYLADARRA RPHHKQRFSQ ISSFLRQRPA	AAAQQLDPQE LGSAGCSQLL TCTDLTGRPY GTVGAGGEDA	960 1020 1080 1140 1200
50	DFQRCQACWQ ACPAAGAGCT		ACHTASRKQS AGRRDRGAAG	VMQVFWPEPH	KDHEGAGGAR	DVVPFQCPAC PVAAVPGVGA DVWPVSTAPL	1260 1320 1380 1400
55	Protein Acc	228 Proteicession #:   11	NP_057518.1 21 	31 	41 	51 	
60	EHLRDGISAR QVINELRNTS KSLEQELASP DLKGTVVIFD	KIAERAQGEL YRPKVCVLGS ILDIEDLVKS EAHNVEKMCE	FPDRALSSWG REQLCIHPEV GSKHRVCPYY ESASFDLTPH	NAAAAAGDPI KKQESNHLQI LSRNLKQQAD DLASGLDVID	ACYTDIPKII HLCRKKVASR IIPMPYNYLL QVLEEQTKAA	CLLCTTLAWR YASRTHSQLT SCHFYNNVEE DAKSRRAHNI QQGEPHPEFS LFAEAQITFQ	60 120 180 240 300 360
65	TKGCILDSLD YKVHIHPDAG TLAPVSSFAL LGKALGNIAR TISAYYARVA	QIIQHLAGRA HRRTAQRSDA EMQIPPPVCL VVPYGLLIFF APGSTGATFL	GVFTNTAGLQ WSTTAARKRG ENPHIIDKHQ PSYPVMEKSL AVCRGKASEG	KLADIIQIVF KVLSYWCFSP IWVGVVPRGP EFWRARDLAR LDFSDTNGRG	SVDPSEGSPG GHSMHELVRQ DGAQLSSAFD KMEALKPLPV VIVTGLPYPP	SPAGLGALQS GVRSLILTSG RRPSEECLSS EPRSKGSPSE RMDPRVVLKM	420 480 540 600 660
70	RAQLPSWVRP GPFFSTRKAK SEQRAGSPGE VAVKQELSQA	HVRVYDNFGH SLDLHVPSLK EQAHSCSTLS NPATFTQALQ	VIRDVAQFFR QRSSGSPAAG LLSEKRPAEE DYKGSDDFAA	VAERTMPAPA DPESSLCVEY PRGGRKKIRL LAACLGPLFA	PRATAPSVRG EQEPVPARQR VSHPEEPVAG EDPKKHNLLQ	CDHRFAFADA EDAVSEAKSP PRGLLAALEH AQTDRAKLFM GFYQFVRPHH	720 780 840 900 960
75	HLNQGRPHLS AALTAYKQDD	PRPPPTGDPG DLDKVLAVLA ERLAVPPVLT	SQPQWGSGVP ALTTAKPEDF	RAGKQGQHAV PLLHRFSMFV	SAYLADARRA RPHHKQRFSQ	AAAQQLDPQE LGSAGCSQLL TCTDLTGRPY GTVGAGGEDA	1020 1080 1140 1200 1219
80		229 Protei cession #: 11		31	41	51	
	 MPAPAPRATA	   PSVRGEDAVS	1	1	1	   SPAAGDPESS	60
•	LCVEYEQEPV	PARQRPRGLL	AALEHSEQRA	GSPGEEQAHS	CSTLSLLSEK	RPAEEPRGGR	120

5	GPLPAEDPKK PTGRTAPDPK GQHAVSAYLA FSMFVRPHHK KTQSKISSPL	EPVAGAQTOR I HNLLQGPYQF I LTVSTAAAQQ I DARRALGSAG I QRFSQTCTDL I RQRPAGTVGA I GCGAEDVVPF I	VRPHHKQQFE LDPQEHLNQG CSQLLAALTA IGRPYPGMEP GGEDAGPSQS	EVCIQLTGRG RPHLSPRPPP YKQDDDLDKV PGPQEERLAV SGPPHGPAAS	CGYRPEHSIP TGDPGSQPQW LAVLAALTTA PPVLTHRAPQ EWGEPHGRDI	RRQRAQPVLD GSGVPRAGKQ KPEDFPLLHR PGPSRSEKTG AGQQATGAPG	180 240 300 360 420 480 540 545
10		230 Protein ession #: N 11		31 	41 	51 	
15	PCRRDSPTTC AHAGFCLEHA LNVPGSSSHD	LLCLVLALPA GPCPPRHYTQ SCPPGAGVIA TLCTSCTGPP AALQLKLRRR	PWNYLERCRY PGTPSQNTQC LSTRVPGAEE	AETPTYPWRD CNVLCGEREE QPCPPGTFSA CERAVIDFVA	EARACHATHN SSSSSEQCOP PQDISIKRLQ	RACRCRTGPF HRNCTALGLA RLLQALEAPE	60 120 180 240 300
20		231 Protein cession #: N 11		31 	41 	51 	
25	PCRRDSPTTC AHAGFCLEHA LNVPGSSSHD	LLCLVLALPA GPCPPRHYTQ SCPPGAGVIA TLCTSCTGFP AALQLKLRRR	FWNYLERCRY PGTPSQNTQC LSTRVPGAEE	CNVLCGEREE QPCPPGTPSA CERAVIDPVA	EARACHATHN SSSSSEQCQP FQDISIKRLQ	RACRCRTGFF HRNCTALGLA RLLQALEAPE	60 120 180 240 300
30		232 Proteir cession #: 1					
	1	11	21	31	41	51	
35	MASSRCPAPR GLSRWAVLWL APGSADSTRL	ACSWDFPRAP GCRCLPGASL GACGVLRATV LHWGSHPTAF LVLVVLSSLG	AWLGTVLLLL GSKSENAGAQ VVSYAAALPA	ADWVLLRTAL GWLAALKPLA AALWHKLGSL	PRIFSLLVPT AALGLALPGL WVPGGQGGSG	ALPLLRVWAV ALFRELISWG NPVRRLLGCL	60 120 180 240 300
40	ENLSLFLWYL AKSSQVAIEA LLKVGILYIG	NTMGHVHSHL VRGLCLLGIM LSAMPTVRSF GQLVTSGAVS	LWGSVSLTMV ANEEGEAQKF SGNLVTFVLY	TLITLPLLFL REKLQEIKTL QMQFTQAVEV	LPKKVGKWYQ NQKEAVAYAV LLSIYPRVQK	LLEVQVRESL NSWTTSISGM AVGSSEKIFE	360 420 480 540 600
45	GSGKSTVAAL YGLTQKPTME PCVLILDDAT	LQNLYQPTGG	QLLLDGKPLP AHSFISGLPQ VEQLLYESPE	GYDTEVDEAG	VAAVGQEPQV SQLSGGQRQA	GEVTALVGPN FGRSLQENIA VALARALIRK HILFLEGGAI	660 720 780 808
50		233 Protei					
	1     MRLTVLCAVO	11     LLPGSLALPL	21     PQEAGGMSEL	31   . QWEQAQDYL!		51     NANSLEAKLK   YRIVSYTRDL	60 120
55	PHITVDRLVS APGTGLGGDA	KALNMWGKEI	GSSLGINFLY	TADIMIGFA	GAHGDSYPF1	GPGNTLAHAF VMYPTYGNGD	180 240 267
60		234 Proteices					
	1 	11	21 	31     GAVAPGAAPI	41     DLATFASTS	51     LHGLGRACGP	60
65	GPHGLRRTLA NRFRHSALSI NFSGHHCSAS ETNETSFEAG	N ALALLTSLAA D ADIFHLANLT S NFSVVYTRYC G IRVQIHSQEE	FLYQAAGLAI GLPPKDRDGI KCYTFNADPI PPYIHQLGFO	R GYLTRPHLVA H RAAGLRYPE R SSLPSRAGG G VSPGFQTFV	A MDPAAPAPV. P DMVDILNRT M GSGLEIMLD S CQEQRLTYL	A GFPAVTLCNI G HQLADMLKSC I QQEEYLPIWR P QPWGNCRAES	120 180 240 300 360
70 ·	LGGGPEGPCI EALTSEAME	F CPTPCNLTRY C RAAYGLSALI	GKEISMVRI GDLGGQMGL	P NRGSARYLA F IGASILTLL	R KYNRNETYI E ILDYIYEVS	Y IECADHTLDS R ENFLVLDVFF W DRLKRVWRRP P GGLFEDFAC	420 480 539
		: 235 Protei ccession #:					
75	1	11 	21 	31   O PSPSGGTAG	41   D PGGLSDPPY	51    P PRSGSLALGD	60
	PSSDPACSQ	S GPMEABEDSI	L PEQPEDSAQ	L QQEKPSLYI	G VRGTVVRSM	Q EVLWTRLREL	120
80	TPYDLVRMS DQTLTLEDL AAKSCGDNI EGVLDMFS1	S MQLAPQELAI V GPQMFMDCS! F QKALSQTPM! K RFRARAQLV!	R WRDQEEKRG P QALPIASED P APEMPKTRE S GHSCRLVQA	L NIIEQQQKE T TGQHDHHFL L SPTEPQDRV L PTVIRSAGC	P CRLPASKHT D PNCHICKDH P PSGLHVPAA I PSNIVWDLL	D LFLKVVHGDV H KGEVEIQRDM E PSNELLGSFE P TKALPCLPPW A SICPAKAKDV L PTRLRPLGGP	300 360

5	GLEVTHSSLL GTPPPGGAWQ QHPYSVAPAG RLSSALAAPE	QSQGRGS I AP HGFGRGQH FH	RGISAWQRPP   RDSCPHQALL	rgrgrlwpep Rhleslatms	ENWOHPGRGQ	WPPEPGLRQS	540 600 660 696
	Seq ID NO: Protein Acc		P_005282	31	41	51	
10	SGNHWPFGEI AFLWVVVAVA	ILALVGNTLA ACRLTGPLPY MAPLLVSPQT	LWLFIRDHKS LNMYASIYFL VQTNHTVVCL	GTPANVPLMH TCI SADRFLA QLYREKASHH	LAVADLSCVL IVHPVKSLKL ALVSLAVAFT	VLPTRLVYHF RRPLYAHLAC FPPITTVTCY	60 120 180 240
15	RILALANRIT LSAKSEL	SCLTSLNGAL	AVRMIAIVLA DPIMYFFVAE	KFRHALONLL	OGKRLKGPPP	SFEGKTNESS	300 360 367
20		237 Proteir ession #: h 11		31	41	51	
25	GEMPKTLACT EPHMLFDRIR	ERPSKNSHPV LVVTKGFSGT	ATKLTEEKYE QVGRIILEDY PGSNENSTQN	HDHGLLRVRM VYKIPPTTTK	VNLQVEDSGL ALCPLYTSPR	YQCVIYQPPK TVTQAPPKST	60 120 180
23	Seq ID NO:	238 Protei		AGGFLSKSLV	FSVLFAVTUR	SFVP	234
20	l	cession #: 1 11	21	31	41	51	
30	LVMGYQKKLR	SMTDKYRLHL	 YDSMKEPCFR SVADLLFVIT	LPFWAVDAVA	NWYFGNFLCK	AVHVIYTVNL	60 120
	YSSVLILAFI	SLORYLAIVH	ATNSQRPRKL FOH IMVGLIL	LAEKVVYVGV	WIPALLLTIP	DFIFANVSEA GHQKRKALKT	180 240
35	TVILILAFFA	CWLPYYIGIS	IDSPILLEII SRGSSLKILS	KQGCEFENTV	HKWISITEAL	AFFHCCLNPI	300 352
		239 Protei	n Sequence NP_036338.1				
40	1	11	21	31	41	51	
	IVWTNGTHVT	YRKDTRYKLL	GDLSRRDVSL	TIENTAVSDS	GVYCCRVEHR	SCSLFTCQNG GWFNDMKITV	60 120
45	TTTSVPTTTS IRREPTSSPL	IPTTTSVPVT YSYTTDGNDT	TTVSTFVPPM	PLPRQNHEPV NNQTQLFLER	ATSPSSPQPA	TTVPTTMTVS ETHPTTLQGA IYAGVCISVL IENSLYATD	180 240 300 359
50	Seq ID NO:	240 Protei	n Sequence				
30	1 	11 	NP_004923.1	31 	41	51 	60
55	FLLEEYTGSE KPVYILRAQA VTATDADDP1	YQYVGKLHSE INRRTGRPVE YGNSAKVVYS	QDRGDGSLKY PESEFIIKIF LLQGQPYFSV	ILSGDGAGDI IDINDNEPIF ESETGIIKT	FIINENTGDI KEVYTATVPI LLNMDRENRI	R SKRSWMWNQF QATKRLDREE MSDVGTFVVQ QYQVVIQAKD KASDADVGEN	120 180 240 300
60	AEIEYSITO LGPPKDSATV VDRHTDMDRI VNDNAPEFAI	G EGLDMFDVIT V RIVVEDVDEI I FNIDSGNGS: B FYETFVCEK	r doetoegiit P PVPSKLAYII I PTSKLLDRET A KADOLIOTLI	r vkklldfeki L qiredaqin' r llwhnitvi: H avdkddpys	K KVYTLKVEA: I TIGSVTAQD! A TEINNPKQS: G HQFSFSLAP!	S NPYVEPRFLY P DAARNPVKYS S RVPLYIKVLD E AASGSNFTIQ A CDHHGNMQSC	360 420 480 540 600
65	HAEALIHPTO DEGGGEEDTO	G LSTGALVAII D AFDIGTLRNI P PYDSLATYA	L LCIVILLVIT P EAIEDNKLRI	V VLFAALRRO R DIVPEALFL	R KKEPLIISK P RRTPTARDN	E DIRDNIVSYN T DVRDFINQRL W GPRFKKLADM	660 720 780 790
70	Protein A	: 241 Prote ccession #: 11	BAB14227.1 21	31 	41 	51 	
75	VPVSPTPPY LITFHNEAR RQGLVRSRI	Q RGHLPTGGH S TLLRTIRSV R GADIAQGTT	L AVCHFPCLL L NRTPTHLIR L TFLDSHCEV	Q EAQPHLQTQ E IILVDDFSN N RDWLQPLLH	V FLQVRCTLL D PDDCKQLIK R VKEDYTRVV	K VAGMSPWAPQ V YCTDLPPTSI L PKVKCLRNNE C PVIDIINLDT P VIDKAWFDYL	60 120 180 240 300
80	GKYDMDMDI KRTAEVWMD ESSIQKGNI CLSVITLFP	W GGENFEISF E YKQYYYAAR R QRQKCLESQ	R VWMCGGSLE P FALERPFGN R QNNQETPNL	I VPCSRVGHV V ESRLDLRKN K LSPCAKVKG	P RKKHPYVFF L RCQSFKWYL E DAKSQVWAF	D GNANTYIKNT E NIYPELSIPK T YTQQILQEEL D GTENGKEIVV	360 420 480 540 557

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Seq ID NO: 242 Protein Sequence Protein Accession #: AAH10659

	1 1	1	21 I	31 !	41 	51 	
	MRRLTRRLVL I	PVFGVLWITV	LLFFWVTKRK	LEVPTGPEVQ	TPKPSDADWD	DLWDQPDERR	60 120
5	YLNAKKWRVG I NEARSTLLRT	IRSVLNRTPT I	HLIREIILVD	DPSNDPDDCK	<b>QLIKLPKVKC</b>	LRNNERQGLV	180
	RSRIRGADIA ( SASELRGGFD	QGTTLTFLDS !	HCEVNRDWLQ	PLLHRVKEDY	TRVVCPVIDI	INLOTETYIE WEDYLGKYDM	240 300
	DMDIWGGENF !	EISFRVWMCG (	GSLEIVPCSR	VGHVPRKKHP	YVFPDGNANT	YIKNTKRTAE	360
10	KGNIRQRQKC I	YAARPFALER :	PFGNVESRLD TPNI.KI.SPCA	LRKNLRCQSF KVKGEDAKSO	WAFTYTOOI	LSIPKESSIQ	420 480
10	TLFPGAPVVL	VLCKNGDDRQ	QWTKTGSHIE	HIASHLCLDT	DMFGDGTENG	KEIVVNPCES	540
	SLMSQHWDMV :	SS					552
15	Seq ID NO:						
13	Protein Acc		21 21	31	41	51	
	 MRRLTRRLVL	DUDOUI WEEK	I I DEMINITURE	LEVENCERVO	TOKOSDADWO	DIMDOFDERR	60
20	YLNAKKWRVG	DDPYKLYAFN	QRESERISSN	RAIPDTRHLS	VLNRTPTHLI	REIILVDDFS	120
20	NDPDDCKQLI	KLPKVKCLRN VCPVIDITNI.	NERQGLVRSR DTPTY LESAS	IRGADIAQGT ELRGGFDWSL	HEOWEOLSPE	ONROWLOPLL OKARRLOPTE	180 240
	PIRTPIIAGG	LFVIDKAWFD	YLGKYDNDHD	INGGENFEIS	FRVWMCGGSL	EIVPCSRVGH	300
	VFRKKHPYVF NLRCQSFKWY	PDGNANTYIK	NTKRTAEVWM PKESSIQKGN	IRQRQKCLES	QRQNNQETPN	nvesrldlrk Lklspcakvk	360 420
25	GEDAKSQVWA	PTYTQQILQE	ELCLSVITLP	PGAPVVLVLC	KNGDDRQQWT	KTGSHIEHIA	480 519
	SHUCLDTUMF	GDGTENGKEI	VVNPCESSEM	SUMMASS			31,7
		244 Proteir ession #: N					
30	1	11	21	31	41	51	
	i Mngkvwsgpg	   FGALTSPRAH	SDFLDSHCEV	i Nrdwlopilih	RVKEDYTRVV	Chaidiinrd	60
	TETTIESASE	LRGGFDWSLH	POWEQLSPEQ	KARRLDPTEP	IRTPIIAGGL   FRKKHPYVFP	FVIDKAWFDY DGNANTYIKN	120 180
35	TKRTAEVWMD	EYKQYYYAAR	PFALERPFGN	VESRLDLRKN	LRCOSFKWYL	ENIYPELSIP	240
	KESSIQKGNI	RQRQKCLESQ	RONNOETPNL	KUSPCAKVKG TGSHIEHIAS	EDAKSQVWAF HLCLDTDMFG	TYTQQILQEE DGTENGKEIV	300 360
	VNPCESSLMS						378
40		245 Protei					
	Protein Acc	cession #:     11	NP_001209.3 21	31	41	51	
	Ī	1	1	1	Ĩ	Ī	
45	MPRRSLHAAA HSDILOYDAS	VLLLVILKEQ LTPLEFOGYN	PSSPAPVNGS LSANKOFLLT	KWTYFGPDGI NNGHSVKLNI	S NSWSKKYPSO PSDMHIQGLO	GGLLQSPIDL SRYSATQLHL	60 120
	HWGNPNDPHG	SEHTVSGQHF	AAELHIVHYN	SDLYPDAST/	NKSEGLAVI	, AVLIEMGSFN	180 240
	NPVQISQEQL	LALETALYCT	HMDDPSPREA	1 INNFRQVQK	F DERLVYTSF	NPTVLWTVFR QVQVCTAAGL	300
50	SLGIILSLAL	AGILGICIVV	VVSIWLFRR	C SIKKGDNKG	/ IYKPATKMET	ГЕАНА	354
		246 Protei					
	Protein Ac	cession #: 11	21	31	41	51	
55	MDDDC1 UAAA	VILLATI PEO	 	 	 	GGLLQSPIDL	60
55	HSDILQYDAS	LTPLEFQGYN	LSANKQFLL	I NNGHSVKLN	L PSDMHIQGL	2 SRYSATQLHL	120
	HWGNPNDPHG PSYDK I FSHL	SEHTVSGQHE OHVKYKGOEA	AAELHIVHY	N SDLYPDAST. L LPERTAEYY	A SNKSEGLAV R YRGSLTTPP	L AVLIEMGSFN C NPTVLWTVFR	180 240
60	NPVQISQEQL	LALETALYCT	HMDDPSPRE	M INNFRQVQK	F DERLVYTSF	S QGIILSLALA	300 343
UU	GILGICIVV	VSIWLFRRKS	i ikkgunkgv	1 YKPATKMET	E ADA		343
		: 247 Proteicession #:					
65	1	11	21	31	41	51	
03	MOVDETLIPE	KGPSLCSAR	   GIALVLHFC	 N PTTIAQNVI	) M NITMVAMVŅ	S TSPQSQLNDS	60
	SEVLPVDSFO	GLSKAPKSL	P AKSSILGGQ	F AIWEKWGPP	O ERSRLCSIN	SGMLLGCFTA K EYIISSLKQQ	120 180
<b>~</b> ^	VGSSKQPLP1	I KAMLRSLPI	W SICLGCFSH	Q WLVSTMVVY	I PTYISSVYH	V NIRDNGLLSA	240
70	LPFIVAWVIO	MVGGYLADF	L LTKKFRLIT	V RKIATILGS	L PSSALIVSL	P YLNSGYITAT V SGFLLSQDPE	300 360
		L FAVNLLGLL					401
	Seq ID NO	: 248 Prote	in Sequence	<b>:</b>			
75	Protein A	ccession #:		1	41	51	
	1	Ī	1	31 	ł	i	
	MPTTVDDVL	E HGGEFHFFQ E LNYTVDGDG	K QMFFLLALI P AGEASDDO	S ATFAPIYVO	SI VFLGFTPDI ST FDCVDPLAS	IR CRSPGVAELS SL DTNRSRLPLG	60 120
80	PCRDGWVYE	T PGSSIVTEF	N LVCANSWMI	D LFQSSVNV	GF FIGSMSIG	(I ADRFGRKLCL	180
						/G RRYRRTVGIF /L ISQNKNAEAM	
	RIIKHIAKK	N GKSLPASLQ	R LRLEEETGI	KK LNPSFLDL	VR TPQIRKHT	4I LMYNWFTSSV	360
	LYQGLIMHM	G LAGUNIYLD	r FYSALVEFI	PA AFMIILTI	DK IGKKYPWAJ	AS NMVAGAACLA	420

	SVPIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII TPPLVYRLTN IWLELPLMVF GVLGLVAGGL VLLLPETKGK ALPETIEEAE NMQRPRKNKE KMIYLQVQKL DIPLN	480 540 555
5	Seq ID No: 249 Protein Sequence Protein Accession 8: Eos sequence 1 11 21 31 41 51	
10	MOPAIQVWFG EDLPLSPRSP LIPRKGFGLA NVCQYDEWIA VRHEATLLEM GEDLSIWLSG LLGIKVKAEK LLEELDNOVL LCQLIDVLQN MVKTCNSEES GNFPMRKVPC KKDAASGSFF ARDITANFLH MCRDIGVOET YLFESEGLVL HKDPRQVYLC LLEIGRIVSR YGVEPPVLVK LEKEIELEET LLNTSGPEDS ISIPKSCCRH EELHEAVKHI AEDPPCSCSH RFSIEYLLSEG RYRLGDKILF IRMLRGKKVM VRVGGGWDTL GGFLLKYDPC RILQFATLEQ KILAFQKGVS	60 120 180 240 300
15	NESVPDSPAR TPOPPEMNPL SAVNMFOKON SKRSVPVSIP KSKEKGORPP GALVPASSLK GGNLGSMSVR SKLPNSPAAS SHPKLKSSKG ITKKPOAPSN NASSLASLN PVGKNTSSPA LPRTAPCISE SPRKCISSPN TPKARVIPAQ NSADLPESTL LPHKCSGKTO PKYLIGHNIIS SRDNAVSHLA AHSNSSSKCP KLPKANIPVR PKPSFOSSAK MTKTSSKTIA TGLGTOSOPS DGAPOAKNVP AQKLKSALNL NQPVSVSSVS PVKATOKSKD KNIVSATKKQ PONKSAFOKT GPSSLKSPGR TPLSIVSLPQ SSTKTOTAPK SAQTVAKSOH STKOPPRSGK TPASITKPPS	360 420 480 540 600 660
20	SVKDADSGDK KPTAKKKEDD DHYFVMTGSK KPRK	694
25	Seq ID NO: 250 Protein Sequence Protein Accession #: NP_001035.1  1 11 21 31 41 51	60 120 180
30	NISMISPICS DAHPGDSSGD SSGLMDTFGT TPAAEFFERG VLHLHQSHGI DDLGPFMQL TACLVLVIVL LYFSLMKGVK TSGKVVWHITA TMPTVVULTAL LLRGVTLPGA IDGIRFMGL DFYRLCEASV WIDAATQVCP SLGVGFGVLI AFSSYNKFIN NCYRDAIVTT SINSLTSFSS GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAMAVV FPIMLLTLGI DEAMCHMEN LTGLIDEFDI. LHBHELFTI. PIVLATFLLS LFCVTNGGIY VFTLLDHFAA	240 300 360 420 480
35	GTSILFGVLI EAIGVANFYG VGQFSDDIQQ MTGQRPSLYW RLCMKLVSPC FLLFVVVVSI VTFRPPHYGA YIFPDMANAL GWVIATSSMA MVPIYAAYKP CSLPGSFREK LAYAIAPEKD RELVDRGEVR QFTLRHWLKV	540 600 620
40	Seq ID NO: 251 Protein Sequence Protein Accession #: NP_071356.1  1 11 21 31 41 51	60 120
45	LAGPRAGVSK RHLRGDQITW IGGNEEGCEA ISFLLSLIDR LVLYCGSRIG KYYVKERSKA MVACYEGNOT GYVRHVDNPN GDGRCITCIY YLNKWMDAKL HGGILRIFPE GKSFIADVEP IFDRLLFFWS DRRNPHEVQP SYATRYAMTV WYFDAEERAE AKKKFRNLTR KTESALTED	180 239
50	Seq ID NO: 252 Protein Sequence Protein Accession #: NP_647475.1  1 11 21 31 41 51	60 120 180
55	HKVAQQQRHE EKQHEKIQHE QSQEGLEDHA HEDEVARIA MAREKESAN TOTALIHLERDCQE LFQVGERQSG LFEIQPGSSP PFLVNCKNTS DGGATTIQRR HEGSVDFMRP MEAYKAGFGD PHGEFWLGLE KVHSITGDRN SRLAVQLRDM DGNAELLQFS VHLGGEDTAY SLQLTAPVAG QLGATTVPPS GLSVPFSTMD QDHDLRRDKN CAKSLSGGWM FGTCSHSNLN GQYFRSIPQQ RQKLKKGIFW KTWRGRYYPL QATTMLIQPN AAEAAS	240 300 360 406
60	Seq ID NO: 253 Protein Sequence Protein Accession #: NP_001207.1 1 11 21 31 41 51	
65	MAPLCPSPHL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL GEEDLPSKED SPREEDPPGE EDLPGEBOLP GEEDLPSKEP KSEEGSLKL EDLPTVEAPG DPGEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRP QSPVDIRPQL AAGFALREL ELLGFQLPPL PERRLRNNGH SVQLTLPPGL EMALGPGREY RALQHLHUMG AAGRPGSEHT VEGHRPPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPENSAYE QLLSRLEETA BEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS DTLWGPGDSR LQLNPRATQP LMGRVIEASF PAGVDSSPRA AEPVQLMSCL AAGDILALVF	120 180 240 300 360 420
70	GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA	459
75	Seq ID NO: 254 Protein Sequence Protein Accession #: NP_003030.1  1 11 21 31 41 51                           MEQQDOSMIC GRITIVULALA TLIAAFGSSF QYGYNVAAVN SPALLMQQFY NETYYGRTGE FMEDFPLILL WSVTVSMFPF GGFIGSLLVG PLVNKFGRKG ALLFNNIFSI VPATLMGCSF VATSFELIII SRLLVGICAG VSSNVVPMUL GELAPKNURG ALGVVPQLFI TVGILVAQIF	120
80	GERNLLANVD GWPILLGLTG VPAALQLELL PFFPESPRYL LIQKKDEAAA KKALQTLRGG DSVDREVAEI RQEDEAEKAA GFISVLKLFR MRSENGLLS IIVLMGGQQL SGVMAIYYY DQIYLSAGVP EEHVQYYTAG TGAVNVVMTF CAVFVVELLG RELLLLGFS ICLIACCYVL AALALQDTVS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVH LSMFTYGLIF PFIQEGLGPY SFIVFAVICL LTTIYIFLIV PETKAKTFIE INQIFTKOMI VSEVYPEKEE LKELPPVTSE Q	240 300 360 4420

		255 Protein					
	Protein Acc	ession #: N 11	21	31	41	51	
5	 MPEEGSGCSV QLNHTGPQQD	 RRRPYGCVLR PRLYWQGGPA GICSPASRSI	 AALVPLVAGL LGRSFLHGPE	LDKGQLRIHR	   PAQAQQQLPL   DGIYMVHIQV   LARGDTLCTN	TLAICSSTTA	60 120 180 193
10	Seq ID NO:	256 Proteir cession #: N		31	41	51	
15	NKTGFQEVFD SSVKQSRTNL	PPHYELFSLR	DKEISADLAD FAQPQPMKTF	LSEELDNYQR	SILVQVKQPR MRRSSTASRC FKQGHECPEQ	IHDHHCGSQA	60 120 180 201
20		257 Protein ceasion #: 1 11		e 31 	<b>41</b> 	51 	
25	HELQSVLAMQ DIKTRLEVEI	SSPEGTLADT ETYHRLLGGE	EAGYVAQLSE GGSEAREAES	IKMYISILEE	AVSSAKSEIM QICQIRGETE		60 120 152
30		258 Protei: cession #: 1 11		31	41	51	
	 MRQTLPCIYF NQLRRLPAAN FCTNLTELHL	   WGGLLPFGML   PTRYSQLTSL   MSNSIOKIKN	CASSTIKCTV DVGFNTISKL NPFVKQKNLI	SHEVADOSHL EPELCOKLPM TLDLSHNGLS	KLTQVPDDLP KKYLNLQHNE STKLGTQVQL	† TNITVLNLTH LSQLSDKTFA ENLQELLLSN	60 120 180
35	NKIQALKSEE LCLELANTSI EYFFLEYNNI NMEDNDIPGI	LDIFANSSLK RNLSLSNSQL QHLFSHSLHG KSNMFTGLIN	KLELSSNOIK STTSNTTFLG LFNVRYLNLK LKYLSLSNSF	EFSPGCFHAI LKWTNLTMLD RSFTKQSISL TSLRTLTNET	GRLFGLFLNN LSYNNLNVVG ASLPKIDDFS FVSLAHSPLH	VQLGPSLTEK NDSFAWLPQL FQWLKCLEHL ILNLTKNKIS	240 300 360 420
40	SLQRLMLRRV NLARLWKHAN LPASVFNNQV	ALKNVDSSPS PGGPIYFLKG SLKSLNLQKN	PFQPLRNLTI LSHLHILNLE LITSVEKKVE	LDLSNNNIAN SNGFDEIPVE GPAFRNLTEI	VFKDLFELKI	CESIAWFVNW	480 540 600 660 720
45	LLIHFEGWRI DQSLKFCLEE	SFYWNVSVHR RDFEAGVFEL	VLGFKEIDRO EAIVNSIKRS	TEQFEYAAYI RKIIFVITH	I HAYKDKOW\ LLKOPLCKRE	WEHPSSMEKE KVHHAVQQAI HKLQVALGSK	780 840 900 904
50		: 259 Protei ccession #: 11		31 I	<b>41</b> 1	51 	
55	LKSMTDIYLI LLTIDRYLAV HFPYSQYQFI MIVYFLFWAI	L NLAISDLFFI V VHAVFALKAI W KNFQTLKIVI P YNIVLLLNTI	L LTVPFWAHY/ R TVTFGVVTSV I LGLVLPLLVI F QEFFGLNNC	A AAQWDFGNTH / ITWVVAVFA: 4 VICYSGILK: S SSNRLDQAM	M CQLLTGLYF: 5 LPGIIFTRS( F LLRCRNEKK)	VILILINCKR GFFSGIFFII KEGLHYTCSS HRAVRLIFTI CINPIIYAFV	60 120 180 240 300 352
60		: 260 Prote: ccession #: 11		ce 31	41	, 51 1	
65	ADGLKGEKG GERGPSGLP	E SASDSLQES	L AQLIVEPGP L PGTKGEKGR	P GPPGPPGPM P GEPGLDGFP	G LQG1QGPKG	A GEMGLSGLPG L DGAKGEKGAS E RGEKGERGVP	60 120 180 216
70	Protein A 1	: 261 Prote ccession #: 11	NP_004852.	31 	41 	51	
75	AVIRANGSA FARSLVQDY VPLTWKLSA EVERRFHLV NMLDSHLYR	G ECOPRRNIV R PGACFNIIC G DKLTEFLOD L LOEYFDESL H FNASFWRKV	F LKTHKTASS N HMRFHYDEV P DRYYDPNGF V LLKDLLCWE E AFGRERMAR	T LLNILFRFG R GLVPTNAIF N AHYLRNLLF L EDVLYFKLN E VAALRHANE	C KHRLKFAFF I TVLRDPARL P DLGYDNSLD IA RRDSPVPRL R MRTICIDGO	A SCSPPALEPE N GRNDFDYPTF F ESSFHYFGPV P SSPQVQEHIL S GELYGRATAW H AVDAAAIQDE V TKLWKFIRDF	240 300
80	LRW						423
		): 262 Prote accession #: 11			41	51	

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	MASVLSRRLG	i Krsllgarvl	GPSASEGPSA	APPSEPLLEG	AAPQPFTTSD	DTPCQEQPKE	60
	VLKAPSTSGL (	QQVAFQPGQK	VYVWYGGQEC	TGLVEQHSWM	EGQVTVWLLE -	QKLQVCCRVE	120
5	EVWLAELQGP PVVQSPPGTE	CPQAPPLEPG	AQALAYRPVS	RNIDVPKRKS	DAVENDENMA	AMVLTSLSCS CDDUDOASPK	180 240
,	YLGDAFGSPO	TDHGFETDPD	PFLLDEPAPR	KRKNSVKVMY	KCLWPNCGKV	LRSIVGIKRH	300
	VKALHLGDTV	DSDQFKREED	FYYTEVQLKE	ESAAAAAAA	AGTPVPGTPT	SEPAPTPSMT	360
	GLPLSALPPP	LHKAQSSGPE	HPGPESSLPS	GALSKSAPGS	<b>FWHIQADHAY</b>	QALPSFQ1PV	420
10	SPHIYTSVSW				KSHLIVTSPP	RAQSGARKAR	480 513
10	GEAKKCRKVY	GIERROQWCI	ACRWANACOR	FLD			
	Seq ID NO:						
	Protein Acc				43	E3	
15	1	11	21	31 i	41	51 1	
13	MRENYETLVS	VGTAELLPLS	AFLSPSEPGR	AVGGGSHADE	GQEPAGCGDP	QGGQPRHSLH	60
	LTALVOLVKE	<b>IPEFLFGEVK</b>	GAMDSPESES	RGASLDGERA	SPEAAAAREP	CPLRGLLSCL	120
	PDGPTSQPHL	ATTPTDSSCS	SGPTGDGVQG	SPLPIKTADK	PWPTRKEGPG	ALGGEPSPPT	180 240
20	HSPSRRKSHR TCDI.TDADIG	PCSPPWAVKT	PAVSCOCPLO	GLLHCLKELD	PGPRHPETSP EAQDRHPSPS	GVGNRRLQEN	300
20	PGAWKRGSGG	<b>PGYLLTPPPH</b>	PDLGAGGLLS	VICHENSWVQS	PPGPASCOPG	RQPLSPSATG	360
	DTRGVPQPSW	<b>GPEAQAASAS</b>	SSPLEALEAC	LKGIPPNGSS	PSQLPPTSCS	QNPQPGDSRS	420
	QKPELQPHRS	HSEEATREPV	LPLGLQSCVR	DGPSRPLAPK	GTPTSPSSSS CSSAADRGPR	RAEPRNWTAD	480 540
25	KEGLRAEACE	SARLGOGRGE	APTRSLHLVS	POVFTSSCVP	ACHORGEKOP	GATRPGVWRW	600
	LPFCSAPKPS	PLHCLESALR	GILPVRPLRF	ACVGGPSPSP	SPGSSSSFSG	SEGEDPRPEP	660
	ELWKPLPQER	DRLPSCKPPV	PLSPCPGGTP	AGSSGGSPGE	DPRRTEPRYC	SGLGAGTAQD DDF1.DDDFAA	720 780
	PCPVSQLEKR PPVI.PASSIA	PRVSEASRGL	OELHSIGAAL	ARTHERLLPU	GPPELPSESP LAGLAQEVAT	MRTQVNRLGR	840
30	RPOGPGPMGQ	ASWMWTLPRG	PRWAHGPGHR	HLPYWRQKGP	TRPKPKILRG	QGESCRAGDL	900
	QGLSRGTARR	ARPLPPDAPP	AEPPGLHCSS	SQQLLSSTPS	CHAAPPAHPL	LAHTGGHQSP	960
	LPPLVPAALP EHRDPRWGAH		ADADVPTSGV	APDGIPERPK	EPSSLIGGVQ	RALQEELWGG	1020 1030
	ENROPEMONE						
35	Seq ID NO:	264 Protei	n Seguence				
		cession #:		•	41	51	
	1	11	21 i	31 	î.	î	
	PAGCGDPQGG	QPRHSLHLTA	LVQLVKEIPE	PLFGEVKGAN	DSPESESRGA	SLOGERASPE	60
40	AAAREPCPLR	GLLSCLPDGP	TSQPHLATTE	TOSSCSSGPT	GDGVQGSPLP	IKTADKPWPT	120
	RKEGPGALGG	EPSPPTHSPS	RRKSHRGQE	R GTSEAGISPO	CDCPLOGLING	LKEILVPGPR CLKELPEAQD	180 240
	RHPSPSGVGN	RRLQENPGA	KRGSGGPGYI	LTPPPHPDLO	AGGLLSVKME	NSWVQSPPGP	300
45	ASCOPGROPL	SPSATGDTRO	VPQPSWGPE	A QAASASSSPI	. EALEACLKGI	PPNGSSPSQL	360
45	PPTSCSQNPQ	PGDSRSQKPE	LOPHRSHSE	E ATREPVLPLO	LOSCVRDGPS	RPLAPRGTPT	420 480
	ADROPPRAER	PNWTADKEC	APKPSPLHCI	L ESALRGILP	RPLRFACVGO	LRPAWPCSSA PSPSPSPGSS	540
	SSFSGSEGED	PRPEPDLWK	LPQERDRLP	S CKPPVPLSP	PGGTPAGSSC	GSPGEDPRRT	600
50	EPRYCSGLGA	GEPGVS					616
30	Sea ID NO:	265 Prote	in Sequence				
			AAH29071.1				
	1	11	21	31	41	51	
55	(	Poctoren N	E NONT NOCCO	D CAMEUACIII	) 	LLMVRASRRS	60
33	GKTSAVLKA	ROSVSGRKN	S TSKDLVTLG	A SSLREERGH	P LHPRHRKAVI	LRTRGRTRGW	120
	VOTLARMSRI	R TRGPVERAA	A AAAAAAGGD	A GHAPFPPPP.	A ADGARAPRS	GQVTPRGLRL	180
			L GFRESDSAK	P ASLRLLQHT	P SARRNYRIA	ARLMRSNYPP	240 256
60	PLSSAALRG	A GPIRKN					
•			in Sequence				
			NP_002095.		41	51	
	1	11	21 1	31 !	i.	1	
65	MTKPSSFSL	P FLIVGAYMT	H VCFNMEIIG	G KEVSPHSRP	F MASIQYGGH	H VCGGVLIDPQ	60
	WVLTAAHCO	Y RFTKGQSPT	V VLGAHSLSK	N EASKQTLEI	K KFIPFSRVT	S DPQSNDIMLV	120
	KLQTAAKLN	K HVKMLHIRS	K TSLRSGTKO	K VTGWGATDF	D SLRPSDTLR	E VTVTVLSRKL G GHECGVATKP	180 240
		Y QTWIKSNLV		C KGDSGGPD1	C KOVINALVO	G GILDCOTTILL	264
70							
			in Sequence				
		ccession #:	NP_443179. 21	.1 31	41	51	
	1	ī	Ì	1	1	- 1	
75	MOVNTLFET	S OVPDWSDPE	O VOVOETVRE	T ISCSOMPA		T GTTTISFSNL	
	GGVHKENAS	L AQHSEVKPO	T CGPQQEEK(	D ROGNIPONE	R EDLKYEQSI	S EANDETMSPG	120 180
	VFSRHLPKD CEDTIDSIN	A KAUFKEPVA G TPVDNYSPA	N SVASPEPTI DE ICSVDTELJ	AE GONKVSDIA	S SNDKTLEVE	M ECFEASDQGT P QTQVSETSVS	240
	TCKSSKDGN	S VMSPLFIST	F TLNISHTA	SE GATGENLAI	CV EKSTYPLAS	T VHAGQEQPSP	300
80	SNSGGLDET	Q LLSSENNPI	V QFKEGGDK	SP SPSAADTT	T PASYSSIVS	P PWEKPTTLTA	360
	NNECFOATR	E TVTIATEVI	IP AKYLAVSII	PE DICHAGGTEI	K FPRASHEKV	S QFPSQVQVDH D KSQTVDRADF	420
	RSYEENFOR	R GSETKOGV	O OSLSOOGS	LS APDFOOSLI	T TSAAQEER	L VPTAPSPASS	540
	REGAGORSO	W GTRVSVVA	ET AGEEDSQA	LS NVPSLSDII	L EESKEYRPO	N WEAGNKLKII	600

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5	PEDAESALAD SRESHKGEEP TISVIMRSLS SRGFSQPRLL ESSVDPVDEK ELSVTDSLSA ASETGGKENV NNVSQDQEK QLKMDHTAFF KKPLTCPKIL ESSVDPIDEI SVIETTRAGK PEPSETTPGG AREGGSMDG NNGHEAEIQS AILQVPCLQG TILSENRISR SQGSMKQEA EQIQPEBAKT AIWQVLQPSE GGERIPSGCS IGQIQESSDG SLGEARQSKK DKAELISPTS PLSSCLPIMT MSSLGVDTHN STGQIHDVPE MDIVEPRKRQ YVFPVSQKRG TIENERGKPL	660 720 780 840 900 960
10	RELEKAPKLL ODPOCKGTIG CAKKSREREK SLEARAGKSP GTLTAVTGSE EVERKPEAPG SGHLAEGVKK KILSRVAALR LKLEEKENIR KNSAFLKKMP KLETSLSHTE EKQDPKKPSC KREGRAPVLL KKIQAEMPPE HSGNVKLSCQ FAEIHEDSTI CHTKDSKSIA QVQRSAGDNS TVSPAIVQAS PKDQGLYYCC IKNSYGKVTA EFNLTABVLK QLSSRQDTKG CEELEFSQLI FKEDFLIDSY FGGRLRGQIA TEELHFGEGV HRKAFRSTVM HGLMPVFKPG HACVLKVHNA LAYGTRINDE LIQRYYKLAA QECYVONTAR YYAKIYAAEA QPLEGFGEVP EIIPIFLIHR	1080 1140 1200 1260 1320 1380
15	PENNIPYATV EEELIGEFVK YSIRDGKEIN FLRRESEAGQ KCCTFQHWVY QKTSGCLLVT DMQGVGMKLT DVGIATLARG YKGFKGNCSM TFIDQFKALR QCNKYCKMLG LKSLQNNNQK QKQPSIGKSK VQTNSMTVKK AGPETPGEKK T	1440 1500 1531
20	Seq ID NO: 268 Protein Sequence Protein Accession #: NP_602293.1  1 11 21 31 41 51                                 MGKQNSKLRP EVLQDLRENT EFTDHELQEW YKGFLKDCPT GHLTVDEFKK IYANFFPYGD ASKFAEHVPR TFDTNGDGTI DFREFIIALS VYSRGKLEQK LKWAFSMYDL DGNGYISRSE	60 120 180
25	MLEIVQAIYK MVSSVMKMPE DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV RLLQCDPSSA SQF	193
30	Seq ID NO: 269 Protein Sequence Protein Accession #: NP_002140.2  1 11 21 31 41 51	60
35	ASKFAEHVFR TFDTNGDGTI DFREFIIALS VTSRGKLEQK LKWAFSMYDL DGNGYISRSE MLEIVQAIYK MVSSVMKMPE DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV RLLQCDPSSA SQF	120 180 193
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40	MGNAQERPSE TIDRERKRLV ETLQADSGLL LDALLARGVL TGPEYEALDA LPDAERRVRR LLLLVGKGE AACQELLRCA QRTACAPDPA WOWQHVGPGY RDRSYDPPCP GHWTPEAPGS GTTCPGLPRA SDPDEAGGPE GSEAVQSGTP EEPEPELEAE ASKEAEPEPE PEPELEPEAE AEPEPELEPE PDPEPEPFE ERDESEDS	60 120 180 208
45	Seq ID NO: 271 Protein Sequence Protein Accession #: NP_004198.1 1 11 21 31 41 51	
50	MGGAVVDEGP TGVKAPDGGM GMAVLFGCFV ITGFSYAFFK AVSVFFKELI QEFGIGYSDT AMISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGLFASL GMVAASFCRS IIQVYLTTGV ITGGELALMF QPSLIMLMRY FSKRRPMANG LAAAGSPVPL CALSPLGQLL ODRYGWRGGF ELLGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFRDRGFVL YAVAASVMVL GLFVPPVFVV SYAKOLGVPD TKAAFLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSF	60 120 180 240 300
55	SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSSAIGLVL LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLLGNFFCI RKKPKEPQPE VAAAEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV	360 420 465
60	Seq ID NO: 272 Protein Sequence Protein Accession #: NP_060705.1 1' 11 21 31 41 51	60
65	LVDIGKOKLP DOSETPLPPI LLGRLGSDPO KKTVCIYGHL DVQPAALEGG MDSEPFTLVE RDGKLYGRGS TDDKGPVAGH INALEAYQKT GQEIPVNVRF CLEGMEESGS EGLDELIFAR KDTFFKOVDY VCISDNYMLG KKKPCITYGL RGICYPFIEV ECSNKOLHSG VYGGSVHEAM TDLILLAGSL VDKRGNILIP GIMEAVAAVT EEEHKLYDDI DFDIEFFAKD VGAQILLLASH LTKKPAELRS PREFKVYMCH GGKPWWSDFS RBHYLAGRRA MKTVFGVEPD LTREGGSIPV	120 180 240 300 360 420
70	TLTFQEATGK NVMLLPVGSA DDGAHSQNEK LNRYNYIEGT KMLAAYLYEV SQLKD	475
	Seq ID NO: 273 Protein Sequence Protein Accession #: AP258592_1 1 11 21 31 41 51	
75	MAALTILFKY IDENQDRYIK KLAKHVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE LVDIGKQKEI PVNVRFCLEG MEESGSEGLD ELIFARKDTF FKDVDYVCIS DNYMLGKKKP CITYGLRGIC YFFIEVECSN KDLHSGVYGG SVHEANTDLI LLMGSLVDKR GNILIPGINE AVAAVTEEEH KLYDDIDFDI EEFAKDVGAQ ILLHSHKKDI LMHRWRYPSL SLHGIEGAFS	240
80	GSGAKTVIPR KVVGKFSIRL VPNMTPEVVG EQVTSYLTKK FAELRSPNEF KVYMCHGGKP WYSDFSHPHY LAGRRAMKTV FGVEPDLTRE GGSIPVTLTF QEATGKNVML LPVGSADDGA HSQNEKLNRY NYIEGTKMLA AYLYEVSQLK D	300 360 391
	Seq ID NO: 274 Protein Sequence Protein Accession #: NP_060871.1	

	1 11 21 31 41 51	
		60 120
5	EKDEAKHALK EPOINOGPEN ALPANDAISL ARCEDITAGE ARCEDITAGE CONTRACTOR	180
_	AGTKPYMAPE VFQVYMDRGP GYSYPVDMWS LGITAYELLR GWRPYEIHSV TPIDEILNMF	240
		300 360
	ALMYONING PILEPEDITE CONTENTION WINDOWS MEDICAL MEDICA	414
10		
	Seq ID NO: 275 Protein Sequence Protein Accession #: NP_004198.1	
	1 11 21 31 41 51	
1.5	1 I I I I I I I I I I I I I I I I I I I	60
15	MOGWANDOB ICAVIEDOGM CHMARIGETA TICEDINTER VICTIONER STATEMENT	120
	ITGLGLALNF OPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGWRGGF	180
	LILGGLLINC CVCAALMRPL VVTAQPGSGP PRPSRRLLDL SVFRDRGFVL YAVAASVMVL GLFVPPVFVV SYAKDLGVPD TKAAFLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSF	240 300
20	SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSSAIGLVL	360
20	LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLLGNFFCI RKKPKEPQPE	420
	VAAAEEEKLH KPPADSGVDL REVEHFLKAB PEKNGEVVHT PETSV	465
	Seq ID NO: 276 Protein Sequence	
25	Protein Accession #: NP_006589.1	
	1 11 21 31 41 51	
	MPTNFTVVPV BAHADGGGDE TAERTEAPGT PEGPEPERPS PGDGNPRENS PFLNNVEVEQ	60
30	ESFFEGINMA LFEEEMDSNP MYSSLLIKLA NYTHLSQGVV EHEEDESSR REAKAPRMGT FIGVYLPCLQ NILGVILFLR LTWIVGVAGV LESFLIVAMC CTCTMLTAIS MSAIATNGVV	120 180
30	PAGGSYYMIS RSLGPEFGGA VGLCFYLGTT FAGAMYILGT IEIFLTYISP GAAIFQAEAA	240
	GGEAAAMLHN MRVYGTCTLV LMALVVFVGV KYVNKLALVF LACVVLSILA IYAGVIKSAF	300 360
	DPPDIPVCLL GNRTLSRRSF DACVKAYGIH NNSATSALWG LFCNGSQPSA ACDEYFIQNN VTEIQGIPGA ASGVFLENLW STYAHAGAFV EKKGVPSVPV AEESRASTLP YVLTDIAASF	420
35	TLLVGIYFPS VTGIMAGSNR SGDLKDAQKS IPTGTILAIV TTSFIYLSCI VLFGACIEGV	480
	VLRDKFGEAL QGNLVIGMLA WPSPWVIVIG SPFSTCGAGL QTLTGAPRIL QAIARDGIVP	540 600
	FLOVFGHGKA NGEPTWALLL TVLICETGIL IASLDSVAPI LSMFFLMCYL FVNLACAVQT LLRTPNWRPR FKFYHWTLSP LGMSLCLALM FICSWYYALS AMLIAGCIYK YIEYRGAEKE	660
40	WGDGIRGLSL NAARYALLRV EHGPPHTKNW RPQVLVMLNL DAEQAVKHPR LLSFTSQLKA	720
40	GKGLTIVGSV LEGTYLDKHM EAQRAEENIR SLMSTEKTKG FCQLVVSSSL RDGMSHLIQS AGLGGLKHNT VLMAWPASMK QEDNPFSWKN FVDTVRDTTA AHQALLVAKN VDSFPQNQER	780 840
	FGGGHIDVWW IVHDGGMLML LPFLLRQHKV WRKCRMRIFT VAQVDDNSIQ MKKDLQMFLY	900
	HLRISAEVEV VEMVENDISA FTYERTLMME QRSQMLKQMQ LSKNEQEREA QLIHDRNTAS	960
45	HTAAAARTQA PPTPDKVQMT WTREKLIAEK YRSRDTSLSG FKDLFSMKPD QSNVRRMHTA VKLNGVVLNK SQDAQLVLLN MPGPPKNRQG DENYMEPLEV LTEGLNRVLL VRGGGREVIT	1020 1080
73	IYS	1083
	Seq ID NO: 277 Protein Sequence Protein Accession #: NP_004576.1	
50	1 11 21 31 41 51	
	MASPHQEPKP GDLIEIFRLG YEHWALYIGD GYVIHLAPPS EYPGAGSSSV FSVLSNSAEV	60
	KRGRLEDVVG GCCYRVNNSL DHEYQPRPVE VIISSAKEMV GQKMKYSIVS RNCEHFVAQL	120
55	RYGKSRCKQV EKAKVEVGVA TALGILVVAG CSFAIRRYQK KATA	164
22	Seq ID NO: 278 Protein Sequence	
	Protein Accession #: NP_004687.1	
	1 11 21 31 41 51	
60	MUKREGKVOP YTKTLDGGMG WMIVIHPFLV NVFVMGMTKT FAIFFVVFQE EFEGTSEQIG	60
	WIGSIMSSLR FCAGPLVAII CDILGEKTTS ILGAFVVTGG YLISSWATSI PFLCVTMGLL	120 180
	PCLGSAFLYQ VAAVVTTKYF KKRLALSTAI ARSGMGLTFL LAPFTKFLID LYDMTGALIL FGAIALNLVP SSMLLRPIHI KSENNSGIKD KGSSLSAHGP EAHATETHCH ETEESTIKDS	240
	TTOKAGLPSK NLTVSQNQSE EFYNGPNRNR LLLKSDEESD KVISWSCKQL PDISLFRNPF	300
65	PYIPTWSFLL SQLAYFIPTF HLVARAKTLG IDIMDASYLV SVAGILETVS QIISGWVADQ NWIKKYHYHK SYLILOGITN LLAPLATTFP LLMTYTICFA IFAGGYLALI LPVLVDLCRN	360 420
	STVNRFLGLA SFFAGMAVLS GPPIAGWLYD YTQTYNGSFY FSGICYLLS VSFFFVPLAE	480
	RWKNSLT	487
70	Seq ID NO: 279 Protein Sequence	
	Protein Accession #: NP_000349.1	
	1 11 21 31 41 51	
		60
75	YFTNCKOWYO RKICGKSTVI SYECCPGYEK VPGEKGCPAA LPLSNLYETL GVVGSTTTQL	120
	YTDRTEKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSLV SNVNIELLNA LRYHMVGRRV LTDELKHGMT LTSMYQNSNI QIHHYPNGIV TVNCARLLKA DHHATNGVVH LIDKVISTIT	180 240
	NNIOOIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLLAP TNEAFEKIPS ETLNRILGDP	300
80	EALROLLNIH ILKSAMCAEA IVAGLSVETL EGTTLEVGCS GDMLTINGKA IISNKDILAT	360 420
٥V	NGVIHYIDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF KDGTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLETLGG KKLRVFVYRN SLCIENSCIA	480
	AHDKRGRYGT LFTMDRVLTP PMGTVMDVLK GDNRFSMLVA AIQSAGLTET LNREGVYTVF	540
	APTNEAFRAL PPRERSRLLG DAKELANILK YHIGDEILVS GGIGALVRLK SLOGDKLEVS LIGHTVVSVNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF	600 660
	PRINAASANY ELAMELITAN TAPAANATIN APALANNAS EKONETYDON PETLYNWONE	500

	SRASQRSVRL A	PVYQKLLER I	икн				683
5	Seq ID NO: 2 Protein Acce	ession #: N	P_663623		11	51	
J	   MEGSGGGAGE     FLNGAPFCWE (	RAPLLGARRA	AAAAAAAGAP	AGRRAACGAV I	LLTELLERAA	 FYGITSNLVL	60 120
10	PLLAAPATRA / DQVKDRGPEA : LCGQSVFITK / MSHGGPFTEE !	TRRPFNWPYW PPDGSAFTDH	SINLGAILSL FKILTYSCCS	GGIAYIQQNV QKRSGERQSN	SFVTGYAIPT GEGIGVFQQS	VCVGLAFVVF SKQSLFDSCK	180 240 300 360
15	PHTLPAAWLT I ILESKRLNLV I PKSMQSAIMG AIQGATLLLF	MFDAVLILLL KEKTINQTIG LFPFPSGVGS	IPLKDKLVDP NVVYHAADLS FVGSGLLALV	ILRRHGLLPS LWWQVPQYLL SIKAIGWMSS	SLKRIAVGMF IGISEIFASI	PVMCSAFAAG AGLEFAYSAA	420 480 540 577
	Seq ID NO:	281 Protein	Sequence				
20	Protein Acc		P_001241.1 21	31	41	51	
		WNRETHCHOH	EPPTACREKQ KYCDPNLGLR TICEPCPVGF	VQQKGTSETD	TICTCEEGWH	CTSEACESCV	60 120 180
25	KTDVVCGPQD	RLRALVVIPI	IFGILFAILL VTQEDGKESR	VLVPIKKVAK			240 277
	Seq ID NO: Protein Acc						
30	1	11	21	31	41	51 1	
	MEQRGQNAPA	ASGARKRHGP	GPREARGARP CPPGHH1SED	GLRVPKTLVL	VVAAVLLLVS	AESALITOOD	60 120
25	SCEVELSPCT	TTRNTVCQCE	EGTFREEDSP	EMCRKCRTGC	PRGMVKVGDC	TPWSDIECVH	180
35			SPGTPASPCS SSQRPGAEDN				240 300
			QRRRLLVPAN TLYTML1KWV				360 420
40	HLLSSGKFMY		1D11hD1kwv	MKI GKDIIS VII	120071007120		440
40	Seg ID NO:	283 Protei	n Sequence				
	Protein Acc	ession #: 1	NP_671716.1 21	31	41	51	
4.5	i	11	1	1	1	1	
45	MEQRGQNAPA LAPOORAAPO	ASGARKRHGP OKRSSPSEGL	GPREARGARP CPPGHHISED	GLRVPKTLVL GRDCISCKYG	ODYSTHWNDL	LFCLRCTRCD	60 120
	SGEVELSPCT	TTRNTVCQCE	EGTPREEDSP	EMCRKCRTGC	PRGMVKVGDO	TPWSDIECVH	180 240
	NVLNEIVSIL	OPTOVPEQEM	EVQEPAEPTG	VNMLSPGESE	HLLEPAEAER	RSSQRPGAED SQRRRLLVPA	300
50			PFDSWEPLMR GERLAKQKIE			DTLYTMLIKW	360 411
		284 Protei	n Sequence NP_002002.2				
55	1	11	21	31	41	51	
	   MRLLLALLGV	LLSVPGPPVL	   SLEASEEVEL	   EPCLAPSLEC	QEQELTVALA	QPVRLCCGRA	60
						QNLTLITGDS RCPAAGNPTP	120 180
60	TIRWLKDGQA	PHGENR IGG1	RLRHQHWSLV	MESVVPSDRO	TYTCLVENA	GSIRYNYLLD	240
						N GSSFGADGFP V LPEEDPTWTA	300 360
	AAPEARYTDI	ILYASGSLAI	AVLLLLAGLY	RGQALHGRHE	RPPATVQKL	S RFPLARQFSL S KPLGEGCFGQ	420 480
65	VVRAEAFGMD	PARPDOAST	AVKMLKDNAS	DKDLADLVSE	MEVMKLIGR	H KNIINLLGVC	540
	QYLESRKCIH	RDLAARNVL	/ TEDNVMKIAL	FGLARGVHH	DYYKKTSNG	V SCAYQVARGM R LPVKWMAPEA	600 660
						R PPHCPPELYG D ASSTCSSSDS	720 780
70		SSSFPFGSG		J SEELEDLINE	101101000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	802
			in Sequence NP_075252.				
75	1	11	21	31	41	51	
75	   MRLLLALLG	   LLSVPGPPV	 L SLEASEEVE	l L EPCLAPSLE	QEQELTVAL	G QPVRLCCGRA	60
	ERGGHWYKEC	SRLAPAGRV	R GWRGRLEIA	S FLPEDAGRY	L CLARGSMIV	L QNLTLITGDS F RCPAAGNPTP	120 180
0Λ	TIRWLKDGQA	FHGENRIGG	I RLRHQHWSL	V MESVVPSDR	G TYTCLVENA	V GSIRYNYLLD	240
80						N GSSFGADGFP V LPGTGRIPHL	360
	TCDSLTPAGE	R TKSPTLQFS	L ESGSSGKSS	S SLVRGVRLS	S SGPALLAGE	V SLDLPLDPLW S DKDLADLVSE	420
						P DLSPDGPRSS	

	The second of th	600
	EGPESTPVLV SCATOVARGA QUESTRACTA REMARESTED	660
	LLREGHRNDR PPHCPPELYG LMRECWHAAP SQRPTFKQLV EALDKVLLAV SEEYLDLRLT	720
5	FGPYSPSGGD ASSTCSSSDS VPSHDPLPLG SSSFPFGSGV QT	762
,	Seq ID NO: 286 Protein Sequence	
	Protein Accession #: NP_002836.2	
	1 11 21 31 41 51	
10	MRGLGTCLAT LAGLLLTAAG ETFSGGCLFD EPYSTCGYSQ SEGDDFNWEQ VNTLTKPTSD	60
	PWMPSGSLML VNASGRPEGO RAHLLLPOLK ENDTHCIDFH YFVSSKSNSP PGLLNVYVKV	120
	NNGDIGNDIN NISCOPTRIW NRAELAISTF WPNFYOVIFE VITSGHQGYL AIDEVKVLGH	180 240
	PCTRTPHFLR IQNVEVNAGQ FATFQCSAIG RTVAGDRLML QGIDVRDAPL KEIKVTSSRR PIASPNVVNT TKRDAGKYRC MIRTEGGVGI SNYAELVVKE PPVPIAPPQL ASVGATYLMI	300
15	OLNANSINGO GPIVAREVEY CTASGSWNDR OPVDSTSYKI GHLDPDTEYE ISVLLTRPGE	360
	CCTCSPCPAL RTRTKCADPM RGPRKLEVVE VKSROITIRW EPPGYNVTRC HSYNLTVHYC	420 480
	YOVGGQEQUR EEVSMOTENS HPOHTITNLS PYTNVSVKLI LMNPEGRKES QELIVQTDED LPGAVPTESI QGSTFEEKIF LQWREPTQTY GVITLYEITY KAVSSFOPEI DLSNQSGRVS	540
	KLZENETHPLF FGLYPGITYS FTIRASTAKG FGPPATNOFT TKISAPSMPA YELETPLNOT	600
20	DNTVTVMLKP AHSRGAPVSV YQIVVEEERP RRTKKTTEIL KCYPVPIHFQ NASLLNSQYY	660 720
	PAAEFPADSI QAAQPFTIGD NKTYNGYWNT PLLPYKSYRI YFQAASRANG ETKIDCVQVA TKGAATPKPV PEPEKQTDHT VKIAGVIAGI LLFVIIPLGV VLVMKKRKLA KKRKETMSST	780
	POEMTUNUNG MOKSVAFOGT NCDEAFSFMD THNLNGRSVS SPSSFTMKTN TLSTSVPNSY	840
25	VEDETUTMAC DISCLUSCHI VERREPADVP YOTGOLHPAI RVADLLOHIT QMKCAEGYGP	900 960
25	REEYESFFEG QSAPMDSAKK DEWRMKNRYG NIIAYDHSRV RLQTIEGDTN SDYINGNYID GYHRPNHYIA TQGPMQETIY DFWRMVWHEN TASIIMVTNL VEVGRVKCCK YWPDDTEIYK	1020
	DIKYTLIETE LLAEYVIRTF AVEKRGYHEI REIRQFHFTG WPDHGYPYHA TGLLGFYRQY	1080
	KSKSPPSAGP LVVHCSAGAG RTGCFIVIDI MLDMAEREGV VDIYNCVREL RSRRVNMVUT	1140 1200
30	EEQYVFIHDA ILEACLCGDT SVPASQVRSL YYDMNKLDPQ TNSSQIKEEF RTLNMVTPTL RVEDCSIALL PRNHEKNRCM DILPPDRCLP FLITIDGESS NYINAALMDS YKQPSAFIVT	1260
50	OHPLPNTVKD FWRLVLDYHC TSVVMLNDVD PAQLCPQYWP ENGVHRHGPI QVEFVSADLE	1320
	EDIISRIFRI YNAARPODGY RMVQQFQFLG WPMYRDTPVS KRSFLKLIRQ VDKWQEEING	1380 1440
	GEGPTVVHCL NGGGRSGTFC AISIVCEMLR HQRTVDVFHA VKTLRNNKPN MVDLLDQYKF CYEVALEYLN SG	1452
35	CIEVALETIA	
	Seq ID NO: 287 Protein Sequence	
	Protein Accession #: NP_057635.1 1 11 21 31 41 51	
40	MGFLOLLVVA VLASEHRVAG AAEVFGNSSE GLIEFSVGKF RYFELNRPPP EEAILHDISS	60 120
	NVTFLIFOIH SOYONTTVSP SPTLLSNSSE TGTASGLVFI LRPEQSTCTW YLGTSGIOPV ONMAILLSYS ERDPVPGGCN LEFDLDIDPN IYLEYNFFET TIKFAPANLG YARGVDPPPC	180
	DAGTDODSRW RLOYDVYOYF LPENDLTEEM LLKHLQRMVS VPQVKASALK VVTLTANDKT	240
45	SVSFSSLPGQ GVIYNVIVMD PFLNTSAAYI PAHTYACSFE AGEGSCASLG RVSSKVFFTL FALLGFPICF FGHRFMKTEL PFIGPIIMGP PPYILITRLT PIKYDVNLIL TAVTGSVGGM	300 360
43	PLVAVWWRFG ILSICMLCVG LVLGFLISSV TPFTPLGNLK IFHDDGVFWV TFSCIAILIP	420
	VVFMGCLRIL NILTCGVIGS YSVVLAIDSY WSTSLSYITL NVLKRALNKD FHRAPTNVPF	480
	QTNDFILLAV WGMLAVSGIT LQIRRERGRP FFPPHPYKLW KQERERRVTN ILDPSYHIPP	540 570
50	LRERLYGRLT QIKGLFQKEQ PAGERTPLLL	
•••	Seq ID NO: 288 Protein Sequence	
	Protein Accession #: NP_003811.1 1 11 21 31 41 51	
55	MEPPGDWGPP PWRSTPRTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG	60
	YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCQMCD PAMGLRASRN CSRTENAVCG CSPGHFCIVQ DGDHCAACRA YATSSPGQRV QKGGTESQDT LCQNCPPGTF SPNGTLEECQ	120 180
	HOTKCSWLVT KAGAGTSSSH WVWWFLSGSL VIVIVCSTVG LIICVKRRKP RGDVVKVIVS	240
60	VORKROEAEG EATVIEALQA PPDVTTVAVE ETIPSFTGRS PNH	283
60	Seq ID NO: 289 Protein Sequence	
	Protein Accession #: NP_000943.1	
	$\frac{1}{1}$ $\frac{11}{1}$ $\frac{2\overline{1}}{1}$ $\frac{31}{1}$ $\frac{41}{1}$ $\frac{51}{1}$	
65	MEPHDSSHMD SEFRYTLFPI VYSIIFVLGV IANGYVLMVF ARLYPCKKFN EIKIFMVNLT	60
-	MADMLFLITL PLWIVYYONO GNWILPKFLC NVAGCLFFIN TYCSVAFLGV ITYNRFQAVT	120
	RPIKTAQANT RKRGISLSLV IMVAIVGAAS YFLILDSTNT VPDSAGSGNV TRCFEHYEKG	180 240
	SVPVLIIHIF IVFSFFLVFL IILFCNLVII RTLLMQPVQQ QRNAEVKRRA LWMVCTVLAV FIICFVPHHV VQLPWTLAEL GFQDSKFHQA INDAHQVTLC LLSTNCVLDP VIYCFLTKKP	300
70	RIGHLTEKFYS MRSSRKCSRA TTDTVTEVVV PFNQIPGNSL KN	342
	Co. ID NO. 200 Protein Company	
	Seq ID NO: 290 Protein Sequence Protein Accession #: NP_003262.1	
75	1 11 21 31 41 51	
75	GCLGAIKENK CLLLTFFLLL LLVFLLEATI AILFFAYTDK IDRYAQQDLK KGLHLYGTQG	60
	NVGLTNAWSI IQTDFRCCGV SNYTDWFEVY NATRVPDSCC LEFSESCGLH APGTWWKAPC	120
	YETVKVMLQE HLLAVGIFGL CTALVQILGL TFAMTHYCQV VKADTYCA	168
80	Seq ID NO: 291 Protein Sequence	
	Protein Accession #: NP_005620.1	
	1 11 21 31 41 51	
	MAKKSAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTROMD	60
	TEA	

	FIMSCVGFAV	GLGNVWRPPY I	LCYKNGGGVF	LIPYVLIALV	GGIPIFFLEI	SLGQFMKAGS	120
	INVWNICPLF	KGLGYASMVI '	VEYCNTYYIM '	<b>/LAWGFYYLV</b>	KSFTTTLPWA	TCGHTWNTPD	180
	CUETERHEDC .	ANASLANLTC I	DOLADRRSPV	IEFWENKVLR	LSGGLEVPGA	Lnwevtlcll	240
_	ACWVLVYFCV	WKGVKSTGKI '	VYPTATFPYV '	<b>VLVVLLVRGV</b>	LLPGALDGII	<b>AATKbom2kt</b>	300
5	GSPOVWIDAG	TOIFFSYAIG	LGALTALGSY	NRFNNNCYKO .	AIILALINSG	TSFFAGYVVF	360
	SILGFMAAEQ	GVHISKVAES	GPGLAFIAYP	RAVTLMPVAP	LWAALFFFML	LLLGLDSQFV	420
	GVEGFITGLL	DLLPASYYFR	FQREISVALC	CALCEVIDLS	MVTDGGMYVF	QLFDYYSASG	480 540
	TTLLWQAFWE	CVVVAWVYGA	DRIMODIACM	IGYRPCPWMK	WCWSFFTPLV	CMCTLILIAAA	600
10		YVYPWWGEAM			DIOUNG I FOREK	MOUDIGEING	635
10	THHTRAKAGD	ADVRGLTTLT	PVSESSKVVV	AFDAM			033
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	MKHVLNLYLL	GVVLTLLSIF	VRVMESLEGL	LESPSPGTSW	TTRSQLANTE	PTKGLPDHPS	60
	RSM						63
00		293 Protein					
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	ļ	11	21	31	41	51	
			1	POCE EL VIII	INDEDDUCM	DOMINIDEDWN	60
	MAGASLGARF	YRQIKRHPGI	IPMIGLICLG	MUSAALTELK	IMERSPOVC*	DKKMMF LE WA	87
25	KISPADQIKI	LAVSTDYKKL	KAURPUF				•
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30	MGPGPSRAPR	APRLMLCALA	LMVAAGGCVV	SAFNLDTRFL	VVKEAGNPGS	LFGYSVALHR	60
	QTERQQRYLL	LAGAPRELAV	PDGYTNRTGA	VYLCPLTAHK	DDCERMNITV	KNDPGHHIIE	120
	DMWLGVTVAS	QGPAGRVLVC	AHRYTQVLWS	GSEDQRRMVG	KCYVRGNDLE	LDSSDDWQTY	180 240
	HNEMCNSHTD	YLETGMCQLG	TSGGFTQNTV	YFGAPGAYNW	KGNSYMIQKK	EWDLSEYSYK	300
35	DPEDQGNLYI	GYTMQVGSFI	LHPKNITIVT	GAPKHKHMGA	ATVUENDO	DLRRRQVLEG TSFPAHPSLL	360
33	SQVGAYFGSA	INTADIANNO	OCCOUNT AVG	ADDECLCKA	TANGGERET	RQPQQVIHGE	420
	LHGPSGSAFG	LOANSIGNIN	DENEVERTAL O	CST.SDHIVE.	. RARPVINIVI	KTLVPRPAVL	480
	TATOLIGIA	UNVELCEAVN	OSAGNPNYRR	NITLAYTLEA	DRDRRPPRLE	FAGSESAVFH	540
	GEESMPEMRO	OKLELLLMON	LRDKLRPIII	SMNYSLPLRM	PORPREGERS	LDAYPILNQA	600
40	OALENHTEVO	FOKECGPDNK	CESNLOMRAA	FVSEQQQKLS	RLQYSRDVR	LLLSINVTNT	660
	RTSERSGEDA	HEALLTLVVP	PALLLSSVRF	PGACQANET I	FCELGNPFK	R NORMELLIAF	720
	EVIGVTLHTE	DLQVQLQLST	SSHQDNLWPH	<b>ILTLLVDYT</b> I	. QTSLSHVNHI	R LOSFFGGTVM	780
	GESCHICTVEL	VGSPLKYEFO	VGPMGEGLVC	LGTLVLGLEV	PYEVSNGKW	LYPTEITVHG	840
4.5	NGSWPCRPPC	DLINPLNLTI	. SDPGDRPSSE	QRRRRQLDPC	GGQGPPPVT	LAAAKKAKSET	900
45	VLTCATGRA	CVWLECPIPE	APVVTNVTVI	ARVWNSTFI	DYRDFDRVR	V NGWATLFLRT	960 1020
	SIPTINMEN	TTWFSVDIDS	ELVEELPAE	ELWLVLVAVO	AGLLLLGLI	I LLLWKCGFFK	1020
	RARTRALYE	KRQKAEMKS(	PSETERLIDE	, x			1031
	Co- ID NO.	295 Protei	n Comience				
50		cession #:		ı			
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	MGPGPSRAPI	R APRLMLCAL	A LMVAAGGCV	/ SAFNLDTRF	L VVKEAGNPG	S LFGYSVALHR	60
	OTEROORYL	L LAGAPRELA	V PDGYTNRTG	VYLCPLTAH	K DDCERMNIT	V KNOPGHHIIE	120
55	DMWLGVTVA:	S QGPAGRVLV	C AHRYTQVLW	GSEDQRRMV	G KCYVRGNDL	E LDSSDDWQTY	180
	HNEMCNSNT	D YLETGMCQL	G TSGGFTQNT	V YPGAPGAYN	W KGNSYMIQR	K EWDLSEYSYK	240
	DPEDQGNLY	I GYTMQVGSF	I LHPKNITIV	T GAPRHRHMG	A VFLLSQEAG	G DLRRRQVLEG	300 360
	SQVGAYFGS	A IALADLNND	G WQDLLVGAP	Y YFERKEEVG	G ALIVEMNUM	G TSFPAHPSLL	420
60	LHGPSGSAF	G LSVASIGDI	N QUGFQDIAV	G APPEGLOKY	I IINSSSAUL	L RQPQQVIHGE H KTLVPRPAVL	480
00	RUGLPGLAT	r GislsGGMD	A DEWLIADER	V GSESDAIVE D NITLAYTLE	A DRDRRPPRI	R FAGSESAVFH	540
	CEECHDEND	C OKIETTIME	N USAGNENIK	T SMNYSLPLR	M PDRPRIGLE	S LDAYPILNQA	600
	OALENHTEV	O FOKECGPON	K CESNLONRA	A FVSEOOOKL	S RLOYSRDVF	K LLLSINVTNT	660
	RTSERSGED	A HEALLTLVV	P PALLLSSVR	P PGACQANET	I FCELGNPF	CR NORMELLIAF	720
65	EVICUTIAT	R DIAVOLOLS	T SSHODNLWP	M ILTLLVDYT	L OTSLSMVNI	IR LOSFFGGTVM	780
	GESGMKTVE	D VGSPLKYEF	Q VGPMGEGLV	G LGTLVLGLE	W PYEVSNGK	IL LYPTEITVHG	840
	NGSWPCRPP	G DLINPLNLT	L SDPGDRPSS	P QRRRRQLDP	G GGQGPPPV7	il aaakkakset	900
	VLTCATGRA	H CAMPECAIS	D APVVTNVTV	K ARVWNSTFI	E DYRDFDRVI	NGWATLFLRT	960
70						II LLLWKCDFFK	1020 1066
. 70	RTRYYQIME	K YHAVRIREE	E RYPPPGSTI	P TKKHWVTSV	IQ TRDQYY		1000
	C	. 306 5	in Coming				
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, ,	MDALCGSGI	L GSKEWDSNI	S VHTENPOLT			LP CYLLYLRHHO	60
	RGYIILSHI	S KLKMVLGVI	LL WCVSWADLI	Y SFHGLVHG	RA PAPVFFVT	PL VVGVTMLLAT	120
	LLIQYERL	G VQSSGVLI:	IF WFLCVVCA	V PFRSKILL	AK AEGEISDP	PR FTTFYIHPAL	. 180
	VLSALILA	F REKPPFFS	AK NVDPNPYPI	ET SAGFLSRL	PF WWFTKMAI	YG YRHPLEEKDI	, 240
80	WSLKEEDR	SQ MVVQQLLE	AW RKQEKQTAI	RH KASAAPGKI	NA SGEDEVLL	GA RPRPRKPSFI	. 300
	KALLATFG	S FLISACFK	LI QDLLSFIN	Q LLSILIRF	IS NPMAPSWW	GF LVAGLMFLCS	360
	MMQSLILQI	HY YHYIFVTG	VK FRTGIMGV	LY RKALVITN	SV KRASTVGE	IV NUMSVDAQRI	420
	MOLAPFLN	LL WSAPLQIII	LA IYFLWONL	SP SVLAGVAF	MV LLIPLNGA	VA VKMRAFQVK	480
	MKLKDSRI	KL MSEILNGI	KV LKLYAWED	SF LKQVEGIR	QG ELQLLRTA	WTTTTTHLL YA	1 540

		600
		660 720
	QQTLEACALL ADLEMLPGGD QTEIGEKGIN LSGGQRQRVS LARAVYSDAD IPLLDDPLSA	780
5	VDSHVAKHIP DHVIGPEGVL AGKTRVLVTH GISFLPQTDF IIVLADGQVS EMGPYPALLQ	840
	RNGSFANFLC NYAPDEDOGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTYVVQ	900
	WALLEY GROUP STROKE ALVINOROLDS WALLESTED THE STROKE TH	960 1020
		1080
10	EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTLVQRFYA ATSRQLKRLE	1140
	SVSRSPIYSH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYFYII SNRWLSIGVE	1200
	LAGICALDIA ADIVATORDO MILODADDO DIDENTINO	1260 1320
	IVGRTGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTIIP QDPILFSGTL	1380
15	RMNLDPFGSY SEEDIWMALE LSHLHTFVSS QPAGLDFQCS EGGENLSVGQ RQLVCLARAL	1440
	LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLTI AHRLNTIMDY TRVLVLDKGV	1500
	VAEFDSPANL IAARGIFYGM ARDAGLA	1527
	Seq ID NO: 297 Protein Sequence	
20	Protein Accession #: NP_002692.1	
	1 11 21 31 41 51	
	HHFYRLFLGA TRRPLNPEWK GEIDNWCVYV LTSLLPFKIQ SQDIKALQKE LEQFAKLLKQ	60
	KRITLGYTQA DVGLTLGVLF GKVFSQTTIC RFEALQLSFK NMCKLRPLLQ KWVEEADNNE	120
25	NLQEICKAET LVQARKRKRT SIENRVRGNL ENLFLQCPKP TLQQISHIAQ QLGLEKDVVR	180 240
	VWPCNRRQKG KRSSSDYAQR EDFEAAGSPF SGGPVSFPLA PGPHFGAPGY GSPHFTALYS SVPFPEGEAF PPVSVTTLGS PLHSN	265
	SVEELIGIME ECOVERIOUS FAILUR	
20	Seq ID NO: 298 Protein Sequence	
30	Protein Accession #: NP_005449.1 1 11 21 31 41 51	
	MASPRRSGOP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG	60
35	LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA IKYGPNHLMV FGGVCPSVTS IIAESLQGNN LVQLSFAATT PVLADKKKYP YFFRTVPSDN	120 180
33	AVNPAILKLL KHYOWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV	240
	KKLKGNDVRI ILGQFDQNMA AKVPCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTBANSS	300
	RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG PSKFHGYAYD	360 420
40	GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL NAMNETNFFG VTGQVVFRNG ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP	480
	LYSILSALTI LGMIMASAPL FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIPLFGLD	540
	GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MPAKTWRVHA IPKNVKMKKK IIKDQKLLVI	600
	VGGMLLIDLC ILICMQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIMLGIV YAYKGLLMLF GCFLAWETRN VSIPALMDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ	660 720
45	FCIVALVIIF CSTITLCLVF VPKLITLRIN PDAATQNRRF QFTQNQKKED SKTSTSVTSV	780
	NQASTSRLEG LQSENHRLRM KITELDKOLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL	840
	CNFTESTOGG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH	900 941
	HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L	741
50	Seq ID NO: 299 Protein Sequence	
	Protein Accession #: NP_055632	
	1 11 21 31 41 51	
	MEAARALRLL LVVCGCLALP PLAEPVCPER CDCQHPQHLL CTNRGLRVVP KTSSLPSPHD	60
55	VLTYSLGGNF ITNITAFDFH RLGQLRRLDL QYNQIRSLHP KTFEKLSRLE ELYLGNNLLQ	120
	ALAPGTLAPL RKLRILYANG NEISRLSRGS FEGLESLVKL RLDGNALGAL PDAVFAPLGN LLYLHLESNR IRFLGKNAFA QLGKLRFLNL SANELQPSLR HAATFAPLRS LSSLILSANS	180 240
	LOHLGPRIFO HUPRIGLISL RGNOLTHLAP EAFWGLEALR ELRLEGNRLS QLPTALLEPL	300
<b>60</b>	HSLEALDISG NELSALHPAT FGHLGRIREL SIRNNALSAL SGDIFAASPA LYRLDIDGNG	360
60	WTCDCRLRGL KRWMGDWHSQ GRLLTVFVQC RHPPALRGKY LDYLDDQQLQ NGSCADPSPS	420 480
	ASLTADRRRQ PLPTAAGEEM TPPAGLAEEL PPOPOLOGOG RFLAGVAWDG AARELVGNRS ALRLSRRGPG LOOPSPSVAA AAGPAPQSLD LHKKPQRGRP TRADPALAEP TPTASPGSAP	540
	SPAGDPWORA TKHRLGTEHO ERAAQSDGGA GLPPLVSDPC DFNKFILCNL TVEAVGADSA	600
65	SVRWAVREHR SPRPLGGARF RLLFDRFGQQ PKFHRFVYLP ESSDSATLRE LRGDTPYLVC	660 720
03	VEGVLGGRVC PVAPRDHCAG LVTLPEAGSR GGVDYQLLTL ALLTVNALLV LLALAAWASR WLRRKLRARR KGGAPVHVRH MYSTRRPLRS MGTGVSADFS GFQSHRPRTT VCALSEADLI	780
	EFPCDRFMDS AGGGAGGSLR REDRLLQRFA D	811
70	Seq ID NO: 300 Protein Sequence Protein Accession #: NP 001783.2	
,,	1 11 21 31 41 51	
	MCRIAGALRI LLPLLAALLQ ASVEASGEIA LCKTGFPEDV YSAVLSKDVH EGQPLLNVKF SNCNGKRKVO YESSEPADPK VDEDGNVYAV RSPPLSSEHA KPLIYAQDKE TQEKWQVAVK	60 120
75	SNCNGKRKVQ YESSEPADFK VDEDGMVYAV RSFPLSSEMA KFLITAQUAE IQEAMQVAVA LSLKPTLTEE SVKESAEVEE IVFPRQFSKH SGHLQRQKRD MVIPPINLPE NSRGPFPQEL	180
	VRIRSDRDKN LSLRYSVTGP GADQPPTGIF IINPISGQLS VTKPLDREQI ARFHLRAHAV	240
	DINGNOVENP IDIVINVIDM NDNRPEFLHQ VWNGTVPEGS KPGTYVMTVT AIDADDPNAL	300
	NGMLRYRIVS QAPSTPSPNM FTINNETGDI ITVAAGLDRE KVQQYTLIIQ ATDMEGNPTY GLSNTATAVI TVTDVNDNPP EFTAMTFYGE VPENRVDIIV ANLTVTDKDQ PHTPAMNAVY	360 420
80	RISGGDPTGR FAIQTDPNSN DGLVTVVKPI DFETNRMFVL TVAAENQVPL AKGIQHPPQS	480
	TATVSVIVID VNENPYFAPN PKIIRQEEGL HAGTMLTTFT AQDPDRYMQQ NIRYTKLSDP	540
	ANWLKIDPYN GQITTIAVLD RESPNYKNNI YNATPLASDN GIPPMSGTGT LQIYLLDIND	600 660
	NAPOVLPQEA ETCETPDPNS INITALDYDI DPNAGPFAFD LPLSPVTIKR NWTITRLNGD FAQLNLKIKF LEAGIYEVPI IITDSGNPPK SNISILRVKV CQCDSNGDCT DVDRIVGAGL	720

	GTGATIATLL EDQDYDLSQL KAADNDPTAP YGGGDD	ADGSVTDGQQ	IKPVGIRRMD	erpihaepqy :	PVRSAAPHPG	DIGDFINEGL	780 840 900 906
5							
	Seq ID NO:						
	Protein Acc			31	41	51	
	ī	î .	ī	1	i	Ĩ.	
10	MVSPRMSGLL	SQTVILALIF	LPQTRPAGVF	ELQIHSFGPG	PGPGAPRSPC	SARLPCRLFF	60
			AALSARGPVY				120
			SLLARVAGRR GPGLRPCAPL				180 240
			RGPSSATTGC				300
15			CFNGGLCVGG				360
			AGPAGPRCEH				420
			GGRCYAHFSG				480 540
	PGLRPGDPQR	FESCHERSS	VAAGVAGAAL VDWNRPEDVD	POGIYVISAP	SIYAREVATO	I.FPPI.HTGRA	600
20	GOROHLLFPY		VDMIKE EDVD	1001111011	DINEDVALE	Di 11 0.10.0.	618
		302 Proteir					
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			LOPYPPEHAQ				60
	KRLERKYPSL HVEGMVNISK		KTSSLELPSC	DLVTADGSTE	VTISENLPAV	GPH1CQQQDS	120 136
	HVEGMANISK	ASSOQM					130
30		303 Protein					
		cession #: 1			41	<b>6</b> 1	
	1	11	21 	31 	ï	51 	
	MGCGGSRADA	IEPRYYESWT	RETESTWLTY	TOSDAPPSAA	APDSGPEAGG	LHSGMLEDGL	60
35				QSLSSGPLTQ	KQNGLQTTEA	KRDAKRMPAK	120
	EVTINVTDSI	QQMDRSRRIT	KNCVN				145
	Seg ID NO:	304 Protei	n Sequence				
40		cession #:	XP_040550.1				
40	1	11	21	31	41	51	
	MCADGETUVI.	KNMLIGINI.I	LIGSMIKESE	COLEVETERY	OROSVEEEGG	I ANYNTSSKE	60
						QVTFTHRINP	120
45						YIPHCSGHGN	180
45						SELRCPTDCS	240 300
						AVTEYVISYQ	360
	PTALGGLQLQ	QRVPGDWSGV	TITELEPGLT	YNISVYAVIS	NILSLPITAK	VATHLSTPQG	420
50						QTGLKPGEEY	480
50						VDFILLKYGL TTEIDAPKNL	540 600
						ATLTDLVPGT	660
						GPIDHYRITF	720
55						FTGFRPISHL	780
"						IMGLQPATEY FDYYRVSYRP	840 900
						TAMONPVOLI	960
						LLPSTHYTAT	1020
60						YVLTYKSTDG	1080 1140
00						FRKWADYRVG	1200
						NLYKLRIGSY	1260
					KNCHRTNLN	KYGESRHSQG	1320
65	INWYHWKGH	E FSIPFVEMIO	RPYNHRLMAG	RKRUSLQF			1358
	Seq ID NO	: 305 Protei	n Sequence				
			NP_005874.1				
	1	11	21	31 i	41 1	51 ·	
70	MASSVAPYE	LVRQVEALK	ENSHLROEL	R DNSSHLSKL	E TETSGMKEV	L KHLQGKLEQE	60
	ARVLVSSGQ*	r enteorkard	MDITSLYNLI	C FQPPTLGPE	P AARTPEGSP	V HGSGPSKDSF	120
						P HVETQFSMQM	180
						Q DRVQQTEPQA D TARTLLAMSS	240 300
75						A LHNIVFSQPD	360
	QGLARKEMR	V LHVLEQIRA	Y CETCWDWLQ	A RDGGPEGGG	A GSAPIPIEP	Q ICQATCAVMK	420
						L TNLTFGDVAN	480
						E AGSVTALVQC O SNSLAIIESG	540 600
80	GGILRNVSS	L VATREDYRQ	V LRDHNCLQT	L LOHLTSHSL	T IVSNACGTL	w nlsarsardq	660
	ELLWDLGAV	G MLRNLVHSK	H KMIAMGSAA	A LRNLLAHRP	A KHQAAATAV	S PGSCVPSLYV	720
						D YASDSGCFDD	
						E KDTSGEAAVA Q SCSPCRGPEG	
		-					

	GRREAGSRAH PLLRLKAAHA SLSNDSLNSG SASDGYCPRE HMLPCPLAAL ASRREDPRCG	960
	OPRESELDED LEGGOREPPA REATSADARY RTIKLSPTYO HVPLLEGASR AGAEPLAGEG	1020
	ISPGARKOAN LPADHLSKVP EKLAAAPLSV ASKALQKLAA QEGPLSLSRC SSLSSLSSAG	1080
5		1140 1200
)		1260
		1320
	PEFGPAPTGS RPRGAADOEL ELLRECLGAA VPARLRKVAS ALVPGRRALP VPVYMLVPAP	1380
••	APAQEDDSCT DSAEGTPVNF SSAASLSDET LQGPPRDQPG GPAGRQRPTG RPTSARQAMG	1440 1500
10	HRHKAGGAGR SAEDSRGAGK NRAGLELPLG RPPSAPADKD GSKPGRTRGD GALQSLCLTT	1560
	PTEEAVYCFY GNDSDEEPPA AAPTPTHRRT SAIPRAPTRE RPQGRKEAPA PSKAAPAAPP PARTOPSLIA DETPPCYSLS SSASSLSEPE PSEPPAVHPR GREPAVTKDP GPGGGRDSSP	1620
	SPRAAGELLO RCISSALPRR RPPVSGLRRR KPRATRLDER PAEGSRERGE EAAGSDRASD	1680
	LDSVEWRAIO EGANSIVTWL HOAAAATREA SSESDSILSF VSGLSVGSTL QPPKHRKGRQ	1740
15	AEGEMGSARR PEKRGAASVK TSGSPRSPAG PEKPRGTQKT TPGVPAVLRG RTVIYVPSPA	1800
	PRAQPKGTPG PRATPRKVAP PCLAQPAAPA KVPSPGQQRS RSLHRPAKTS ELATLSQPPR SATPPARLAK TPSSSSSQTS PASQPLPRKR PPVTQAAGAL PGPGASPVPK TPARTLLAKQ	1860 1920
	HKTORSPVRI PFMORPARRG PPPLARAVPE PGPRGRAGTE AGPGARGGRL GLVRVASALS	1980
	SGSESSDRSG FRRQLTPIKE SPGLRRRRSE LSSAESAASA PQGASPRRGR PALPAVFLCS	2040
20	SRCEELRAAP ROGPAPAROR PPAARPSPGE RPARRTTSES PSRLPVRAPA ARPETVKRYA	2100
	SLPHISVARR PDGAVPAAPA SADAARRSSD GEPRPLPRVA APGTTWRRIR DEDVPHILRS TLPATALPLR GSTPEDAPAG PPPRKTSDAV VQTEEVAAPK TNSSTSPSLE TREPPGAPAG	2160 2220
	GOLSLIGSDV DGPSLAKAPI SAPFVHEGIG VAVGGFPASR HGSPSRSARV PPFNYVPSPM	2280
	VVAATTDSAA EKAPATASAT LLE	2303
25		
	Seq ID NO: 306 Protein Sequence	
	Protein Accession #: NP_006356.1 1 11 21 31 41 51	
30	MPLTEDLITF NLRNFLLFQL WESSFSPGAG GFCTTLPPSF LRVDDRATSS TTDSSRAPSS	60
	PRPPGSTSHC GISTRCTERC LCVLPLRTSQ VPDVMAPQHD QEKFHDLAYS CLGKSPSMSN	120 156
	QDLYGYSTSS LALGLAWLSW ETKKKNVLHL VGLDSL	130
	Seq ID NO: 307 Protein Sequence	
35	Protein Accession #: AAH32726.1	
	1 11 21 31 41 51	
	MASTRSIELE HFEERDKRPR PGSRRGAPSS SGGSSSSGPK GNGLIPSPAH SAHCSFYRTR	60
	TLOALSSEKK AKKARPYRNG DRYFKGLVFA ISSDRFRSFD ALLIELTRSL SDNVNLPQGV	120
40	RTIYTIDGSR KVTSLDELLE GESYVCASNE PFRKVDYTKN INPNWSVNIK GGTSRALAAA	180
	SSVKSEVKES KDFIKPKLVT VIRSGVKPRK AVRILLNKKT AHSFEQVLTD ITEAIKLDSG	240 300
	VVKRLCTLDG KQVTCLQDFF GDDDVFIACG PEKFRYAQDD FVLDHSECRV LKSSYSRSSA VKYSGSKSPG PSRRSKSPAS VNGTPSSQLS TPKSTKSSSS SPTSPGSFRG LKISAHGRSS	360
	SNVNGGPELD RCISPEGVNG NRCSESSTLL EKYKIGKVIG DGNFAVVKEC IDRSTGKEFA	420
45	LKIIDKAKCC GKEHLIENEV SILRRVKHPN IIMLVEEMET ATELFLVMEL VKGGDLFDAI	480
_	TSSTKYTERD GSAMVYNLAN ALRYLHGLSI VHRDIKPENL LVCEYPDGTK SLKLGDFGLA	540
	TVVEGPLYTV CGTPTYVAPE IIAETGYGLK VDIWAAGVIT YILLCGFPPP RSENNLQEDL	600 660
	FDQILAGKLE FPAPYWDNIT DSAKELISQM LQVNVEARCT AGQILSHPWV SDDASQENNM QAEVTGKLKQ HFNNALPKQN STTTGVSVIM FDLTV	695
50	AUDA LOUDING IN HINCHE HAVE DELL'AUTONIO	
	Seq ID NO: 308 Protein Sequence	
	Protein Accession #: NP_055978.2	
	1 11 21 31 41 51	
55	MEEMEEELKC PVCGSFYREP IILPCSHNLC QACARNILVQ TPESESPQSH RAAGSGVSDY	60
	DYLDLDKMSL YSEADSGYGS YGGFASAPTT PCQKSPNGVR VFPPAMPPPA THLSPALAPV	120
	PRINSCITCPO CHRSLILDDR GLRGFPKNRV LEGVIDRYQQ SKAAALKCQL CEKAPKEATV	180 240
	MCEQCDVFYC DPCRLRCHPP RGPLAKHRLV PPAQGRVSRR LSPRKVSTCT DHELENHSMY CVQCKMPVCY QCLEEGKHSS HEVKALGAMW KLHKSQLSQA LNGLSDRAKE AKEFLVQLRN	300
60	MVQQIQENSV EFEACLVAQC DALIDALNRR KAQLLARVNK EHEHKLKVVR DQISHCTVKL	360
	ROTTGLMEYC LEVIKENDPS GFLQISDALI RRVHLTEDQM GKGTLTPRMT TDFDLSLDNS	420
	PLIQSINGLD FYQYKASSPY PATPILQLEE CCTHNNSATL SWKQPPLSTV PADGYILELD	480 540
	DGNGGOFREV YVGKETMCTV DGLHFNSTYN ARVKAFNKTG VSPYSKTLVL QTSEVAWFAF DPGSAHSDII LSNDNLTVTC SSYDDRVVLG KTGFSKGIHY WELTVDRYDN HPDPAFGVAR	600
65	MDVMKDVMLG KODKAWAMYV DNNRSWFMHN NSHTNRTEGG ITKGATIGVL LDLNRKNLTF	660
	FINDEQQGPI AFDNVEGLFF PAVSLNRNVQ VTLHTGLPVP DFYSSRASIA	710
	a sa un san autolo Comuna	
	Seq ID NO: 309 Protein Sequence Protein Accession #: NP_116025.1	
70	1 11 21 31 41 51	
	MEDLEEDVRF IVDETLDFGG LSPSDSREEE DITVLVTPEK PLRRGLSHRS DPNAVAPAPO	60 120
	GVRLSLGPLS PEKLEEILDE ANRLAAQLEQ CALQDRESAG EGLGPRRVKP SPRRETFVLK DSPVRDLLPT VNSLTRSTPS PSSLTPRLRS NDRKGSVRAL RATSGKRPSN MKRESPTCNL	180
75	FPASKSPASS PLTRSTPPVR GRAGPSGRAA ASPPTPIRSV LAPQPSTSNS QRLPRPQGAA	240
	AKSSSQLPIP SAIPRPASRM PLTSRSVPPG RGALPPDSLS TRKGLPRPST AGHRVRESGH	300
	KVPVSQRLNL PVMGATRSNL QPPRKVAVPG PTR	333
	Seq ID NO: 310 Protein Sequence	
80	Protein Accession #: ref   XP_166946.2	
	1 11 21 31 41 51	
	THE REPORT OF THE PROPERTY OF	60
	MGSDSRLPEM EEKGSGDKAG WSGALLAEVK NQGLKLCEWM LVLKAELVEW YTSVIVGQQG HRLKMDLLKE RHHRKYLQKP IKRCSGLMGL NWSLRPAISS SPLARSQEKH HGAKGNEGVK	60 120
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	ALSFRKLRKL KRPPTPPSQA KSWRGRTGSA ADSPGAAAMA VQAALLSTHP FVPFGFGGSP	180
	DGLGGAFGAL DKGCCYEDDE TGAPAGALLS GAEGGDVREA TROLLSFIDS ASSNIKLALD	240 300
	KPGKSKRKVN HRNAPTVAAP AHGKAAPRRE ASQAAAAASL QSRSLAALFD SLRHVPGGAE PAGGEVAAPA AGLGGAGTGG AGGDVAGPAG ATAIPGARKV PLRARNLPPS FFTEPSRAGG	360
5	GGCGPSGPDV SLGDLEKGAE AVEFFELLGP DYGAGTEAAV LLAAEPLDVF PAGASVLRGP	420
•	PELEPGLPEP PPAVVGNLLY PEPWSVPGCS PTKKSPLTAP RGGLTLNEPL SPLYPAAADS	480
	PGGEDGRGHL ASFAPFFPDC ALPPPPPPPHQ VSYDYSAGYS RTAYSSLWRS DGVWEGAPGE	540
	EGAHRD	546
10	C ID NO. 311 Brokein Company	
10	Seq ID NO: 311 Protein Sequence Protein Accession #: NP 071406.1	
	1 11 21 31 41 51	
1.5	MAPTKPSFOO DPSRRERLOA LRKEKSRDAA RSRRGKENPE PYELAKLIPL PAAITSQLDK	60
15	ASIIRLTISY LKORDPANOG DPPWNLRMEG PPPNTSVKGA QRRRSPSALA IEVFEAHLGS	120 180
	HILQSLDGFV FALNQEGKFL YISETVSIYL GLSQVELTGS SVFDYVHPGD HVEMABQLGM KLPPGRGLLS QGTAEDGASS ASSSSQSETP EPVESTSPSL LITDNTLERS PFIRMKSTLT	240
	KRGVHIKSSG YKVIHITGRL RLRVSLSHGR TVPSQIMGLV VVAHALPPPT INEVRIDCHM	300
	FYTRVNMOLN IIYCENRISD YMDLTPVDIV GKRCYHFIHA EDVEGIRHSH LDLLNKGQCV	360
20	TKYYRWMQKN GGYIWIQSSA TIAINAKNAN EKNIIWVNYL LSNPEYKDTP MDIAQLPHLP	420
	EKTSESSETS DSESDSKOTS GITEDNENSK SDEKGNOSEN SEDPEPDRKK SGNACDNOMN	480 540
	CNDDGHSSSN PDSRDSDDSF EHSDFENPKA GEDGFGALGA MQIKVERYVE SESDLRLQNC ESLTSDSAKD SDSAGEAGAQ ASSKHQKRKK RRKRQKGGSA SRRRLSSASS PGGLDAGLVE	600
	PPRLLSSPNS ASVLKIKTEI SEPINFUNDS SIWNYPPNRE ISRNESPYSM TKPPSSEHPP	660
25	SPOGGGGGG GGGGLHVAIP DSVLTPPGAD GAAARKTQPG ASATAALAPV ASDPLSPPLS	720
	ASPRDKHPGN GGGGGGGG AGGGGPSASN SLLYTGDLEA LQRLQAGNVV LPLVHRVTGT	780
	LAATSTAAQR VYTTGTIRYA PAEVILAMQS NLLPNAHAVN FVDVNSPGFG LDPKTPMEML	840 900
	YHHVHRLMMS GPFGGAVSAA SLTQMPAGNV FTTAEGLFST LPFPVYSNGI HAAQTLERKE D	901
30		
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	1 11 21 31 41 51	
35	MDSDASLVSS RPSSPEPDDL FLPARSKGSS GSAFTGGTVS SSTPSDCPPE LSAELRGAMG	60
33	SAGAHPGDKL GGSGFKSSSS STSSSTSSAA ASSTKKDKKQ MTEPELQQLR LKINSRERKR	120
	MHDLNIAMDG LREVMPYAHG PSVRKLSKIA TLLLARNYIL MLTNSLEEMK RLVSEIYGGH	180
	HAGFHPSACG GLAHSAPLPA ATAHPAAAAH AAHHPAVHHP ILPPAAAAAA AAAAAAAVSS	240
40	ASLPGSGLPS VGSIRPPHGL LKSPSAAAAA PLGGGGGGGG ASGGFQHWGG MPCPCSMCQV	300
40	PPPHHHVSAM GAGSLPRUTS DAK	323
	Seq ID NO: 313 Protein Sequence	
	Protein Accession #: XP 045127.3	
	1 11 $2\overline{1}$ 31 41 51	
45		
	MTVLEESSIS LMSSVVADFS EFEEDPQVFN TLFPSRPIVP LSSRSMEISE TSVGISAEVD	60 120
	MSSVTTTQVP PAHGRLSVPA SLDPTAGSLS VAETQVTPSS VTTAFFSVIT SILLDSSFSV IANKNTPSLA VRDPSVFTPY SLVPSVESSL PSDQERSSFS EHKPRGALDF ASSFFSTPPL	180
	ELSGSISSPS EAPASLSLMP SDLSPPTSQS PSPLVETFTL FDSSDLQSSQ LSLPSSTNLE	240
50	FSQLQPSSEL PLATIMLLPS RSEVSPWSSF PSDSLEFVEA STVSLTDSEA HFTSAFIETT	300
	SYLESSLISH ESAVTALVPP GSESFDILTA GIQATSPLTT VHTTPILTES SLFSTLTPPD	360
	DQISALDGHV SVLASFSKAI PTGTVLITDA YLPSGSSFVS EATPFPLPTE LTVVGPSLTP TEVPLNTSTE VSTTSTGAAT GGPLDSTLMG DAASQSPPES SAAPPLPSLR PVTAFTLEAT	420 480
	VDTPTLATAK PPYVCDITVP DAYLITTVLA RRAVQEYIIT AIKEVLRIHF NRAVELKVYE	540
55	LPTDFTFLVT SGPFVYTAIS VINVLINSKL VRDQTPLILS VKPSFLVPES RFQVQTVLQF	600
	VPPSVDTGFC NFTQRIEKGL MTALFEVRKH HQGTYNLTVQ ILNITISSSR VTPRRGPVNI	660
	IPAVKSTOGP LNGSEVSELL RNLSVVEPSP YLGYPVLQIA EPFQYPQLNL SQLLKSSWVR	720
	TVLLGVMEKQ LQNEVFQAEM ERKLAQLLSE VSTRRRMWRR ATVAAGNSVV QVVNVSRLEG	780 840
60	DDNPVQLIYP VEDQDGERLS AVKSSDLINK MDLQRAAIIL GYRIQGVIAQ PVDRVKRPSP ESQSNNLWVI VGVVIPVLVV MVIVVILYWK LCRTDKLDFQ PDTVANIQQR QKLQIPSVKG	900
00	FDFAKQHLGQ HNKDDILIH EPAPLPGPLK DHTTPSENGD VPSPKSKIPS KNVRHRGRVS	960
	PSDADSTVSE ESSERDAGDK TPGAVNDGRS HRAPQSGPPL PSSGNEQHSS ASIFEHVDRI	1020
	SRPPEASRRV PSKIQLIAMQ PIPAPPVQRP SPADRVAESN KINKEIQTAL RHKSEIEHHR	1080
65	NKIRLRAKRR GHYEFPVVDD LSSGDTKERH RVYRRAQMQI DKILDPTASV PSVFIEPRKS	1140
05	SRIKRSPKPR RKHQVNGCPA DAEKDRLITT DSDGTYRRPP GVHNSAYIGC PSDPDLPADV QTPSSVELGR YPALPPPASQ YIPPQPSIEE ARQTMHSLLD DAFALVAPSS QPASTAGVGP	1200 1260
	GYPPGLPANS TPSQEERRAT QWGSFYSPAQ TANNPCSRYE DYGMTPPTGP LPRPGFGPGL	1320
	LOSTELVPPD POOPOASAEA PFAARGIYSE EMPSVARPRP VGGTTGSQIQ HLTQVGIASR	1380
70	IGAQPVEIPP SRGSQYGGPG WPSYGEDEAG RREAVPRTSG REPSAPSGNL PHRGLQGPGL	1440
70	GYPTSSTEDL QPGHSSASLI KAIREELLRL SQKQSTVQNF HS	1482
	O. TO MO. 314 Dantain Company	
	Seq ID NO: 314 Protein Sequence Protein Accession #: BAC04820.1	
_	1 11 21 31 41 51	
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	MAPRPLOPLY LALCGAAAVL GSVLFILMKT YFGRGRERRW DRGEAWWGAE AARLPEWDEN	60
	DPEDEEDEEP ALEELEGREV LVLGLDGAGK STFLRVLSGK PPLEGHIPTW GFNSVRLPTK	120
	DFEVDLLEIG GSQNLRFYWK EFVSEVDVLV FVVDSADRLR LPWARQELHK LLDKDPDLPV VVVANKQDLS EAMSMGELQR ELGLQAIDNQ REVFLLAASI APAGPTFEEP GTVHIWKLLL	180 240
80	ELLS	244
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	Seq ID NO: 315 Protein Sequence	
	Protein Accession #: NP_066563.1	
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	MARRAGGARM F LEPSSPSHWG Q K	GSLLLFALL LPTPPLRDQ	 AAGVAPLSWD RLQLSHDLLG	i Lpeprsrask Illikkalgv	I IRVHSRGNLW SLSRPAPQIQ	I ATGHFMGKKS YRRLLVQILQ	60 120 121
5			_				
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10	MERRRITSAA F	RRSYVSSGEM	MVGGLAPGRR	LGPGTRLSLA	i Rmppplptrv	deslagalna	60
	GFKETRASER A	AEMMELNDRP	ASYIEKVRFL	EQQNKALAAE	LNQLRAKEPT	Kladvyqael	120 180
	RELRIRIDOL 1	ransarleve Esleeeirfl	RDNLAQDLAT RKIHEEEVRE	LOEOLAROOV	HVELDVARPD	LTAALKEIRT	240
16	QYEAMASSNM I	HEAEEWYRSK	FADLTDAAAR	NAELLRQAKH	EANDYRROLQ	SLTCDLESLR	300
15	GTNESLEROM I	REQEERHVRE EGEENRITIP	VOTPSNLOIR	ETSLDTKSVS	EMARKIQEYQ	KTVENRDGEV	360 420
	IKESKQEHKO 1						432
	Seq ID NO:	317 Proteir	Sequence				
20	Protein Acc				41	51	
	ī	11 	21 	31 	41	1	
	MRLLSSLSGS IISREOADEL	SVSSDAEEYQ	PPIWKSYLYQ	LOQUEAPRPKR	I I CPREVENR	PKYYGREFHG	60 120
25	INDLVTDGLI						180
	THEEHTAVEK	ISSLVRRAAL	THNDNHFNYE	KTHNPKVHTF	RGPHWCEYCA	NFMWGLIAQG	240 300
	VRCSDCGLNV ARGLKSEGLY	RVSGFTEHIE	DVKMAFDRDG	<b>EKADISANVY</b>	PDINIITGAL	KLYFRDLPIP	360
30	VITYDTYSKP NAENLGIVFG					VTMNEKONFM	420 466
50				Simit dinie			
	Seq ID NO: Protein Acc						
35		11	21	31	41	51	
33	   MKRAHPEYSS	SDSELDETIE	! VEKESADENG	I NLSSALGSMS	PTTSSQILAR	KRRRGIIEKR	60
	RRDR INNSLS	<b>ELRRLVPSAP</b>	EKQGSAKLEK	AEILQMTVDH	LKMLHTAGGK	GYFDAHALAM	120 180
			IEGLDASDPL HGNAGTTASP				240
40	LPVVTSASKL		LSAFPFSFGS				300 304
	IGAF						304
	Seq ID NO:		n Sequence NP_001927.2				
45	1	11	21	31	41	51	
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	NSLSQKKKVT	VEDLESEDER	INDPEAKWIS	DTEFIYREQK	GTVRLWNVET	NTSTVLIEGK	120
50						DPPEVSNAKL YEEEILKTHI	180 240
	AHWWSPDGTR	LAYAAINDSE	VPIMELPTYT	GSIYPTVKPY	HYPKAGSENE	SISLHVIGLN	300
						SNDNIQSITS	360 420
55	GDWDVTKILA	YDEKGNKIYE	LSTEDLPRRE	QLYSANTVG	FNRQCLSCDI	VENCTYFSAS	480
33						KVEYRDIEID HGAVVVKCDG	540 600
	RGSGFQGTKL	LHEVRRRLGI	LEEKDQMEA	RTMLKEQYII	RTRVAVFGKI	YGGYLSTYIL	660
						AHRVSALEEQ QHLYRSIINF	720 780
60	FVECFRIQDK						803
	Seq ID NO:	320 Prote	in Sequence				
	Protein Ac	cession #:	XP_087461.	1 31	41	51	
65	1	Ī	1	Ī	1	1	
						C WPRRPPGPPS R AFFAAAFHRV	60 120
	GPPLLIEHLG	LAAGGAQQD	L RLCVGCGWV	R GRRTGRLRP	A AAPSAAAAT	A GAPTALPAYP	180
70						T LVIVVWSVAA A AVTSGVATK	240 299
			in Sequence				
	Protein Ac	cession #:	NP_036393.	1			
75	1	11	21 	31 	41 	51 	
	MDLQGRGVPS					V RENGTTCLMA	
						W VDRAYALKML S ALVTPAGKSY	
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οU	LGLILGLVIN	4 VTLAIYHVH	H KMTANQVQI	P RDRSQYKHM	IG		280
			in Sequence NP_653187				
	1	11	21	31	41	51	

5	MANUGIAATP CGLFLLPGFA LQIQCYQCEE PQLHNDCSSP EFIVNCTVNV QDMCQKEVME QSAGIMYRKS CASSAACLIA SAGYQSFCSP GKLNSVCISC CNTPLCNGPR PKKRGSSASA LRPGLRTTIL FLKLALFSAH C	60 120 141
10	Seq ID NO: 323 Protein Sequence	60
15	SRISMIISIC VFVLTFSAPL ATVLSNRFGH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA IGIISGLGYC FSFLFTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGNR YSLLFVGLLQ LNIVIFGALL RPIIIRGPAS PKIVIQENKK EAQYMLENEK TRTSIDSIDS GVELTTSFKN VFTHTNLELE PKADMQQVLV KTSPRPSKK APLLDFSILK EKSFICYALF GLFATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFF LNREPIRKIY	120 180 240 300 360 420
20	IELICVILLT VSLPAFTFAT EFNGLMSCSI FFGFMVGTIG GLIFHCLLKM MSNALQKMSS AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ RHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV	480 523
20	Seq ID NO: 324 Protein Sequence Protein Accession #: NP_004824.1  1 11 21 31 41 51	40
25	MESKYKEILL LTGLDNITDE ELDREKFELS DERNIATOKL HTABRIGVAT LHIONAGAVS AVMKTIRIFO KLAYMLLAKR LQEEKEKVDK QYKSVTKPKP LSQAEMSPAA SAAIRNDVAK QRAAPKUSH VKPEGKOMVA QQESIREGFQ KRCLPVMVLK AKKPFTETO ECKQEMFHAT VATEKEPFFV KVPNTLLKOK FIPKRIIIIA RYYRHSGFLE VNSASRVLDA ESDOKVNVPL	60 120 180 240 300
30	NIIRKAGETP KINTLQTQPL GTIVNGLEVV QKVTEKKNNI LFDLSDNTGK MEVLGVRNED THKCKEGDKV RLTFFTLSKN GEKLQLTSGV RSTIKVIKAK KKT  Seq 1D NO: 325 Protein Sequence	343
35	Protein Accession #: NP_005400.1  1 11 21 31 41 51                        MSVKGMAIAL AVILCATUVQ GPPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNP	60 94
40	Seq ID NO: 326 Protein Sequence Protein Accession #: NP_002553.1  1 11 21 31 41 51                    MPACCSCSDV FQYETNKVTR IQSMNYGTIK WFFHVIIFSY VCFALVSDKL YQRKEPVISS	60
45	VHTKVKGIAE VKEEIVENGV KKLVHSVFDT ADYTFPLQGN SFFVMTNFLK TEGQEQRLCP EYPTRETLCS SDRGCKKGWM DPQSKGIQTG RCVVHEGNQK TCEVSAMCPI EAVEEAPRPA LLNSAENFTV LIKNNIDPPG HNYTTRNILP GLMITCTFHK TQNPQCPIFR LGDIFRETGD MFSDVALQGG IMGIEIYMC NLDRWPHHCH PKYSFRRLDD KTTNVSLYPG YNFRYAKYYK ENNVEKRTLI KVFGIRFDIL VPGTGGKFDI IQLVVYIGST LSYFGLAAVF IDFLIDTYSS	120 180 240 300 360
50	NCCRSHIYPM CKCCOPCVUN EYYYRKKCES IVEPKPTLKY VSFVDESHIR MVNQQLLGRS LQDVKQGEVP RPAMDFTDLS RLPLALHDTP PIPGQPEEIQ LLRKEATPRS RDSPVMCQCC SCLPSQLPES HRCLEELCCR KKPGACITTS ELFRKLVLSR HVLQFLLLYQ EPLLALDVDS INSRLRHCAY RCYATWRFGS QDMADFAILP SCCRWRIRKE PPKSEGQYSG FKSPY	420 480 540 595
55	Seq ID NO: 327 Protein Sequence Protein Accession #: NP_001784.2 1 11 21 31 41 51	
60	MCLPRGPLAS LLLLQVCMLQ CAASEPCRAV FREAEVTLEA GGAEQEFGQA LGKVFMGCFG  GPPALFSTDN DDFTYRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVENG  KGPPFQRLNQ LKSNKDRDTK IFYSITOFGA DSPPEGVFAV EKETGHLLN KPLDREEIAK  YELFGHAVSE NGASVEDPMN ISIIVTOOND HKPKFTQDTF RGSVLEGVLF GTSVMQVTAT  DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIRRSTGTIS VISSGLDREK VPEYTLTIQA  TDMGDGGSTT TAVAVVEILD ANDNAFMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAFNSP	60 120 180 240 300 360 420
65	AMRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNOHTLYVEV THEAPFVLKL PTSTATIVVH VEDVHEAPVP VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR DPAGHLAMDP DSGQYTAVGT LDREDEQFVR NNIYEVMULA MDNGSPFTTG TGTLLILLID VNDHGPVEPP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY MTAEVNEEGD TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGEED QDYDITQLHR	480 540 600
70	GLEARPEVVL RNDVAPTIIP THMYRPRAN PDEIGHFILE NLKAANTDPT APPYDTLLVF DYEGGGSDAA SLSSLTSSAS DQDQDYDYLN EMGSRFKKLA DMYGGGEDD	780 629
75	Seq ID NO: 328 Protein Sequence Protein Accession #: NP_002562.1  1 11 21 31 41 51                    MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR MENNSCVEKK VLGEKTONPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMCQ YLARVLVEDD EIMGGFIRAP RPLPRKLWYL LDLKQMEEPC RF	60 120 162
80	Seq ID NO: 129 Protein Sequence LEK6 Protein Accession #: NP_001318.1 1 11 21 31 41 51	
	1 11 21 11 41 51	. 60

		120 180
	Seq ID NO: 330 Protein Sequence LEK6	
5	Protein Accession #: NP_066274 1 11 21 31 41 51	
	MOAECOGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA	60
••	PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC	120
10	PLPVFLAQAP SGQRR	135
	Seq ID NO: 331 Protein Sequence	
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15		60
	WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG QVIWVNNTII NGSQVWGGQP	120
	VYPQETDDAC IPPDGGPCPS GSWSQKRSFV YVMKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HPLRNQPLTF	180 240
20	ALOLHOPSGY LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGFVTAQV VLQAAIPLTS	300
	CGSSPVPGTT DCHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM TPAEVSIVVL SGTTAAQVTT	360 420
	TEWVETTARE LPIPEPEGPD ASSIMSTESI TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY	480 540
25	GSFSVTLDIV QGIESABILQ AVPSGBGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV	600
	GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG ENSPLLSCQQ	660 661
	V	
30	Seq ID NO: 332 Protein Sequence Protein Accession #: NP_001913.2	
	1 11 21 31 41 51	
	MSPLWWGFLL SCLGCKILPG AQCQFPRVCM TVDSLVNKEC CPRLGAESAN VCGSQQGRGQ	60
35	CTEVRADTRP WSGPYILRNQ DDRELWPRKP FHRTCKCTGN FAGYNCGDCK FGWTGPNCER KKPPVIRQNI HSLSPQEREQ FLGALDLAKK RVHPDYVITT QHWLGLLGPN GTQPQFANCS	120 180
33	VYDFFVWLHY YSVRDTLLGP GRPYRAIDFS HQGPAFVTWH RYHLLCLERD LQRLIGNESF	240
	ALPYWNFATG RNECDVCTDQ LFGAARPDDP TLISRNSRFS SWETVCOSLD DYNHLVTLCN GTYEGLLRRN QMGRNSMKLP TLKDIRDCLS LQKFDNPPFF QNSTPSPRNA LEGFDKADGT	300 360
40	LDSQVMSLHN LVHSPLNGTN ALPHSAANDP IFVVLHSFTD AIFDEWMKRF NPPADAWPQE	420
40	LAPIGHNRMY NMVPPPPPVT NEELFLTSDQ LGYSYAIDLP VSVEETPGWP TTLLVVMGTL VALVGLFVLL AFLQYRRLRK GYTPLMETHL SSKRYTEEA	480 519
	Seq ID NO: 333 Protein Sequence	
45	Protein Accession #: XP_059422.1	
43		
	MNMHLPLFLL ASVILPSICS HFNPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS VLGMLQLGAD GRTKKQLAMV MRYGVNGVGK ILKKINKAIV SKKNKDIVTV ANAVFVKNAS	60 120
	EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TRDMIDNLLS PDLIDGVLTR	180
50	LVLVNAVYFK GLWKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWYN FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRVQ VILPKFTAVA	240 300
	QTDLKEPLKV LGITDMFDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI	360
	LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP	397
55	Seq ID NO: 334 Protein Sequence	
	Protein Accession #: XP_040512.2 1 11 21 31 41 51	
		60
60	MROHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG VELGADGKTV SYTOFLLPTN AFGARRNTID STSSFSQFRN LSHRSLSIGR ASGTQGSLDT	120
	GSDLGDFMDY DPNILDDPQW PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNETPKEKFP HIKLTLSKIR SLKREMRKLA QEDCGLEEPT VAMAFVYFEK LALKGKLNKQ NRKLCAGACV	180 240
	LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEPPV LVALEPALHL PEHEVMPHYR	300
65	RLVQSS	306
05	Seq ID NO: 335 Protein Sequence	
	Protein Accession #: AAH08826 1 11 21 31 41 51	
70		60
70	MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGGGRVNQ LGGVFINGRP LPNHIRHKIV EMAKHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY	60 120
	KRENPGMFSW EIRDKLLKDA VCDRNTVPSV SSISRILRSK FGKGEEEEAD LERKEAEESE	180 240
	KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAFERT HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARWRKQAGAN QLMAFNHLIP GGFPPTAMPT	300
75	LPTYQLSETS YQPTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH	360 420
	GFSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRHNLSLH SKFIRVQNEG TGKSSWMLN PEGGKSGKSP RRRAASMDNN SKFAKSRSRA AKKKASLQSG QEGAGDSPGS QFSKWPASPG	480
	SHSNDDFDNM STFRRTSSN ASTIGRLSP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMMQ QTPCYSFAPP NTSLMSPSPN	540 600
80	YOKYTYGOSS MSPLPOMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV	660
	TO THE RESERVE THE PROPERTY OF	720
	DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNKMMNPS SHTHPGHAQQ TSAVNGRPLP HTVSTMPHTS GMRRLTQVKT PVQVPLPHPM QMSALGGYSS VSSCNGYGRM GLLHQEKLPS	

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	1 11 21 31 41 51	
5	MEVSRRKAPP RPPRPAAPLP LLAYLLALAA PGRGADEPVW RSEQAIGAIA ASQEDGVFVA	60
	SGSCLDQLDY SLEHSLSRLY RDQAGNCTEP VSLAPPARPR PGSSFSKLLL PYREGAAGLG GLLLTGWTFD RGACEVRPLG NLSRNSLRNG TEVVSCHPQG STAGVVYRAG RNNRWYLAVA	120 180
	ATYVLPEPET ASRONPAASD HDTAIALKOT EGRSLATQEL GRLKLCEGAG SLHFVDAFLW	240 300
10	NGSIYPPYYP YNYTSGAATG WPSMARIAQS TEVLFQQQAS LDCGHGHPDG RRLLLSSSLV EALDVWAGVF SAAAGEGQER RSPTTTALCL PRMSEIQARA KRVSWDFKTA ESHCKEGDQP	360
	ERVOPIASST LIHSDLTSVY GTVVMNRTVL FLGTGDGQLL KVILGENLTS NCPEVIYEIK EETPVFYKLV PDPVKNIYIY LTAGKEVRRI RVANCNKHKS CSECLTATDP HCGNCHSLQR	420 480
	CTFOGDCVHS ENLENWLDIS SGAKKCPKIQ IIRSSKEKTT VTMVGSFSPR HSKCMVKNVD	540
15	SSRELCONKS OPERICUS PERATYKOVS VVNVMFSFGS WILSDRFNFT NCSSLKECPA CVETGCAWCK SARRCIHPFT ACDPSDYERN QEQCPVAVEK TSGGGRPKEN KGNRTNQALQ	600 660
	VPYIKSIEPO KVSTLGKSNV IVTGANFTRA SNITMILKGT STCDKDVIQV SHVLNDTHMK	720
	FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITHMGRNFD VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLQY	780 840
20	REDPRFTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LFHGENGQLN CSFENITRNQ	900 960
20	DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF AAVGVTRHKS KELSRKQSQQ LELLBSELRK EIRDGPAELQ MDKLDVVDSF GTVPFLDYKH	1020
	PALRTFPPES GGPTHIFTED MENRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS	1080 1140
	VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKLMLRRTE SVVEKLLTNM MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDMLL WQVPEPSTVA	1200
25	LNVVFEKIPE NESADVCRNI SVNVLDCDTI GQAKEKIFQA FLSKNGSPYG LQLNEIGLEL QMCTRQKELL DIDSSSVILE DGITKLNTIG HYBISNGSTI KVFKKIANFT SDVEYSDDHC	1260 1320
	HLILPDSEAP ODVOGKRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLFR SIWSLPNSRA	1380
	PPAIKYPPDF LDAQAENKKI TDPDVVHIMK TNSLPLRFWV NILKNPQFVF DIKKTPHIDG CLSVIAQAFM DAFSLTEQQL GKEAPTNKLL YAKDIPTYKE EVKSYYKAIR DLPPLSSSEM	1440 1500
30	EEPLTQESKK HENEFNEEVA LTEIYKYIVK YPDEILNKLE RERGLEEAQK QLLHVKVLFD	1560
	EKKKCKM	1568
	Seq ID NO: 337 Protein Sequence	
35	Protein Accession #: XP_063670.1 1 11 21 31 41 51	
		60
	MORILEEPAD DCTWSTRILL TLSEFIMSLQ RTVYPHSEKW RALSVPSSSY FQELVGTSQE LALTFWHLLS MPGFFIVSYG FLTAFGRTLF HLDLLQPNLT PSRFDKYTGL PIYEIEGDGL	120
40	DPCFOSHVOG ILEVLWHSKV ESAYHTNDGD TAGEGVENGT SQTRGGGGAA RSRCREMEEP	180 235
40	TPEPVYVDVD KGLTLACFVF LCLFLVVMII RCAKVIMDPY SAIPTSTWEE QHLDD	233
	Seq ID NO: 338 Protein Sequence Protein Accession #: FGENESH predicted	
4 ~	1 11 21 31 41 51	
45		60
	APRAPRARAP VTGKRRSRRS AVALGSAPAQ PGPRERTGRA SPALENNSDL LSKASAIATG	120
	TPPCEDSTIA RPYLPPPLTT HPELVGTSQE LALTFWHLLS MFGFFIVSYG FLTAFGRTLF HLDLLQPNLT PSRFDKYTGQ LLELPVHSKY VLTIHWSQGL CIWSSHPCEA GVENGTSQTR	180 240
50	GGGGAARSRC REMEEPTPEP VYVDVDKGLT LACFVFLCLF LVVMIIRCAK VIMDPYSAIP	300 311
	TSTWEEQHLD D	311
	Seq ID NO: 339 Protein Sequence Protein Accession #: FGENESH predicted	
55	1 11 21 31 41 51	
	MGKDFMSKTP KAMATQAKID KWDLIKLKSP CTAKETTIRV NRQPTEWEKI FAIYSSDEGL	60
	ISRIYNEPKQ IYKKKTNNPI NKWAKDMNRH PSKEDIYAAN RHMKKCSSSL AIREMQIKTT	120
60	TRCHLTPVRM AIIKKSGNNR TAEEQPKLRK EAVGSIEIFR FADGLDITLM ILGILASLVN GACLPLMPLV LGEMSDNLIS GCLVQTNTTN YQNCTQSQEK LNEDMTLLTL YYVGIGVAAL	180 240
	IFGYIQISLW IITAARQTKR IRKQFFHSVL AQDIGWFDSC DIGELWTRMT DDIDKISDGI	300 360
	GDKIALLFON MSTFSIGLAV GLVKGWKLTL VTLSTSPLIM ASAAACSRMV ISLTSKELSA YSKAGAVAEE VLSSIRTVIA FRAQEKELQR YTONLKDAKD FGIKRTIASK VSLGAVYFFM	420
65	NOTYGLAFWY GTSLILNGEP GYTIGTVLAV FFSVIHSSYC IGAAVPHFET FAIARGAAFH IFQVIDKKPS IDNFSTAGYK PESIEGTVEF KNVSFNYPSR PSIKILKGLN LRIKSGETVA	480 540
03	LVGLNGSGKS TVVQLLQRLY DPDDGFIMVD ENDIRALNVR HYRDKIGYVS QEPVLFGTTI	600
	SMNIKYGROD VTDEEMERAA REANAYDFIM EPPNKFNTLV GEKGAQMŠGG QKQRIAIARA LVRNPKILIL DEATSALDSE SKSAVQAALE KDTPRYSF	660 698
70		
70	Seq ID NO: 340 Protein Sequence Protein Accession #: XP_166496.1	
	1 11 21 31 41 51	
		60
75	FIMEPPNKFN TLVGEKGAQM SGGQKQRIAI ARALVRNPKI LILDEATSAL DSESKSAVQA	120
	ALEKDTPRYS F	131
	Seq ID NO: 341 Protein Sequence	
80	Protein Accession #: XP_166305.1 1 11 21 31 41 51	
		60
	LALFLIGYVL SARTWRLLTG CCSSARASCG SALRGSLVCT QISAAAALAP LTWVAVALLG	120
	GAFYECAATG SAAFAQRLCL GRNRSCAAEL PLVPCNQAKA SDVQDLLKDL KAQSQVLGWI	180

	LIAVVIIILL FEGSHPKEYN LGFVDSSGIN	TPSMKEWQQI	PVSFLQLKFW SSLYTFNPKG	ÖAAZWTHKAA Kiapeõeõõi	LKSKATEHAT NRKEKTHSIR	ELAKENIKCF STEGDTVIPV	240 300 315
5	Seq ID NO: Protein Acc			31	41	51	
10	NFAIQEATVA DCSHSEDVGV VKYEGHWRQV KNSFWIHQVT	CRQLGFEAAL ICHPRRHRGY CDQGWTMINS CLGTEPHMAN	TWAHSAKYGQ LSETVSNALG RVVCGMLGFP CQVQVAPARG	KLRLVGPESK GEGPIWLDNV POGRRLEEVR SEVPVDSHYY KLRPACPGGM	QCVGTESSLD LKPILASAKQ RKVWDLKMRD HAVVSCVAGP	QCGSNGWGVS HSPVTEGAVE PKSRLKSLTN HFRPPKTKPQ	60 120 180 240 300
15	LFGARLGQGL VRLAGGRIPE WSGTPRAQEV LVQETAYLED	GPIHLSEVRC EGLLEVQVEV VMSGVRCSGT RPLSQLYCAH	RGYERTLSDC NGVPRWGSVC ELALQQCQRH EENCLSKSAD	QWGTVCDHRW PALEGSQNGC SENWGLTEAM GPVHCSHGGG HMDWPYGYRR	QHENAAAVRC VACRQLGLGP RFLAGVSCMD LLRFSTQIYN	NVPNMGFQNQ AIHAYKETWF SAPDLVMNAQ LGRTDFRPKT	360 420 480 540 600
20	FGEQGVTVGC	WDTYRHDIDC	QWVDITDVGP AELSLEQEQR	SKVAEGHKAS GNYIFQVIVN LRNNLI	PHYEVAESDP	SNNMLQCRCK	660 720 756
25		343 Protein cession #: 1	n Sequence NP_001789.2				
25	1	11 	21 	31 	41 	51 {	
30	PNIVKLLDVI HRVLHRDLKP STAVDIWSLG	HTENKLYLVF QNLLINTEGA CIFAEMVTRR	EFLHQDLKKF IKLADFGLAR ALFPGDSEID	ALKKIRLDTE MDASALTGIP AFGVPVRTYT QLFRIFRTLG PNKRISAKAA	LPLIKSYLFQ HEVVTLWYRA TPDEVVWPGV	PEILLGCKYY TSMPDYKPSF	60 120 180 240 298
35	Protein Ac	11	NP_439892.1 21 	31 	41 	51 	
40	PNIVKLLDVI HRVLHRDLKP IFRTLGTPDE	HTENKLYLVF QNLLINTEGA	PEFLHODLKKI IKLADFGLAI DYKPSFPKW	MDASALTGIF AFGVPVRTY	LPLIKSYLFO HEVTRRALFF	EISLLKELNH LLQGLAFCHS GDSEIDQLFR QMLHYDPYKR	60 120 180 240 264
45		345 Proteicession #:	n Sequence NP_116127 : 21	1 31	41	51	
50	QVKAYTFSEE PPGPNREFSI EPQAGSPMTI	ALYLSLGVLM FHLIVSYDMI TVVQKADSGI SCQTKLPLQI	L ILQGPAKPV H YHCSGIFQS R SAARLLFSF	P EGDLLVLRC P GPGIPETAS Y KDGRIVQSR	Q AWQDWPLTQ\ V VAITVQELF\ 3 LSSEFQIPT\	DITDAREAGF TFYRDGSALG APILRAVPSA SEDHSGSYWC	60 120 180 240
	SEDPGFSSPI	L GMPDPHLYHO	3 WGTFFKHWG	D VRVLLGHLL	A APGTAPEEAI M ELRELSGHQI	P GPLPPPPTPS K PGTTKATAE	300 359
55	Protein Ad	ccession #: 11	in Sequence NP_002337. 21	1 31 	41 	51 	•
60	MKIFLPVLL VTFGHSLSK SLLPALLRF	T CSPACPIPE	S LMCFSCLNQ G VNVGVASMG	K SNLYCLKPT I SCCQSFLCN	I CSDQDNYCV P SAADGGLRA	T VSASAGIGNL S VTLLGAGLLL	60 120 131
			in Sequence XP_113526.				
65	1	11	21 	31 	41 1	51 	
	KSHLIQVER	E KMQMELSHK	R ARVELERA	S TSARNYERE	V DRNQELLTR	Q LEERAEQIRS I RQLQEREAGA Q WSVMDQEMRV	60 120 180
70	KRLESEKQE IVKNMKSEL VGLELENER GLEKARQQL	L QEQLDLQHK V RLPRLEREL L LAKLQSWER Q EELRQVSGQ	k cqeanqki( k qlreesahi kl dqtmglsii pl leerkkret	DE LOASQEARA LR EMRETNGLI RT PEDLSRFVA TH EALARRLO	D HEQQIKDLE Q EELEGLQRK /E LQQRELALK CR VLLLTKERE	XX KLSLQEQDAA XL GRQEKMQETL XD KNSAVTSSAR XG MRAILGSYDS VA DMLEMELKML	300 360 420
75	KSQSSSAEQ KVLHMSLNF VAELKKQVE	S FLFSREEAD T SVARQRLRE S AELKNORLE	OT LRLKVEELI ED HSQLQAECI CE VFQTKIQEI	EG ERSRLEEEN ER LRGLLRAM FR KACYTLTG	CR MLEAQLERS ER GGTVPADLE (Q IDITTENQ)	PA LOGDYDOSRT EA AAASLPSSKE VR LTSLYAEHPG LE LFSROTVA	540 600
80	Seq ID NO Protein A	): 348 Prote Accession #: 11	ein Sequence : NP_000264 21	e .1 31	41	51	
	Ĭ	1	1	1	1	i i	
	MTQAGRRGI LALGLLQLI	G TPEPRPRT( LP GRRPAGPG!	OP MASPRIGT SP ATSPPASV	FC CPTRDAATO RI LRAAAACD	OL VLSFQPRAT LL GCLGMVIR	FH ALCLGSGGLR ST VWLGFPNFVD	60 120
						760	

5	SVSDMNHTEI WPAAFCVGSA MWIQLLYSAC FWHLFCYAVD AYLVIRRSAG LSTILLYHIM AMGLATLLCV EGAANLYYPS VSRCERGLDH AIPHYVTMYL PLLLVLVANP ILFQKTVTAV ASLLKGRQGI YTENERRMGA VIKIRFPKIM KVLIICMLSN IINESLLFYL EMQTDINGGS LKPVRTAAKT TMFIMGILMP AQGFLLSLAF YGMTGCSLGF QSPRKEIQME SLTTSAAEGA HPSPLMPHEN PASGKVSQVG GQTSDEALSM LSEGSDASTI EIHTASESCN KNEGDPALPT HGDL	180 240 300 360 420 424
10	Seq ID NO: 349 Protein Sequence	60
15	PLTEEEEEG AGATISRGPA FPGMGSEELR LASFYDWPLT AEVPPELLAA AGPFHTGHQD KVRCFFCYGG LQSWKRGDDP WTEHAKWFPS COFLLRSKGR DFVHSVQETH SQLLGSWDPW EEPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGGVS PAEAQRAWWV LEPPGARDVE AQLRRLQEER TCKVCLDRAV SIVFVPCGHL VCAECAPGLQ LCPICRAPVR SRVRTFLS	120 180 240 298
20	Seq ID NO: 350 Protein Sequence Protein Accession #: NP_071444.1  1 11 21 31 41 51	60
25	PLTEEEEEEG AGATLSRGPA FPGMGSEELR LASFYDMPLT AEVPELLAA AGFFHTGROD KVRCFFCYGG LQSWKRGDDP WTEHAKWPPS CQFLLRSKGR DFVHSVQETH SQLLGSWDPW EEPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGARD VEAQLRRLQE ERTCKVCLDR AVSIVFVPCG HLVCAECAPG LQLCPICRAP VRSRVRTFLS	120 180 240 280
30	Seq ID NO: 351 Protein Sequence Protein Accession #: NP_066300.1 1 11 21 31 41 51	
35	MGSVSSLIGG HSPHSKECRA SQYKLRKSSH LKKLINYSDG LLRFGFSQDS GHGKSSSING KEEDFFYIKV SQKARGSHHP DYTALSSGDL GQAGVDFDP STPPKLMPFS NQLEMGSEKG AVRPTAFKEV LPRSGAILHS SPESASHQLH PAPPDKPKEQ ELKPGLCSGA LSDSGRNSNS SLPTHSTSSS YQLDPLVTPV GPTSRFGGSA HNITOGIVIQ DSNMMSLKAL SPSDGGSKLD HSNKADKGPS CVRSPISTDE CSIQELEQKL LEREGALQKL QRSFEEKELA SSLAYEERPR RCDDELEGFE PKGGNKLKQA SQKSQRAQQV LHLQVLQUQ EKRQLRQELE SLMKEQDLLE	60 120 180 240 300 360
40	TKLRSYEREK TSFGPALEET OMEVCOKSGE ISLLKQOLKE SOTEVNAKAS EILGLKAQLK DTRGKLEGLE LRTQDLEGAL RTKGLELEVC ENELQRKONE AELLREKVNL LEGELQELRA QAALARDMGP PTPPEDVPAL QRELERLRAE LREERGGEDO MSSGGOHERL VMKEEKEKVI QYQKQLQQSY VAMYQRNQRL EKALQQLARG DSAGEPLEVD LEGADIPYED IIATEI	420 480 540 596
45	Seq ID NO: 352 Protein Sequence	60
50	RPAWNSKLQY ILAQVGFSVG LGNVWRFPYL CQKNGGGAYL LPYLILLMVI GIPLFFLELS VGQRIRRGSI GYMNYISPKL GGIGFASCVV CYFVALYYNV IIGMSLPYFS QSFQQPLPMD QCPLVKNASH TFVEPECCQS SATTYYWYRE ALMISSSISE SGGLMWKHTI CLLAAWVMVC LAMIKGIQSS GKIIYFSSLF PYVVLICFLI RAFLLMGSID GIRHWFTPKL SIMLEPKVMR EAATOVFFAL GLGFGGVIAF SSYNKRDNNC HFDAVLVSFI NFFTSVLATL VVFAVLGFKA	120 180 240 300 360
55	NVINEKCITO NSETIMKPIK MGNISQDIIP HHINISTYTÄ EDYHLVYDII QKVKEEEFPÄ LHINSCKIEE ELNKAVQCTG LAPIAPTEAN THFPASPFMS VMFFLMLVNL GLGSMFGTIE GIVTPIVDTF KVRKEILTVI CCLLAPCIGL IFVQRSGMYP VTMFDDYSÄT LPLLIVVILE NIAVCFVYGI DKFMEDLKOM LGFAPSRYYY YMRKISPIM LLSLLIASVV NMGLSPPGYN AMIEDKASEE PLSYPTMGLV VCVSLVVFAI LPVPVVFIVR RFMLIDDSSG NLASVTYKRG RVLKEPVNLE GDDTSLIHGK IPSEMPSPNF GKNIYRKOSG SPTLDTAPMG RYGIGYLMAD	420 480 540 600 660 720
60	IMPDMPESDL	730
	Seq ID NO: 353 Protein Sequence Protein Accession #: NP_005594.1 1 11 21 31 41 51	
65	MEGGERSPLL SQETAGGKPL SVHRPPTSGC LGPVPREDQA EAMGCSCCPP ETKHQALSGT PKKGPAPSLS PGSSCVKYLI FLSNPPFSLL GLLALAIGLM GLAVKGSLGS DLGGPLPTDP MLGLALGGLV VSAASLAGCL GALCENTCLL RGFSGGILAF LVLEAVAGAL VMAHGPLQD	60 120 180 240
70	SLEHTLRVAI AHYODDPDLR FLLDQVQLGL RCCGAASYQD WQQNLYFNCS SPGVQACSLP ASCCIDPRED GASVNDQCGF GVLRLDADAA QRVVYLEGGG PPLRRWLRAN LAASGGYATA VVLLQGAELL LAARLLGALA ARSGAAYGPG AHGEDRAGPQ SPSPGAPPAA KPARG	300 355
75	Seq ID NO: 354 Protein Sequence Protein Accession #: AAL84622.1  1 11 21 31 41 51	60 120
80	WKLAIQILKI AMVTIQLVLF GLSNQMVVAF KEENTIAPKH LFLKGYMDRM DDTYAVYTOS DVYDQLIFAV NQYLQLYNVS VGMHAYENG TKOSANAICO HFYRRGNIYP GNDTFDIDDE IETECFFVEP DEPFHIGTPA ENKLNILIDF HRLITVELQF KLKAINLQTV RHGELPDCYD FTLTITFDNK AHSGRIKISL DNDISIRECK DMYSGSIQK NTHYMMIFDA FVILTCLVSL ILCIRSVIRG LQLQQEFVNF FLLHYKKEVS VSDQMEFVNG WYIMIIISDI LTIIGSILKM EIQAKSLTSY DVCSILLGTS TMLVMLGVIR YLGFFAKYNL LILTLQAALP NVIRFCCCAM MIYLGYCPCG WIVLGPYHDK FRSLNMYSEC LFSLINGDDM FATFAKMOQK SYLVMLFSRI YLVSFISLFI YMILSLFIAL ITDTYETIKQ YQQDGFPETE LRTFISECKD LPNSGKYRLE	180 240 300 360 420 480

	DDPPVSLFCC	CKK					553
	Seq ID NO: Protein Acc						
5		11	21	31	41	51	
10		LQGPSPGSPG NYRGSPRGKR	QEQAAEGAPE SAGPLPGNLQ		TYKOKECVYY CVGRYDKACL	CHLDIIWINT HFCTQTLDVS	60 120 180 238
10	Seq ID NO: Protein Acc	356 Proteir	Sequence				
15	1	11	31	31	41	51	
	LQDNLVIALH SLEPEPWFFK	SYEPSHDGDL NLSRKDAERQ	GFEKGEPLRI LLAPGNTHGS		QSLTTGQEGF GSFSLSVRDF	yegsnppasp Ipfnfvakan Donogevvkh Kpwwedewev	60 120 180 240
20	VRLYAVVTQE IHRDLRAANI SDVWSFGILL	PIYIITEYME LVSDTLSCKI	NGSLVDFLKT ADFGLARLIE YPGHTNPEVI	PSGIKLTINK DNEYTAREGA	LLDMAAQIAE KFPIKWTAPE	LMKQLQHQRL GMAPIEERNY AINYGTPTIK QLMRLCWKER	300 360 420 480 509
25	PEDRFIFDIO	KOVDEDITIN	120019191				202
		357 Protein cession #: 1 11 1		31 	41 1	51 	
30	IQPVGTPFEE VPATVATATP LDTEAPTPRL	LPSERPTLEP STPAAPPFTA VSTATSRPRA	ATSPLVVTEV TTAVIRTTGV LPRPATTQEP	PEEPSQRATT RRLLPLPLTT DIPERSTLPL	VSTTMATTAA VATARATTPE GTTAPGPTEV	TTPAVLPTIN TSTGDPTVAT APSPPTTAAV AQTPTPETFL TLPKGARPGP	60 120 180 240 300
35	GLLDNAIDSG YTLEEPKQAS		ILERKEVLVA EFYA			YRMKKKDEGS	360 384
40	1 	cession #: 11     PPAGYGGSPG	21 ⁻ 	31 	41   SHPSYTDTPV	51     SAPRTLSAVG	60
45	ignmnypsts Clidkrornr Eaelavepkt Llragwnell	PGSLVKHICA CQYCRYQKCL ESYGDMNMEN IASFSHRSVS	ICGDRSSGKH VMGMKREAVQ STNDPVTNIC VQDGILLATO	YGVYSCEGCK EERQRSRERA HAADKQLFTL LHVHRSSAHS	GFFKRTIRKE ESEAECATSO VEWAKRIPHE AGVGSIFDRV	DIKPLPGLPG LIYTCRDNKD HEDMPVERIL SDLTLEDQVI LTELVSKMKD EQPGRFAKLL	120 180 240 300 360 420
50	Seq ID NO:	359 Protei	n Sequence	' FLMEMLETPL	QIT		463
	Protein Ac	cession #:	NP_002176.1 21	31	41	51	
55	DPDVNTTNLE IDLTTIVKPE	FEICGALVEV APFDLSVIY	KCLNFRKLQE EGANDFVVTI	YFIETKKFL NTSHLQKKYV	LIGKSNICVI KVLMHDVAYI	S SQHSLTCAFE VGEKSLTCKK QEKDENKWTH	60 120 180
60	ILLTISILSF ESFLDCQIHE FGRDSSLTCI	PSVALLVIL	CVLWKKRIKI FEGFLQDTFP( FILSSSRSLD)	OLEESEKORI RESGKNGPH	GGDVQSPNC	E INNSSGEMDP P RKNLMVSFNP P SEDVVVTPES T TNSTLPPPFS	240 300 360 420 459
65	Protein Ac	: 360 Protes cession #:	NP_006263.			<b></b>	
70	LDNDGDGECI	) FQEFMAFVAI	M VTTACHEFF		41   E LSHFLEEIK	E GEVADKAWEL	60 92
		: 361 Prote ccession #:		. 1			
75	1     MPMDLILVV	11     FCVCTARTV	21   V GFGHDPDLQ	31   M DIVTELDLV	41   N TTLGVAQVS	51   G MENASKAFLF	60
80	QDIEREIHAL LRDEIRYHY NLPPGINLM MDLQELLAKI AVECRRMSC LVKITEMCP	A PHVSEKLIQ I HNGKPRTEA L GQRNQKHGL M TAKLNYAET P PLNCSPDSL P LNCSEKDHI	L FQNKSEFTI L PYRMADGQW P KGIIQDGKI R LSQLENCHC P VHIAGQCCK L PENQCCRVC	L ATVQOKPST H KVALSVSAS I FMPNGYITQ E KTCQVSGLL V CRPKCIYGG R GHNFCAEGP	S GVILSIREL H LLLHVDCNR C PNLMHTCPT Y RDQDSWVDG K VLAEGQRIL K CGENSECKN	E HSYFELESSG I YERVIDPPDT C SDFLSLVQGI D HCRNCTCKSG T KSCRECRGGV W NTKATCECKS D DFSCTEHDEC	120 180 240 300 360 420 480

5	GSGQHNCDEN I FTGSHCEKDI I ALRTHTCWND I DGKIFCRRTA I GEVDCWPLTC I WTMAGSPCTT	DECSEGIIEC   BACINLAGGP   CDCQNPSADL PNLSCEYTAI	HINHSRCVNLP DCLCPSGPSC FCCPECDTRV LEGECCPRCV	GWYHCECRSG SGDCPHEGGL TSQCLDQNGH	FHDDGTYSLS ( KHNGQVWTLK : KLYRSGDNWT	GESCIDIDEC EDRCSVCSCK HSCQQCRCLE	540 600 660 720 780 810
10	ī	ession #: N 11 	P_057264.1 21 	31 	Ĭ.	51 	
15 20	LSVGLPSSLY LNGATVVAAL HYHALFTGFG PLTEVAKGIP MTLKSLLRAL LIYERGVEVG VYSTLVLCSL	SIVWPLSPIL IANPRRKLVM GALGYLLGAI PQQTPQDPPL VNMPPHYRYL CWGFCINSVP	GFLLQPVVGS AISVTMIGVV DWAHLELGRL SSDGMYEYGS CISHLIGWTA SSLYSYFQKV VPFNLITEYH	ASDHCRSRWG LFDFAADFID LGTEFQVMFP IEKVKNGYVN FLSNMLPFTD LVSYIGLKGL REEEKERQQA	AMFGREFCYA RRRPYILTLG GPIKAYLFDV PSALVLTLCP PELAMQGAKN PMGQIVYRGD YPTGYLLFGL PGGDPDNSVR PVALPVRYVD	VMMLVGMALY CSHQDKEKGL TVHLCSISEA KNHAEQTRRA PYSAHNSTEF GTGFIGLFPN	60 120 180 240 300 360 420 480 530
20		363 Protein					
		ession #: 1		31	41	51	
25	ī	ī	Ī	ī	1	Ī	
	DMCCQTHDCC	VMAGVIPIQG YDHLKTQGCS RFYWRPHCRG	IYKDYYRYNF	SOGNIHCEDK	YWPYGCHCGL GSWCEQQLCA	GGRGQPKDAT CDKEVAFCLK	60 120 145
30		364 Protei					
		cession #: 1		••	41	51	
	1	11	21 	31 	ì.	i	
	MRLPDLRPWT	SLLLVDAALL	NLLOGPLGTL	LPOGLPGLML	EGTLRLGGLW	GLLKLRGLLG	60
35	FVGTLLLPLC	LATPLTVSLR	ALVAGASRAP	PARVASAPWS	WLLVGYGAAG	LSWSLWAVLS	120
	PPGAQEKEQD	QVNNKVLMWR	LLKLSRPDLP	LLVAAFFFLV	LAVLGETLIP	HYSGRVIDIL	180 240
	GGDFDPHAFA	SAIFFMCLFS	FGSSLSAGCR	GGCFTYTMSN	INDRIKEQUE	SSLLRQDLGF RLTLLSLLKM	300
	POPTIAREN	PKP22DIIF	TODAYARAGO	VVREAVGGLO	TVRSFGAEEH	EVCRYKEALE	360
40	OCROLYWRRD	LERALYLLIR	RVLHLGVQMI	MLSCGLOOM	DGELTQGSLL	SFMIYQESVG	420
	SYVOTLVYIY	GDMLSNVGAA	EKVFSYMDRO	PNLPSPGTL	<b>PTTLQGVVKF</b>	QDVSFAYPNR	480
	PDRPVLKGLT	FTLRPGEVTA	LVGPNGSGKS	TVAALLQNLY	QPTGGQVLLD	EKPISQYEHC	540 600
		GEPVLFSGSV GKORLAIARA			( QAAAAADF IQ	EMEHGIYTDV	630
45	GENGSQEMO	ONLINENDAD	Dimiration	•			
	Seq ID NO:	365 Protei	n Sequence				
		cession #:		••		51	
	1	11	21	31	41 	1	
50	MKKSGVLFLI	. GIILLVLIG	/ QGTPVVRKGI	R CSCISTNOG	T İHLQSLKOLI	QFAPSPSCEK	60
		VQTCLNPDS/	DAKETIKKM	E KQVSQKKKQ	K NGKKHQKKK	LKVRKSQRSR	120
	QKKTT						
	Seq ID NO	366 Prote	in Sequence				
55		cession #:			4.5	51	
	1	11	21	31	41 [	1	
	MARSLVCIA	i V IILLSAFSGI	P GVRGGPMPK	L ADRKLCADO	E CSHPISMAV	A LODYMAPDCR	60
60	FLT I HRGQV VKTDKWDFY	V YVFSKLKGR	G RLFWGGSVQ	G DYYGDLAAR	L GYFPSSIVR	E DQTLKPGKVD	120 131

It is understood that the examples described above in no way serve to limit the true

scope of this invention, but rather are presented for illustrative purposes. All publications,
sequences of accession numbers, and patent applications cited in this specification are herein
incorporated by reference as if each individual publication or patent application were
specifically and individually indicated to be incorporated by reference.





## WHAT IS CLAIMED IS:

1	1.	A method for determining the presence or absence of a pathological cell in a
2	patient, said n	nethod comprising detecting a nucleic acid comprising a sequence at least 80%
3	identical to a	sequence as described in Tables 2A-68 in a biological sample from said patient,
4	thereby deterr	nining the presence or absence of said pathological cell.
1	2.	The method of Claim 1, wherein:
2	a) said	d pathology is described in Table 1, including a cancer; and/or
3	b) sai	d biological sample comprises isolated nucleic acids.
1	3.	The method of Claim 1, wherein said biological sample is tissue from an organ
2	which is affect	eted by said pathology of Table 1, including a cancer.
1	4.	The method of Claim 2, wherein said nucleic acids are mRNA
1	5.	The method of Claim 2:
2	a) fur	ther comprising a step of amplifying nucleic acids before said step of detecting
3	sa	id nucleic acid; or
4	b) wh	nere said detecting is of a protein encoded by said nucleic acid.
1	6.	The method of Claim 1, wherein said nucleic acid comprises a sequence as
2	described in	Γables 2A-68.
1	7.	The method of Claim 2, wherein:
2	a) sai	d detecting step is carried out by:
3	i)	using a labeled nucleic acid probe;
4	ii)	utilizing a biochip comprising a sequence at least 80% identical to a sequence
5		as described in Tables 2A-68, Sir
6	iii	detecting a polypeptide encoded by said nucleic acid; or
7	b) sa	id patient is:
8	i)	undergoing a therapeutic regimen to treat said pathology of Table 1; or
9	ii	is suspected of having said pathology or cancer.
1	8.	An isolated nucleic acid molecule comprising a sequence as described in
2	Tables 2A-68	3. ·



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18.

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9. 1 The nucleic acid molecule of Claim 8, which is labeled. 1 10. An expression vector comprising the nucleic acid of Claim 8. 1 11. A host cell comprising the expression vector of Claim 10. 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule 2 comprising a sequence as described in Tables 2A-68. 1 ·13. An antibody that specifically binds a polypeptide of Claim 12. 14. The antibody of Claim 13: 1 2 a) conjugated to an effector component; 3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a 4 cytotoxic chemical; 5 c) which is an antibody fragment; or 6 d) which is a humanized antibody. 1 A method for specifically targeting a compound to a pathological cell in a 2 patient, said method comprising administering to said patient an antibody of Claim 13, 3 thereby providing said targetting. 1 16. A method for determining the presence or absence of a pathological cell in a 2 patient, said method comprising contacting a biological sample with an antibody of Claim 13. 1 17. The method of Claim 16, wherein: 2 a) said antibody is conjugated to: 3 i) an effector component; or 4 ii) a fluorescent label; or

b) said biological sample is a blood, serum, urine, or stool sample.





3 a) contacting said compound with a pathology-associated polypeptide, said 4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence 5 at least 80% identical to a sequence as described in Tables 2A-68; and 6 b) determining the functional effect of said compound upon said polypeptide. 1 19. A drug screening assay comprising the steps of: 2 a) administering a test compound to a mammal having a pathology of Table 1 or a 3 cell isolated therefrom; and 4 b) comparing the level of gene expression of a polynucleotide that selectively 5 hybridizes to a sequence at least 80% identical to a sequence as described in 6 Tables 2A-68 in a treated cell or mammal with the level of gene expression of said 7 polynucleotide in a control cell or mammal, wherein a test compound that 8 modulates said level of expression of the polynucleotide is a candidate for the 9 treatment of said pathology. 10

## (12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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125138 A3

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.





#### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560 CLASSIFICATION OF SUBJECT MATTER IPC(7) : C12Q 1/68 US ČÍ. 435/6 According to International Patent Classification (IPC) or to both national classification and IPC FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S.: 435/6, 7.1, 287.2; 436/63, 64 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the International search (name of data base and, where practicable, search terms used) Please See Continuation Sheet DOCUMENTS CONSIDERED TO BE RELEVANT Relevant to claim No. Citation of document, with indication, where appropriate, of the relevant passages Category * US 6,426,186 B1 (JONES et al.) 30 July 2002 (30.07.2002), see especially Detailed 1-6 X,P Description of the Invention and Sequence 62. Y,P US 6,194,158 B1 (KROES et al.) 27 February 2001 (27.02.2001), see especially 2-5 X Background of the Invention and Detailed Description of the Invention. 1, 6, 7 Y US 6,440,676 B1 (KROES et al.) 27 August 2002 (27.08.2002), see especially Background 2-5 X,P of the Invention and Detailed Description of the Invention. Y.P 1, 6, 7 US 6,500,938 B1 (AU-YOUNG et al.) 31 December 2002 (31.12.2002), see especially 1-7 Y,P Summary of the Invention and Description of the Invention. 1-7 SMYTH TEMPLETON et al. Cloning and Characterization of Human Tumor Cell Insterstitial Collagenase. September 1990, Volume 50, Number 17, pages 5431-5437, especially Figure 2. Further documents are listed in the continuation of Box C. See patent family annex. later document published after the international filing date or priority date and not in conflict with the application but clied to understand the principle or theory underlying the invention Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone -xearlier application or patent published on or after the international filling date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed **.**&. document member of the same patent family Date of mailing of the international search report Date of the actual completion of the international search 03 March 2003 (03.03.2003) Authorized officer Aram Mansal Name and mailing address of the ISA/US Commissioner of Patents and Trademarks
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Washington, D.C. 20231 Carolyn Smith Facsimile No. (703)305-3230 Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claim Nos.:     because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.:     because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Claim Nos.:  because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet x
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.  2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.  3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7 for Specie A(hemangiomas) and B (SEQ ID NO: 1)  Remark on Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)



International application No.

PCT/US02/29560

This application contains the following inventions or groups of inventions, which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Groups 1-104,648, claim(s) 1-7, drawn to a method for determining the presence or absence of a pathological (Specie A) cell in a patient via detection of polynucleotides that are at least 80% identical to listed sequences (Specie B). If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

Groups 104,649-105,060, claim(s) 8-12, drawn to an isolated nucleic acid molecules from Tables 2A-68, expression vectors, host cells, and polypeptides encoded by nucleic acid molecules with listed sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,061-105,472, claim(s) 13-14, drawn to an antibody that binds to a polypeptide encoded by a polynucleotide with sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,473-105,884, claim(s) 15, drawn to a method for targeting a compound to a pathological cell in a patient via administering an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,885-106,296, claim(s) 16-17, drawn to a method for determining the presence or absence of a pathological cell in a patient via contacting the sample with an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,297-106,708, claim(s) 18, drawn to a method for identifying a compound that modulates a pathology-associated polypeptide encoded by a polynucleotide that hybridizes to a sequence in Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,709-211,356, claim(s) 19, drawn to drug screening assay by administering a compound to a mammal or cell having a pathology (of Table 1) and comparing the level of gene expression of a polynucleotide that hybridizes to a sequence that is 80% identical to sequences as described in Tables 2A-68 (Species B) to gene expression in control cells or mammals. If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

This International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons indicated below:

The inventions listed as all Group Sets (Groups 1-211,356) do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

Groups 1-104,648 and Groups 105,472-211,356 are directed to methods or assays which vary in one or more of the following: reactants, steps, and/or goals which are not coextensive and which do not share the same technical feature. Groups 104,649-105,472 have two separate special technical features, a nucleic acid and an antibody, respectively. These are directed to different chemical entity types regarding the critical limitations featuring different structures and functions. The antibodies undergo recognition and binding reactions

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wherein what is bound is different from what is bound by the compositions including the nucleic acids. Thus, in summary, each Group is directed to a different special technical feature and thus supports this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

The claims in the Groups 1-104,648 and 106,709-211,356 include a series of species A directed to different pathologies which are listed in Table 1. Each of these types of pathologies are separate entities which affect patients differently, meaning each has its own special technical feature.

The claims in all Groups (1-211,356) include a series of species B directed to nucleic acid sequence listed (412 possibilities) which are considered separate as each defines its own special technical feature.

The first listed pathology (Specie A) and SBQ ID NO: 1 (Species B) will be automatically searched. For each additional Group with a specie combination elected, the fee is an additional \$210.00.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, PUBMED, BIOSIS, CAPLUS, MEDLINE, SCISEARCH, EMBASE searching terms: diagnosis, cancer, screen, modulator, pathological cell, patient, nucleic acid, tissue, mRNA, detect, probe, blochip, array, therapeutic

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